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ALIGNMENTS

REFERENCE AUTHORS	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 AF005096 LOCUS DEFINITION
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Malpighiales; Euphorbiaceae; Ricinus. 1 (bases 1 to 1856) Sayanova,O., Smith,M.A., Lapinskas,P., Stobart,A.K., Dobson,G.,	AF005096 AF005096.1 GI:4101625 . Ricinus communis (castor bean) Ricinus communis	AF005096 1856 bp mRNA linear PLN 05-JAN-1999 Ricinus communis desaturase/cytochrome b5 protein mRNA, complete cds.

Pred. No. is the number of results predicted by chance to have a

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Expression of a borage desaturase cDNA containing an N-terminal cytochrome b5 domain results in the accumulation of high levels delta6-desaturated fatty acids in transgenic tobacco Proc. Natl. Acad. Sci. U.S.A. 94 (8), 4211-4216 (1997)
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SPLLHLAGQDVTDAFVAYHPGTAWQYLDKFFTGYHLKDYSVSESTSKDYRRLVARFSKL

GPEKKGH1AF1TLVSWMWLLALSVYGULCSWSTWVHL1SGGLWGFPW1DSGW1GHDSG

HYQVMMSRFPNRLAQILSGNCLAGISIAWWKWNINTHH ACNSLDFDDDLQHMPFFAV

SSKFFSSITSYFYERKOMFDCAARFLVSYGHLTFYPVWCFARTUHVQFCLNHFSSSV

VANTGQEILGVLVFWIMYPFLVSCLDWNGERVMFVAASFSVTRIUFRVGFLNKTSSSV

YLGLLIANDWFENGTKGTLDITGSSWMDWFHGGLQFQWEHHLFRWFLKKVSSFV

YLGLLIANDWFENGTKGTLDITGSSWMDWFHGGLQFQWEHHLFRWFLKKVSSFV

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/product="desaturase/cytochrome
/protein_id="AAD01240.1"
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/db_xref="GI:4101626"
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                                                                       TTTATTCTGTCTTTTAAGGTGGTGTTTTCCAACAACAAAAGGGTATACAAGAGAAGTCAG
                                                                                                                                                                   GGTTCACTCACCTCTCATTTCTATGAGAAAAGGTTGACTTTTGACTCTTTATCAAGATTC
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Sequence 1 from |
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Patent: US 5977436-A 1 02-NOV-1999;
Location/Qualifiers
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1 (bases 1 to 1684)

Thomas, T.L. and Li, Z.
Oleogin 5 regulatory region for the modification of plant seed
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TTTCCCTTGAAGAGTCTTGCTGGTCAAGAGGTAACTGATGCATTTGTTGCATTCCATCCT
                   CTCCCATTGTTAAGTTTTGCCGGCCAAGATGTCACTGATGCGTTCATTGCTTACCATCCT
                                                                      TCTATCAAGGGAAAAGTTTACGATATCTCCAAGTGGACTAAAGAGCATCCCGGTGGTGAG
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                                                      TCGATTCAAGGGAAAGCCTATGATGTTTCGGATTGGGTGAAAGACCATCCAGGTGGCAGC
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Pred. No. 4.7e-148;
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El (bases 1 to 1664)

Thomas T.L., Beremand.P.D. and Nunberg,A.N.
A sunflower albumin 5' regulatory region for the modification plant seed lipid composition
Patent: JP 2001518795-A 1 16-OCT-2001;
RHONE POULENC AGRO
PN JP 2001518795-A/1
PD 16-OCT-2001
PP 09-APR-1998 JP 1998543140
PF 09-APR-1998 JP 1058731570
PI TERRY L THOMAS, PHILLIP D BEREMAND, ANDREW N NUNBERG PC C12N15/82,C12N15/29,C12N15/53,A01H5/00,A01H5/10 CC Strandedn Double;
CC Topology: Linear;
FH Key
FT CDS
FT C
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JP 2001518795-A/1.
GTCTCTGAGATGTCCAAGGACTACAGAAGGCTCGTCTCTGAGTTTTCTAAGATGGGTTTG
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Pred. No. 4.7e-148;
0; Mismatches 522;
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                                                         AACACTTTCGGGTGAACCTTATNAAACATCAAGTGCTGTCTTTCCCGTAAAAGCTTCCAG
                                                                                         GCATTGCAGGCTAGGGATATAACCAAGCCGCTCCCGAAGAATTTGGTATGGGAAGCTCTT
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Db 1435 TGTTTGTGTCTTGTTCTACTTGTT 1464
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Query Match 38.0%;
Best Local Similarity 62.8%;
Matches 885; Conservative
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PN JP 2001519668-A/1
PD 23-OCT-2001
PF 09-APR-1998 JP 1998543141
PF 09-APR-1997 US 08/831575
PI TERRY L THOMAS, ZHONGSEN LI
PC C12N15/82, C12N15/29, C12N15/53, A01
Strandedness: Double;
CC Topology: Linear;
CC An oleosin 5' regulatory region fo
CC seed lipid
CC composition
FH Key Location/Qualifie
FH Key Location/Qualifie
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Thomas, T.L. and Li, Z.
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CTGAGTGTTTACGGTGTTCTCTACTGCAAGAGCACCTGGGCTCATCTTTGCTCTGGTTTG
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                                                                TATGACAAAAAAGGTCATATTATGTTTGCAACTTTGTGCTTTATAGCAATGCTGTTTGCT
                                                                                                     TTCAAGACACCAGGCAAAGGGGTCTACTGCTCAATCTTTTTCGTGTCTGTTGTTTCGCT
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JP 2001519668-A/1

23-OCT-2001

09-APR-1998 JP 1998543141

09-APR-1997 US 08/831575

TERRY L THOMAS, ZHONGSEN LI

C12N15/82, C12N15/29, C12N15/53, A01H5/00, A01H5/10
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
277 c 358 g 61
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Pred. No. 4.7e-148;
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	1440 TCCCAATGTTTCTTTTTTTTTTTTTT 1469 	
TTCCAG 1439 CTCCTA 1434	1380 AACACTTTCGGGTGAACCTTATNAAACATCAAGTGCTGTCTTTCCCGTAAAAGCTTCCAG	
GCAATG 1379 	1320 GCTATGGAAGCTAAGGATGTTACCAAGCCAGTTCCCAAGAACATGGTCTGGGAAGCAATG	
GCTGTG 1319 AACACA 1314	1260 TATGAAACTGCTACCATGTGGGAGGCCAATAAAATGGTATACTCCACCCTGCGTGCTGTG	
TTGTCC 1259	1200 TGCCATTTCAGGAAAATCTCACCCATTGTGAACAAACTTTGCCAGAAGCATAATTTGTCC	
CCTAAG 1199 CCTAGA 1194	1140 TGGTTTCATGGTGGCCTGCACTTTCAGATTGAGCATCATCTGTTTCCAAGGATGCCTAAG	
TGGGAT 1139 	1080 GATTGGTTTCACCAGCAGACAAAGGGCACGCTCAACATAACAGCTTCTGCTTGGTGGGAT	
GGTAAT 1079 	1020 TGGCAGTTCAGCTTGAATCACTTTGCTTCTAATGTTTACACTGGTTTGCCTAGCGGTAAT	
CAACAT 1019 CAACAA 1014	960 aattggcctgaaagggtcatgtatttcacgtcctgtttagcagtcgccgggttccaacat 	
CTACCC 959	900 GAAATTTTAGGCTATGCAGCTTTCTTGACTTGGTATTCTCTACTCCTTTCTCGGCTACCCC	
AGTCAG 899 GCTCAG 894	840 TITATTCTGTCTTTTAAGGTGGTGTTTTCCAACAACAAAAGGGTATACAAGAGAAGTCAG	
TATCTT 839 AATATG 837	780 TITGTTAGCTTTCAGCACIGGACATTTTATCCTGCATTGTTAAGCGTTAGGCTCTATCTT	
AGGTTT 779 	720 AACTCCCTTACATCATACTATCACAACTGCAAAATGACCTATGATCGCCGCTGCCAGGTTT	
	660 GCCAATCTGGATACTGCATATTCAGCACCTTCCTATAATTGCCATATCCCCAAAATTTTTC	
AATAGC 659 AATAGC 657	600 GGTGTTAGTGTTGCATGGTGGAAGTTGGACCATAACACCCCATCACTTTGCCTGTAATAGC	
ATTGCT 599	540 GITATGCCTAACCGTAAGCTTAATCGTCTTTTTCAAATCATTGCAGGAAATGTGATTGCT	
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CTTTCAGCACT	TACATCATACT	GGATCCTGAT/ TGACCCTGAT	TGTTGCATGG	TTATGCCTAACCGTAAGC 	TATGCTATGG	TTACGGTGTTO	ACCAGGCAAA(AAAAGGTCATI	GATGTCCAAGO	TTGGCAATACO	GTTAAGTTTT(GAAGAGTCTT(GGGAAAAGTTT AGGGAAAGCCT	CATTTCGCAA(CATTACCTCA(38.0%; ilarity 62.8%; Conservative	277 c	n of .gammalinole S 5789220-A 4 04-AU Location/Qualifiers 11685	led. 1 to 1685) 1., Reddy,A	from patent GI:3975519
TITGTTAGCTTTCAGCACTGGACATTTTATCCTGCATTGTTAAGCGTTAGGCTCTATCTT	AACTCCCTTACATCATACCACAACTGCAAAATGACCTATGATCGCGCTGCCAGGTTT	GCCAATCTGGATCCTGATATTCAGCACCTTCCTATAATTGCCATATCCCCCAAAATTTTTC	GGTGTTAGTGTTGCATGGTGGAAGTTGGACCATAACACCCATCACTTTGCCTGTAATAGC 	TTATGCCTAACCGTAAGCTTAATCGTCTTTTTCAAATCATTGCAGGAAATGTGATTGCT 	CTAATGGGTATGCTATGGCTCCAGAGTGGTTGGGTGGGGCATGATTCTTGTCACTACCAA	CTGAGTGTTTACGGTGTTCTCTACTGCAAGAGCACCTGGGCTCATCTTTGCTCTGGTTTG 	TICAAGACACCAGGCAAAGGGGTCIACTGCICAATCITITTCGIGTCTGIGTTGTICGCT	GTCTCTGAGATGTCCAAGGACTACAGAAGGCTCGTCTGAGTTTTCTAAGATGGGTTTG 	GCACTGCTTGGCAATACCTTGACAGGTTCTTTACTGGGTACTACGTTCAAGATTACTCT 	CTCCCATIGITAAGITTTGCCGGCCAAGATGTCACTGATGCGTTCATTGCTTACCATCCT	CTATCAAGGGAAAAGTTTACGATATCTCCAAGTGGACTAAAGAGCATCCCGGTGGTGAG 	AAGAAGCACATTTCGCAAGCAGACCTTGCAAAGCATAAGCAACCAGGAGATTTATGGATC 	Score 559.4; DB Pred. No. 4.7e-1 0; Mismatches 5	357 g 6	Production of .gammalinolenic aci Patent: US 5789220-A 4 04-AUG-1998; Location/Qualifiers 11685 /organism_"unknown"	S., Nuccio,	1685 bp 1t US 5789220 .9
CCTGCATTGTT	AAAATGACCTI AGGTTGACTTI	CCTATAATTGO	CATAACACCCI	TTAATCGTCTTTTTCAAATCATTGCAGGAAATGTGATTGCT 	TGGGTGGGGC	AGCACCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	TCAATCTTTTT	CTCGTCTCTG	TTTACTGGGTI	GTCACTGATGO	AAGTGGACTAJ GATTGGGTGAJ	AAGCATAAGCI AACCACGATAI	4; DB 6; 4.7e-148; hes 522;	20 t	acid by a	M., Nunberg,A.	DNA
raagcgttag 	ATGATCGCGC TTGACTCTTT	CCATATCCCC.	ATCACTTTGC	TTGCAGGAAA 	ATGATTCTTG	CTCATCTTTG racattTGTT	CGTGTCTGT	AGTTTTCTAA AGTTTTCTAA	ACTACGTTCA	CGTTCATTGC	AAGAGCATCC	AACCAGGAGA AACCCGGAGA	Length 16 Indels		.DELTA.6-d	g,A.N. and	linear
GCTCTATCTT	TGCCAGGTTT ATCAAGATTC	AAAATTTTTC CAAGTTTTTT	CTGTAATAGC	TGTGATTGCT	TCACTACCAA GCATTATATG	CTCTGGTTTG TTCTGGGTGT	GTTGTTCGCT GCTGTTTGCT	GATGGGTTTG AATGGGTTTG	AGATTACTCT	TTACCATCCT	CGGTGGTGAG AGGTGGCAGC	TTTATGGATC	85; 3; Gaps		esaturase		PAT 05-DEC-1998
839	779 778	719 718	659	599 598	539	479 478	419 418	359 358	299 298	239	179 178	119 118	1,				1998

Ş	Query M Best Lo Matches	BASE CC ORIGIN	AUTHORS TITLE JOURNAL FEATURES	SOURCE ORGANISM	DEFINITION ACCESSION VERSION KEYWORDS	RESULT 7 AR200408	g Q	р У	D &	Qy db	Qy db	Qy Db	Db Qy	g Qy	당 왕	B &	₽ Q	D ₀
60 AAGAAGCACATTTCGCAAGCAGACCTTGCAAAGCATAAGCAACCAGGAGATTTATGGATC 119	Match Jocal Similari 18 885; Cons	rce NT 431 a	Thomas, T.L. Production of g Patent: US 6355	3	Sequence 4 from patent US 6355861. AR200408 AR200408.1 GI:20250482	AR200408	1440 TCCCAATGTTTCTTTTTTTTTTTTTT 1469	1380 AACACTTTCGGGTGAACCTTATNAAACATCAAGTGCTGTCTTTCCCGTAAAAGCTTCCAG 1439	1320 GCTATGGAAGCTAAGGATGTTACCAAGCCAGTTCCCAAGAACATGGTCTGGGAAGCAATG 1379	1260 TATGAAACTGCTACCATGTGGGAGGCCAATAAAATGGTATACTCCACCCTGCGTGCTGTG 1319	1200 TGCCATTTCAGGAAAATCTCACCCATTGTGAACAAACTTTGCCAGAAGCATAATTTGTCC 1259	1140 TGGTTTCATGGTGGCCTGCACTTTCAGATTGAGATCATCTGTTTCCAAGGATGCCTAAG 1199	1080 GATTGGTTTCACCAGCAGACAAAGGGCACGCTCAACATAACAGCTTCTGCTTGGTGGGGAT 1139	1020 TGGCAGTTCAGCTTGAATCACTTTGCTTCTAATGTTTTACACTGGTTTGCCTAGCGGTAAT 1079	960 AATTGGCCTGAAAGGGTCATGTATTTCACGTCCTGTTTAGCAGTCGCCGGGTTCCAACAT 1019	900 GAAATTTTAGGCTATGCAGCTTTCTTGACTTGGTATTCTCTACTCCTTTCTCGCCTACCC 959	840 TTTATTCTGTCTTTTAAGGTGGTGTTTTCCAACAAAAGGGTATACAAGAGAAGTCAG 899	779 TTTGTAAGTTATCAACATTGGACATTTTACCCTATTATGTGTGCTGCTAGGCTCAATATG 838
D Q	b dy	D Q	B 8	B &	g Q	B &	Qy db	Q Qy	da VQ	g Qy	B &	B Q	B 8	D Q	D Qy	Q dd	D Qy	Db
1140 TGGTTTCATGGTGGCCTGCACTTTCAGATTGAGCATCATTTGTTTCCCAAGATGCCTAAG 1199 1136 TGGTTTCATGGTGGATTGCAAATTCCAAATTGAGCATCATTTGTTTCCCAAGATGCCTAGA 1195	GATTGGTTTCACCAGCAGACAAAAGGGCACGCTCAACATAACAGCTTCTGCTTGGTGGGGAT	1020 TGGCAGTTCAGCTTGAATCACTTTGCTTAATGTTTACACTGGTTTGCCTAGCGGTAAT 1079	960 AATTGGCCTGAAAGGGTCATGTATTTCACGTCCTGTTTAGCAGTCGCCGGGTTCCAACAT 1019	900 GAAATTTAGGCTATGCAGCTTTCTTGACTTGGTATTCTCTACTCCTTTCTCGCCTACCC 959	840 TTTATTCTGTCTTTTAAGGTGGTGTTTTCCAACAACAAAGGGTATACAAGAGAAGTCAG 899	780 TITGITAGCITTCAGCACTGGACATTTATCCTGCATTGTTAAGCGTTAGGCTCTATCTT 839	720 AACTCCCTTACATCATACTATCACAACTGCAAAATGACCTATGATCGCGCGCG	660 GCCAATCTGGATGCTGATATTCAGCACCTTCCTATAATTGCCATATCCCCGAAAATTTTTC 719	600 GGTGTTAGTGTTGCATGGTGGAAGTTGGACCATAACACCCATCACTTTGCCTGTAATAGC 659	540 GTTATGCCTAACCGTAAGCTTAATCGTCTTTTTCAAATCATTGCAGGAAATGTGATTGCT 599	480 CTAATGGGTATGGCTCCAGAGTGGTTGGGTGGGGCATGATTCTTGTCACTACCAA 539	420 CTGAGTGTTTACGGTGTTCTCTACTGCAAGAGCACCTGGGCTCATCTTTGCTCTGGGTTTG 479	360 TTCAAGACACCAGGCAAAGGGGTCTACTGCTCAATCTTTTTCGTGTCTGTGTTGTTTCGCT 419	300 GTCTCTGAGATGTCCAAGGACTACAGAAGGCTCGTCTCTGAGTTTTCTAAGATGGGTTTG 359	240 GGCACTGCTTGGCAATACCTTGACAGGTTCTTTACTGGGTACTACGTTCAAGATTACTCT 299	180 CTCCCATTGTTAAGTTTTGCCGGCCAAGATGTCACTGATGCGTTCATTGCTTACCATCCT 239	120 TCTATCAAGGGAAAAGTTTACGATATCTCCAAGTGGACTAAAGAGCATCCCGGTGGTGAG 179	59 AAGAAATACATTACCTCAGATGAACTCAAGAACCACGATAAACCCGGAGATCTATGGATC 118

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Thomas,T.L., Reddy,A.S., Nuccio,M., Nunberg,A.N. and Freyssinet,G.L.
Proyesinet,G.L.
Production of .gamma.-linolenic acid by a .DELTA.6-desaturase Patent: US 5614393-A 4 25-MAR-1997;
LOCALION/Qualifiers
1. .1685
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Db 1316 GCATTGCAGGCTAGGAATATAACCAAGCCTCCCGAAAGAATTTTGGTATGGAAAGCTCTT 1375 Qy 1380 AACACTTTCGGGTGAACCTTATNAAACATCAAGTGCTGTCTTTCCCGTAAAAGCTTCCAG 1439	Oy 1260 TATGAAACTGCTACCATGTGGGAAGCCAATAAAATGGTATACTCCACCCTGCGTGCTGTG 1319	Qy 1200 TGCCATTTCAGGAAAATCTCACCCATTGTGAACAAACTTTGCCAGAAGCATAATTTGTCC 1259	Oy 1140 TGGTTTCATGGTGGCCTGCACTTTCAGATTGAGCATCATCTGTTTCCAAGGATGCCTAAG 1199	Oy 1080 GATTGGTTTCACCAGCAGACAAAGGGCACGCTCAACATAACAGCTTCTGCTTGGTGGGAT 1139	Qy 1020 TGGCAGTTCAGCTTGAATCACTTTGCTTCTAATGTTTACACTGGTTTGCCTAGCGGTAAT 1079	QY 960 AATTGGCCTGAAAGGGTCATGTATTTCACGTCCTGTTTAGCAGTCGCCGGGTTCCAACAT 1019	Oy 900 GAAATTTAGGCTATGCAGCTTTCTTGACTTGGTATTCTCTACTCCTTTCTCGCCTACCC 959	Qy 840 TTTATTCTGTCTTTTAAGGTGGTGTTTTCCAACAAAGGGTATACAAGAGAAGTCAG 899	Qy 780 TTTGTTAGCTTTCAGCACTGGACATTTTATCCTGCATTGTTAAGCGTTAGGCTCTATCTT 839	Qy 720 AACTCCCTTACATCATACTATCACAACTGCAAAATGACCTATGATCGCGCTGCCAGGTTT 779	Qy 660 GCCAAICTGGATCTGATATTCAGCACCTTCCTAFAAITGCCATATCCCCAAAATTTTTC 719	Qy 600 GGTGTTAGTGTTGCATGGTGGAAGTTGGACCATAACACCCATCACTTTGCCTGTAATAGC 659	539 GIAGTGTCTGATTCAAGGCTTAATAAGTTTATGGGTATTTTTGCTGCAAATTGTCTTTCA	Db 479 TTGATGGGGTTTCTTTGGATTCAGAGTGGTTGGATTGGA	Db 419 ATGAGTGTTTATGGGGTTTTGTTGAGGGTGTTTTGTTATTGTTATTGTGTACTACTACTACTACTACTACTACTACTATTGTTTTTGTGAGGGCCATGATTCTTGTCACTACTACTACCAA 539	

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Station, Long Ashton, Bristol BS18 9AF, UK
Location/Qualifiers
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Sayanova, O., Smith, M
Direct Submission
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RNVSYKAHELLGCLVFSIWYPLLVSCLPNWGERIMFVIASLSVTGMQQVQFSLNHFSS
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AACACTTTCGGGTGAACCTTATNAAACATCAAGTGCTGTCTTTCCCGGTAAAAGCTTCCAG
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                                                                                                                                                                                                                                                                                        TGGTTTCATGGTGGCCTGCACTTTCAGATTGAGCATCATCTGTTTCCAAGGATGCCTAAG
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                                                                                                                                                                                                                                                                      TGGTTTCATGGTGGATTGCAATTCCAAATTGAGCATCATTTGTTTCCCAAGATGCCTAGA 1193
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                                                                                                                          TACAATTATGCATCTTTCTCCAAGGCCAATGAAATGACACTCAGAACATTGAGGAACACA
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8	D Q	Query Ma Best Loc Matches	BASE COUNT				mRNA CDS	gene		JOURNAL FEATURES source	AUTHORS TITLE	JOURNAL	REFERENCE AUTHORS	SOURCE ORGANISM	ACCESSION VERSION	RESULT 11 AY055118 LOCUS	D Q	Db 1
120 TCTATCAAGGGAAAAGTTTACGATATCTCCAAGTGGACTAAAGAGCATCCCGGTGGTGAG 179	60 AAGAAGCACATTTCGCAAAGCAACCTTGCAAAGCATAAGCAACCAGGAGATTTATGGATC 119	y Match 37.6%; Score 553; DB 8; Length 1450; Local Similarity 63.9%; Pred. No. 3.1e-146; hes 854; Conservative 0; Mismatches 480; Indels 3; Gaps 1;	SVYVGORGIMFEKOTCGTLDISCPSWIDMFHGGLOFOVEHHLFRLPRCHLRKISP FVMELCKKHNLSYNCASFSQANEMTLRTLRDTALQARDLTKPLPKNLVWEALNTHG" 355 a 252 c 358 g 485 t	MGLFDKKGHĪVLVTVFFIĀMMFAMSVYGVLFCEGVLVHLLĀGGLMGFVWIQSGWIGHD ĀGHYIVMENEKLINKLMGIVĀSNOLSGISIGWRKWHNHAHIACNSLDVEDDDLQYIPFL VVSSKLFSSLYSHFYEKKLTFOSLSRFFVSHQHWTFFYDWGCSARVMWFVQSLIMLITK RNVFYRSQELLGLVVFWIWYPLLVSCLPNWGERIMFVVASLSVTGLQQVQFSLNHFĀA	/protein_id="AALI23581.1" /protein_id="AALI23581.1" /db_xref="G1:17223797" /db_xref="G1:17223797" /translation="MANAIKKYITAEELKKHDKEGDLWISIQGKVYDVSDWLKDHPGG /KFPLKSLAGGOEVTADAFVAEHSGSTWKLLDSFFTGYYLKDYSVSEVSKDYBKIJFEFNK KFPLKSLAGGOEVTADAFVAEHSGSTWKLLDSFFTGYYLKDYSVSEVSKDYBKIJFEFNK	/gene="D6DES" /note="acyl-lipid desaturase" /codon_start=1 /road="tart=1	<8>1354 /gene="b6DES" /product="delta-6-desaturase" 81354	183 (1935)" <pre></pre>	pitardii var. pitardii" c DNA" i" 194255" 155444 1565 1575	Submitted (10-SEP-2001) Biochemistry, Uni Campus Universitario, La Canada s.n., Alm Location/Qualifiers 11450		nd Mol	Asteridae; lamids; Boraginaceae; Echium. 1 (bases 1 to 1450) Maroto, F.G., Alonso, D.L., Garrido, JA.S., Ferron, M.V. and Rulz, J.R.	Echium pitardii var. pitardii Echium pitardii var. pitardii Eukaryota; Viridiplantae; Streptophyta; Embryophyta		AY055118 1450 bp DNA linear PLN 01-DEC-2001	1440 TCCCAATGITTCTTTTTTTTTTTTTT 1469	
ප දි) D Q) B &	D QY	Db Qy	рь	р Q	Db Qy	D 43	? B &	р <i>Q</i>	gb QY	da t	S B 8	?	B Q	Db Qy	D Q	дь
1200 TGCCATTCAGGAAAATCTCACCCATTGTGAACAAACTTTGCCAGAAGCATAATTTGTCC 1259	4) TGGTTTCATGGTGGCCTGCACTTTCAGATTGAGCATCATCTGTTTCCAAGGATGCCTAAG	80 GATTIGGTTICACCAGCAGACAAAAGGCACCCICAACATAAAGCTICIGGTGGATGGAT	TGGCAGTTCACCTTGAATCACTTTGCTTCTAATGTTTACACTGCTTTGCCTAGCGGTAAT	AATTGGCCTGAAAGGGTCATGTATTTCACGTCCTGTTTAGCAGTCGCCGGGTTCCAACAT	900 GAAATTTAGGCTATGCAGCTTTCTTGACTTGGTATTCTCTACTCCTTTCTCGCCTACCC 959	840 TTTATTCTGTCTTTTAAGGTGGTGTTTTCCAACAACAAAAGGGTATACAAGAGAAGTCAG 899	780 TTTGTTAGCTTTCAGCACTGGACATTTTATCCTGCATTGTTAAGCGTTAGGCTCTATCTT 839	683 AGCTCGCTCACTTTCTATGAAAAGAAACTCACATTTGACTCGTTATCGAGATTC 742	GCCAATCTGCATCCTGATATTCAGCACCTTCCTATAATTGCCATATCCCCAAAATTTTTC GCCAATCTGCATCATCATCATCATCATCATCATCCCCAAAATTTTTC GCCAATTATGACCCGGATTTACAATACATACCTTTCTTGTTGTCTCGAAGTTGTTT CTGATTATGACCCGGATTTACAATACATACCATTTCTTGTTGTTCTTGTCGAAGTTGTTT	600 GGTGTTAGTGTTGCATGGTAGGAAGTTGGACCATAACACCCATCACTTTGCCTGTAATAGC 659	540 GTTATGCCTAACCGTAAGCTTATTCGTCTTTTTCAATCATTGCTAGAAATTGCTTTCA 562 503 GTTATGCCTAATCCAAAGCTTAATAAGCTTATGGGTATTGTTGCTAGTAATTGCCTTTCA 562	TTGATGGGGTTTGTCTGGATTCAGAGTGGGTGGATTGGGCATGATGCTGGGCATTATATA	480 CTAANTGGTATGGCTTCTAGGAGTGGTTGGGGGGCATGATTTTCTTGCACCAA 539	TICAMACACCAGGCAAAGGGCIACTGCICAATCIITTICGIGCIGIGIGIGIGGCITTGIICGCITTGIGCACAAAAAAGGGICATATGIGCTTGIGCTGACCAGAAAAAAGGGICATATGIGCTTGIGCTAGCGACTGIGTTTTTATAGCTATGATGTTTGCCT	GTCTCTGAGATGTCCAAGGACTACAGAAGGCTCGTCTCTGAGTTTTCTTAAGATGGGTTTG 	240 GGCACTGCTTGGCAATACCTTGACAGGTTCTTTACTGGGTACTACGTTCAAGATTACTCT 299	180 CTCCCATTGTTAAGTTTTGCCGGCCAAGATGTCACTGATGCGTTCATTGCTTACCATCCT 239	83 TCCATTCAAGGCAAGGTCTATGATGTTTCAGATTGGTTGAAGGACCATCCAGGTGGGAAG 142

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REFERENCE
AUTHORS
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Boraginaceae; Echium.

1 (bases 1 to 1478)
Maroto, F.G., Alonso, D.L., Garrido, J.-A.S., Ferron, M.V. and
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AY055117
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   AAGAAGCACATTTCGCAAGCAGACCTTGCAAAGCATAAGCAACCAGGAGATTTATGGATC 119
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TGGTTTCATGGTGGCCTGCACTTTCAGATTGAGCATCATCTGTTTCCAAGGATGCCTAAG 1199
                                                                               GATTGGTTTCACCAGCAGACAAAGGGCACGCTCAACATAACAGCTTCTGCTTGGTGGGAT
                                                                                                                          GTGCAGTTCTCTTTGAACCATTTCTCGGCGAGTGTTTATGTTGGTCAGCCTAAAGGGAAC 1068
                                                                                                                                            TGGCAGTTCAGCTTGAATCACTTTGCTTCTAATGTTTACACTGGTTTGCCTAGCGGTAAT 1079
                                                                                                                                                                                                                   AATTGGCCTGAAAGGGTCATGTATTTCACGTCCTGTTTAGCAGTCGCCGGGTTCCAACAT 1019
                                                                                                                                                                                                                                                                                         GAAATTTTAGGCTATGCAGCTTTCTTGACTTGGTATTCTCTACTCCTTTCTCGCCTACCC
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B &	D Q	Query M Best Lo Matches	BASE COUNT					FEATURES sou	JOURNAL	REFERENCE AUTHORS	Jour	REFERENCE AUTHORS		SOURCE ORGANI	DEFINITION ACCESSION VERSION	RESULT 13 AY131238	Db	8	B &	B &	}	Qy Db
120 TCTATCAAGGAAAAGTTTACGATATCTCCAAGTGGACTAAAGAGCATCCCGGTGGTGAG 179	60 AAGAAGCACATTTCGCAAAGCAGACCTTGCAAAGCATAAGCAACCAGGAGATTTATGGATC 119	Query Match 36.6%; Score 538.2; DB 8; Length 1347; Best Local Similarity 63.2%; Pred. No. 5.1e-142; Matches 844; Conservative 0; Mismatches 488; Indels 3; Gaps 1;	SVYVGKENGNNWEBTQTDGTLDISCPPM/DWFHGGLQFQIEHHLFPKMPRCNLRTISP YVIELCKKHNLPYNYASFSKANEMTLRTLRNTALQARDITKPLPKNLVWEALHTHG" COUNT 346 a 239 c 298 g 464 t	MGLYDKAGHIMFATLCFIAMLFAMSVYGVLRCEGVLVHLFSGCLMGFLWIQSGWIGHD PGHYMVVSDSRLNKFMGIFAANCLSGISIGNSKMNINAHHIACNSLEYDPDLQYIPFL VVSSKFFGSLTTSHFYEKLTIDSLSRFFVSYQHMTEYTIMCAARLIMYVGSLIMLLTK RNVSYRAHBLLGCLVFSIWYPLLVSCLPIMGGRIMFVIASSVTGMQQVQFSLNHFSS	/protein_id="AAM94345.1" /db_xref="g1:22296826" /translation="MAAQIKKYITSDELKOHDKPGDLMISILGKAYDVSDWVTDHPGG SFPLKSLAGOEVTDAFVAFHPASTWKNLDKFFTGYYLKDYSVSEVSKDYSKLVFEFSK	CDS 1. 1347 /codon_start=1 /product="delta-6-desaturase"	/organism= nighting optinged /nol_type="mRNA" /db xref="taxon:85884"	rce 1.1347	NAL Submitted (12-JUL-2002) Biologie Moleculaire, Faculte des Sciences, Ibn Batouta, Rabat, Rabat 1014, Morocco	2 (bas	spinosa fruit Unpublished	1 (bases 1 to 1347) El Filali, A., Anderson, M. and Abbas, K. Characterization and cloping of delta-6-decaturace in	Sper	Argania spinosa SM Argania spinosa	TION Argania spinosa delta-6-desaturase mRNA, complete cds.	3	1369 AATACTCATGGTTAAGC 1385	1380 AACACTTTCGGGTGAAC 1396	1320 GCTATGGAAGCTAAGGATGTTACCAAGCCAGTTCCCAAGAACATGGTCTGGGAAGCAATG 1379 	1249 TACAATTGTGCATCATTCTCCGAGGCCAATGAAATGACACTCAGAACATTAAGGGACACA 1308	TGCCACCTTAGGAAAATCTCCCCATTCGTGATGGAGTTATGCAAGAAGCACAATTTGTCT	
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JOURNAL
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Best Local Similarity
Matches 850; Conserv
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Station, Long Ashton, Bristol BS41 9AF, UK
Location/Qualifiers
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(bases 1 to 1341)
Longman, A. U., Michaelson, L. V. and Napier, J. A.
Isolation and characterization of a cDNA encoding
sphingolipid desaturase from Aquilegia vulgaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF406816 1341 bp
Aquilegia vulgaris sphingolipid
mRNA, complete cds.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
Ranunculaceae; Aquilegia.
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CCAGGTGGTGAAGCACCTTTATTGAATCTAGCTGGTCAAGATGTTACAGATGCATTTGTT
                  CCCGGTGGTGAGCTCCCATTGTTAAGTTTTGCCGGCCAAGATGTCACTGATGCGTTCATT
                                                                    GATATATGGATCTCAATTCAAGGTAAGATCTATGATGTTTCAGAATGGATTAAAGATCAT
                                                                                           GATTTATGGATCTCTATCAAGGGAAAAGTTTACGATATCTCCAAGTGGACTAAAGAGCAT
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                                                                                                                                            aTGGAAGAGCCAAAGAAGCACATTTCGCAAGCAGACCTTGCAAAGCATAAGCAAACCAGGA
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                                                                                                                                                                                                                      Conservative
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LYDKKGHHILASLTGISTGWKWNHNAHHIAVNSLDYDDDLQHIPFLAV
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VTDRALLIGLAVFWCWYSLLLACLPNWGERAMYVAMSFAVSGYQHIOFCLNHFSAHT
YVGRPPCNDWFFDISCSTWMDWFHGGLQFQVEHHLFPRLPRCHLRKISPFV
KELCRKHNLPYISVSFFEANKWTIATLENAALQARDLTWPIPKNLVWEAVNTHG"
L26 c 293 g 476 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Aquilegia vulgaris"
/mol_type="mRNA"
/db_xref="taxon:3451"
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63.1%;
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                                                                                                                                                                                                                  Score 529.4; DB 8;
Pred. No. 1.6e-139;
0; Mismatches 491;
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                                                   CATAATTTGTCCTATGAAACTGCTACCATGTGGGAGGCCAATAAAATGGTATACTCCACC
                                                                                                            AGGATGCCTAAGTGCCATTTCAGGAAAATCTCACCCATTGTGAACAAACTTTTGCCAGAAG
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Helianthus annuus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; campanulids; Asterales; Asteraceae; Asteroideae;

Heliantheae; Helianthus.
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X87143.1 GI:1040728
cytochrome B5 domain; delta-8 sphingolipid desaturase; sldl gene.
Helianthus annuus (common sunflower)
                                                                                                                                                                                                                                                                                                                                                                                                                             Allgemeine Botanik, Ohnhorststr. 18, 2:
Related sequences: AJ224160, AJ224161,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HACYTB5RN 1591 bp mRNA linear PLN 03-FEB-2001
Helianthus annuus mRNA for stereo-unselective delta 8-sphingolipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (10-MAY-1995) P. Sperling, Univ Hamburg, Allgemeine Botanik, Ohnhorststr. 18, 2269 Hamburg,
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Direct Submission
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/db xref="STTEMBL:Q43469"
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/evidence=experimental
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73. .1449
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/tissue_type="cotyledons of developing sunflower fruits"
/dev_stage="21 DAF"
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/cultivar="inbred line HA89,
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GATTCTTGTCACTACCAAGTTATGCCTAACCGTAAGCTTAATCGTCTTTTTCAAATCATT GTGGCCCGGGTCAACCTCTATTTACAAACAATCCTGTTGCTGATTTCAAAACGAAAGA--AGCGTTAGGCTCTATCTTTTATTCTGTCTTTTTAAGGTGGTGTTTTCCAACAACAAAAGG GATCGCGCTGCCAGGTTTTTTGTTAGCTTTCAGCACTGGACATTTTATCCTGCATTGTTA GTTTCTTCCAAGCTTTTTAACTCAATAACTTCTGTTTTCTATGGGAGACAGTTGACCTTT ATATCCCCAAAATTTTTCAACTCCCTTACATCATACTATCACAACTGCAAAATGACCTAT GCAGGAAATGTGATTGCTGGTGTTAGTGTTGCATGGTGGAAGTTGGACCATAACACCCAT GTGTCGCTACTGCTTTCCGCTTGTGTGTGTATAGCGTGTTATATTCCGGAAGCTTCTGGATT GIGICIGIGITGOTCOGCICTGAGIGITTACGGTGTTCTCTACTGCAAGAGCACCTGGGCT CACTTAAAAGATTACCAGGTTTCTGACATTTCTAGAGACTACCGGAAACTCGCTTCAGAG TACGTTCAAGATTACTCTGTCTCTGAGATGTCCAAGGACTACAGAAGGCTCGTCTGTGAG GAGCATCCGGGTGGCGATGCCCCGTTGATTAATCTCGCGGGCCAGGATGTAACTGACGCA GAGCATCCCGGTGGTGAGCTCCCATTGTTAAGTTTTGCCGGCCAAGATGTCACTGATGCG CCAGGAGATTTATGGATCTCTATCAAGGGAAAAGTTTACGATATCTCCAAGTGGACTAAA AATTCAATTGCTGATGGAAAAAAATACATAACATCAAAAGAGTTAAAGAAGCATAACAAC ACTTCAATGGAAGAGCCAAAGAAGCACATTTCGCAAGCAGACCTTGCAAAGCATAAGCAA 101 - TTCCCGACAGAGGTTTAAACATACTCGGAACCCTAATCTTCTGGACGTGGTTTCCGTTA GTATACAAGAGAAGTCAGGAAATTTTAGGCTATGCAGCTTTCTTGACTTGGTATTCTCTA GACCCGTTAGCCCGGTTCTTCGTGAGCTACCAGCATTACTTATATTACCCCGATCATGTGT CACTTTGCCTGTAATAGCGCCAATCTGGATCCTGATATTCAGCACCTTCCTATAATTGCC ATCGGGAATTGTATAACCGGAATAAGCATCGCGTGGTGGAAATGGACGCATAACGCACAT GACGCGGGTCATTACCAAATGATGGCGACCCGCGGGTGGAACAAGTTTGCCGGAATATTT CATATGCTTTCGGGGGCGATATTGGGATTAGCATGGATGCAAATTGCCTATTTGGGTCAT TTTGCAAAAGCGGGTATGTTTGAGAAGAAAGGTCACGGTGTAATTTACTCACTTTGTTTC TTTTCTAAGATGGGTTTGTTCAAGACACCAGGCAAAGGGGTCTACTGCTCAATCTTTTTC TITATCGCATTTCATCCCGGTACTGCGTGGAAGCATCTAGACAAACTATTCACCGGGTAT TTCATTGCTTACCATCCTGGCACTGCTTGGCAATACCTTGACAGGTTCTTTACTGGGTAC Conservative 31.3%; 0; Mismatches 552; Score 460.8; Pred. No. 6.3 .2e-120; Length Ÿ Gape 161 881 879 821 641 581 521 996 941 937 819 761 699 339 221 159 701 639 579 519 461 459 401 399 341 279 219 759 281

1417 TTAGCTTGGGAAGCTTTCAACACCCATGGTTGAAGCTTCT 1456	Db
1362 ATGGTCTGGGAAGCAATGAACACTTTCGGGTGAACCTTAT 1401	ઇ
1357 AAGACGCTTAGGACAGCGGCTCTACAGGCACGTGACCTTACGAACCCGGCCCCACAGAAT 1416	DЬ
1302 TCCACCCTGCGTGCTGTGGCTATGGAAGCTAAGGATGTTACCAAGCCAGTTCCCAAGAAC 1361	Ş
1297 AAGAAATATAACTTACCTTATGTGAGTTTGTCGTTTTATGATGCGAATGTAACGACCTTG 1356	DЬ
1242 CAGAAGCATAATTTGTCCTATGAAACTGCTACCATGTGGGAGGCCAATAAAATGGTATAC 1301	Ş
1237 TTTCCTAGGTTGCCACGGTGTCACTTGAGGTCGATTTCTCCTATATGTAGAGAACTCTGC 1296	Дb
1182 TTTCCAAGGATGCCTAAGTGCCATTTCAGGAAAAATCTCACCCATTGTGAACAAACTTTGC 1241	Ş
1177 TGTTCTTCTTGGATGGATTGGTTTTTCGGAGGTTTTACAGTTTCAACTTGAGCACCATTTG 1236	дb
1122 GCTTCTGCTTGGTGGGATTGGTTTCATGGTGGCCTGCACTTTCAGATTGAGCATCATCTG 1181	Ş
1117 GGCCCGCCAAAAGGACAATTGGTTCGAGAAACAAACGCGTGGGACCATCGATATCGCG 1176	망
1062 GGTTTGCCTAGCGGTAATGATTGGTTTCACCAGCAGACAAAGGGCACGCTCAACATAACA 1121	Ş
1057 GTAACGGGTATACAACATATTCAGTTTACACTGAACCATTTTTCTGGGGATGTTTACGTG 1116	DЬ
1002 GTCGCCGGGTTCCAACATTGGCAGTTCAGCTTGAATCACTTTGCTTCTAATGTTTACACT 1061	ş
997 CTTGTTTCTCGCTTACCGAACTGGCCCGAACGCGTGGCGTTTGTGTTAGGTTAGCTTCTGT 1056	ф

Search completed: December 31, 2003, 21:04:19 Job time : 3697.2 secs

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Result
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                                                                                                                                                                                                                                           Score
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1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*

4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*

5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*

6: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*

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14225.873 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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ALIGNMENTS

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AAD01349 standard; cDNA; 1471 BP.

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Cahoon EB, Cahoon RE,
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                                                                                                                                                                                                  03-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                    08-JUN-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Picramnia pentandra.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "Delta-6 fatty acid desaturase"
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     Hitz WD,
     Kinney AJ;
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Query Match
Best Local Similarity
Matches 1471; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1471 BP; 353 A; 330 C; 313 G; 474
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                                                                                                               ACACTTTCGGGTGAACCTTATNAAACATCAAGTGCTGTCTTTCCCGTAAAAGCTTCCAGT
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standard; DNA; entry) ВP

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 38.0%; Score 559.4; DB 19; Length Best Local Similarity 62.8%; Pred. No. 3.2e-158; Matches 885; Conservative 0; Mismatches 522; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence is the gene encoding the borage (Borago officinalis) delta-6 desaturase enzyme. The lipid metabolism gene is an example of a heterologous gene which can be expressed at high levels in a seed-specific manner in transgenic plants, when placed under control of the sunflower albumin gene 5' regulatory region (AAV34397).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New sunflower albumin 5' regulatory region - useful for altered lipid metabolism in plant seeds  \label{eq:lipid}
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P-PSDB; AAW67471.
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                           GTTATGCCTAACCGTAAGCTTAATCGTCTTTTTCAAATCATTGCAGGAAATGTGATTGCT
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                                                                                                                       ATGAGTGTTTATGGGGTTTTTGTTTTGTGAGGGTGTTTTGGTACATTTGTTTTCTGGGTGT
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Delta-6 desaturase; borage; oleosin;
                            Borage delta-6 desaturase cDNA
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AAW98130), an enzyme that catalyses the conversion of linoleic acid
to gamma-linolenic acid (GLA). Delta-6 desaturase CDNA was
isolated from a borage membrane-bound polysomal cDNA library
using a partial clone, obtained from an EST database search, as
probe. The borage delta-6 desaturase nucleic acid can be
perably linked to the seed-specific 5' regulatory region (see
coperably linked to the seed-specific 5' regulatory region (see
AAX24916) of the Arabidopsis thaliana oleosin AtS21 gene in claimed
expression cassettes of the invention. Transgenic plants, e.g.
sunflower, soybean, maize, tobacco, cotton, peanut, oilseed
rape or Arabidopsis are obtained that show increased levels of
GIA or octadecatetraeonic acid. The levels of desirable fatty
coils of use in human health and industrial applications.
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid containing oleosin 5'-regulatory region - useful for modulating fatty acid synthesis and lipid metabolism in plants, particularly to increase content of gamma-linolenic acid
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GGCACTGCTTGGCAATACCTTGACAGGGTTCTTTACTGGGTACTACGTTCAAGATTACTCT
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                                                                                         GTCTCTGAGATGTCCAAGGACTACAGAAGGCTCGTCTCTGAGTTTTCTAAGATGGGTTTG
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                                                        GTTTCTGAGGTTTCTAAAGATTATAGGAAGCTTGTGTTTTGAGTTTTCTAAAATGGGTTTG
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Pred. No. 3.2e-158;
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                                                                                                         AACACTTTCGGGTGAACCTTATNAAACATCAAGTGCTGTCTTTCCCGTAAAAGCTTCCAG
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Best Local Similarity
Matches 885; Conserv
                                                                                                                                                                                                                                                                                                                                          A DNA clone (AAT30395) codes for borage delta-6-desaturase (AAR98455), which catalyses the conversion of linoleic acid to gamma-linolenic acid (GLA). It was isolated from a borage membrane-bound polysomal library using probes based on abundantly expressed sed storage protein CDNAs and with an isolated partial cDNA clone. The gene can be incorporated into a vector, pref. incorporating a tissue-specific promoter, for the expression of delta-6-desaturase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT30395 standard;
                                                                                                                                                                                                                                                        Sequence 1685
                                                                                                                                                                                                                                                                                              in transgenic plants, esp. sunflower, soybean, maize, tobacco, peanut, carrot or oilseed rape, resulting in increased GLA prodn. Alteration of plant lipids may also lead to improved chilling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transgenic plants comprising the borage delta-6-desaturase granow increased production of gamma linolenic acid and having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-DEC-1994;
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                                                                                           TCTATCAAGGGAAAAGTTTACGATATCTCCAAGTGGACTAAAGAGCATCCCGGTGGTGAG
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                                                                                                                                  AAGAAATÁCATTACCTCAGATGAACTCAAGAACCACGATAAACCCGGAGATCTATGGATC
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               TTTCCCTTGAAGAGTCTTGCTGGTCAAGAGGTAACTGATGCATTTGTTGCATTCCATCCT
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                                                          TATGAAACTGCTACCATGTGGGAGGCCAATAAAATGGTATACTCCACCCTGCGTGCTGTG
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  Best Local Similarity
                     Query Match
                                                                                                          The invention describes an isolated nucleic acid encoding an evening primrose Delta6-desaturase. The nucleic acid and a vector expressing the nucleic acid are useful for producing a plant such as sunflower, soybean, maize, tobacco, peanut, carrot or oil seed rape plant, with increased gamma linolenic acid (GLA) content, and also for inducing or increasing production of GLA in a bacteria or plant deficient, lacking in or producing low levels of GLA. The nucleic acid is also useful for inducing chilling tolerance in plants. This sequence encodes the borage delta6 desaturase involved in the production of gamma linoleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-JAN-1992;
14-SEP-1994;
28-JAN-1997;
                                                                    Sequence 1685
                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acid encoding evening primrose delta6-desaturase which converts linoleic acid to gamma linolenic acid useful for producing gamma linolenic acid in transgenic plant or bacteria
                                                                                                                                                                                                                                                                                                                                        Example 9; Column 29-32; 53pp; English.
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chilling tolerance;
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peanut; carrot; oil seed rape; gamma linolenic
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10-OCT-1991;
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92US-0307382.
97US-0789936.
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/product= "delta6-desaturase"
/transl_except= (pos:1151..11
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gene; ds; borage.
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                                                                                    GTTCAGTTCTCCTTGAACCACTTCTCTTCAAGTGTTTATGTTGGAAAGCCTAAAGGGAAT
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TGGCAGTTCAGCTTGAATCACTTTGCTTAATGTTTACACTGGTTTTGCCTAGCGGTAAT
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19-SEP-1997;
10-OCT-1991;
08-JAN-1992;
14-SEP-1994;
28-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Delta-6-desaturase; gene; ss; delta-12-desaturase; sunflower; soybean; maize; tobacco; peanut; carrot; oil seed rape; gamma-linolenic acid; Goctadecatetraenoic acid; alpha-linolenic acid; delta-15-desaturase;
                     Novel nucleic acid encoding evening primrose delta-6-desaturase, useful for producing plant with increased gamma linolenic acid content, and for inducing octadecatetraenoic acid production in plant -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Borago officinalis
                                                                                                         P-PSDB;
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97US-0934254.
91US-0774475.
92US-0817919.
94US-0307382.
97US-0789936.
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/product= "Borage delta-6-desaturase #1"
/transl_except= (pos:1151..1153, aa:Ser)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a nucleic acid encoding an evening primrose delta-6-desaturase polypeptide. The nucleic acid, a vector comprising the nucleic acid or a nucleic acid encoding delta-12-desaturase, is useful for producing a plant (such as sunflower, soybean, maize, tobacco, peanut, carrot or oil seed rape plant) with increased gamma-linolenic acid (GLA) content by transforming a plant cell with the nucleic acid or vector and regenerating a plant with increased GLA content from the plant cell, for inducing or increasing production of GLA in an organism lacking in or producing low levels of GLA and for inducing production of or producing low levels of GLA and for inducing production of or producing low levels of GLA and for inducing production of produces alpha-linolenic acid or a bacterium which a bacterium which delta-15-desaturase activity on a GLA substrate. This sequence represents cDNA encoding a borage delta-6-desaturase polypeptide.
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Similarity 62.8%;
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Sequence 1685 BP; 431 A; 277 C; 357 G; 620 T; 0 other;

AAGAAGCACATTTCGCAAGCAGACCTTGCAAAGCATAAGCAACCAGGAGATTTATGGATC Score 559.4; DB 25; Pred. No. 3.2e-158; 0; Mismatches 522; Indels Length ω --Gaps 119

GCCAATCTGGATCCTGATATTCAGCACCTTCCTATAATTGCCATATCCCCAAAATTTTTTC GGTGTTAGTGTTGCATGGTGGAAGTTGGACCATAACACCCATCACTTTGCCTGTAATAGC GTTATGCCTAACCGTAAGCTTAATCGTCTTTTTCAAATCATTGCAGGAAATGTGATTGCT CTAATGGGTATGCTATGGCTCCAGAGTGGTTGGGTGGGGCATGATTCTTGTCACTACCAA 539 ATGAGTGTTTATGGGGTTTTGTTTGTGAGGGTGTTTTGGTACATTTGTTTTTCTGGGTGT CTGAGTGTTTACGGTGTTCTCTACTGCAAGAGCACCTGGGCTCATCTTTGCTCTGGTTTG GTCTCTGAGATGTCCAAGGACTACAGAAGGCTCGTCTCTGAGTTTTTCTAAGATGGGTTTG GGCACTGCTTGGCAATACCTTGACAGGTTCTTTACTGGGTACTACGTTCAAGATTACTCT CTCCCATTGTTAAGTTTTGCCGGCCAAGATGTCACTGATGCGTTCATTGCTTACCATCCT TCTATCAAGGGAAAAGTTTACGATATCTCCAAGTGGACTAAAGAGCATCCCGGTGGTGAG GGTTCACTCACCTCTCATTTCTATGAGAAAAAGGTTGACTTTTGACTCTTTATCAAGATTC CTTGAATATGACCCTGATTTACAATATATACCATTCCTTGTTGTGT GTAGTGTCTGATTCAAGGCTTAATAAGTTTATGGGTATTTTTGCTGCAAATTGTCTTTCA TATGACAAAAAGGTCATATTATGTTTGCAACTTTGTGCTTTATAGCAATGCTGTTTGCT TTCAAGACACCAGGCAAAGGGGTCTACTGCTCAATCTTTTTCGTGTCTGTTGTTCGTCT GTTTCTGAGGTTTCTAAAGATTATAGGAAGCTTGTGTTTTGAGTTTTCTAAAATGGGTTTG GCCTCTACATGGAAGAATCTTGATAAGTTTTTTCACTGGGTATTATCTTAAAGATTACTCT TTTCCCTTGAAGAGTCTTGCTGGTCAAGAGGTAACTGATGCATTTGTTGCATTCCATCCT TCGATTCAAGGGAAAGCCTATGATGTTTCGGATTGGGTGAAAAGACCATCCAGGTGGCAGC **AAGAAATACATTACCTCAGATGAACTCAAGAACCACGATAAACCCCGGAGATCTATGGATC** AACTCCCTTACATCATACTATCACAACTGCAAAATGACCTATGATCGCGCTGCCAGGTTT GGAATAAGTATTGGTTGGTGGAAATGGAACCATAATGCACATCACATTGCCTGTAATAGC CTTCCAAGTTTTT 599 178 659 478 479 179 778 779 718 719 859 598 118 538 418 419 358 359 298 299 238 239

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CGTGCAACAGCCTTGACCATGACCCTGATCTGCAGCACATGCCGGTCTTTGCAGTTTCGT
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Polynucleotide encoding delta-6 desaturase enzyme useful for producing transgenic plants and for producing antibodies specific to which is useful for screening cDNA expression libraries -
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The present sequence is a cDNA encoding sphingolipid desaturase from clone sel.pk0017.D4:fis isolated from soybean seedling cDNA library, sel. The present sequence is useful for producing transgenic plants having altered levels of sphingolipid desaturase whi in turn would alter the fatty acid composition. The enzyme is useful for producing polyclonal or monoclonal antibodies. The polynucleotide is also useful as primer or probe for screening cDNA libraries to isolate desired full-length cDNA clones.

614 T; 0 other;

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                                                                                                              Sphingolipid desaturase; sld1; sphingobase; ceramide; capnoid; transgenic plant; crop plant; delta-8-unsaturated long-chain base; tolerance; resistance; soil salinity; ion stress; toxicity; drought; cold; frost; phytopathogenic microorganism; flowering time; cosmetic; pharmaceutical; food; chemical raw material; ds.
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CC This invention describes a novel sphingolipid desaturase that selectively CC introduces a double bond into the sphingobase of the ceramide residue of csphingolipids and capnoids. A DNA sequence encoding the sphingolipid CC desaturase, or a vector containing the DNA sequence, can be used to CC produce transgenic plants, especially crop plants, with an increased or CC decreased delta-8-unsaturated long-chain base content or an altered CC delta-8-unsaturated long-chain base content or an altered CC compensate for a delta-8-unsaturated long-chain base deficiency, to CC exclude production of delta-8-unsaturated long-chain base deficiency, to CC conditions, cold or frost and/or phytopathogenic microases tolerance CC or resistance to soil salinity, ion stress or toxicity, drought, wet CC conditions, cold or frost and/or phytopathogenic microorganisms, or to CC alter size growth and flowering time. Cells, transgenic organisms or CC can be used in cosmetics, pharmaceuticals and foods and as chemical raw CC can be used in cosmetics, pharmaceuticals and foods and as chemical raw CC described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                New aphingolipid desaturase that selectively introduces double bond into sphingolipids and capnoids -
Sequence 1606 BP; 412 A; 338 C; 370 G; 486 T; 0 other;
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RESULT 9 AAZ44832

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GCAGCGATCCTAAACCTCGCCGGTCAAGACGTCACCGACGCGTTCATCGCTTACCATCCC

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                                                                                                                                                                                                                                                         This invention describes a novel sphingolipid desaturase that selectively controduces a double bond into the sphingolipid desaturase of the ceramide residue of sphingolipids and capnoids. A DNA sequence encoding the sphingolipid codesaturase, or a vector containing the DNA sequence, can be used to compound the sphingolipid codecreased delta-8-unsaturated long-chain base content or an altered codelta-8-unsaturated long-chain base content or an altered codelta-8-unsaturated long-chain base cis/trans ratio, especially to compensate for a delta-8-unsaturated long-chain bases, to increase tolerance codecreased efficiency, to compensate for a delta-8-unsaturated bases, to increase tolerance corresistance to soil salinity, ion stress or toxicity, drought, wet conditions, cold or frost and/or phytopathogenic microorganisms or to calter size growth and flowering time. Cells, transgenic organisms or compensation containing the DNA sequence can be used to produce sphingolipids can decontain cosmetics, pharmaceuticals and foods and as chemical raw materials. This sequence encodes the Brassica napus sphingolipid desaturase sldl protein described in the method of the invention.
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Best Local S
Matches 794
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                                                                                                                                                                                                                                                       Sequence 1594 BP; 382 A; 369
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                                                         TATGAAACTGCTACCATGTGGGAGGCCAATAAAATGGTATACTCCACCCTGCGTGCTGG
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                           TATAGGAGTCTTTCGTGGTGGGAGGCTAATGTGTGGACGCTCAGGACTCTGAGGAAAGCG
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pathway; promoter; termination sequence;
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                       TGGTTCTTTGGTGGATTGCAGTTTCAGTTAGAGCATCATTTGTTTCCTCGGCTTCCTCGT
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                                TGGCAGTTCAGCTTGAATCACTTTGCTTCTAATGTTTTACACTGGTTTGCCTTAGCGGTAAT
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              GAAATTTTAGGCTATGCAGCTTTCTTGACTTGGTATTCTCTACTCCTTTTCTCGCCTACCC
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New sphingolipid desaturase that selectively introduces into sphingolipids and capnoids -
                                                                                                                                                    Heinz E,
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This invention describes a novel sphingolipid desaturase that selectively CC introduces a double bond into the sphingobase of the ceramide residue of sphingolipids and capnoids. A DNA sequence encoding the sphingolipid CC sphingolipid and capnoids. A DNA sequence, can be used to CC produce transgenic plants, especially crop plants, with an increased or CC decreased delta-8-unsaturated long-chain base content or an altered CC compensate for a delta-8-unsaturated long-chain base deficiency, to CC compensate for a delta-8-unsaturated bases, to increase tolerance CC or resistance to soil salinity, ion stress or toxicity, drought, wet CC conditions, cold or frost and/or phytopathogenic microorganisms, or to alter size growth and flowering time. Cells, transgenic organisms or CC alter size growth and flowering time. Cells, transgenic organisms or CC plants containing the DNA sequence can be used to produce sphingolipids and capnoids with unsaturated sphingobases. The sphingolipids or capnoids can be used in cosmetics, pharmaceuticals and foods and as chemical raw materials. This sequence encodes the Arabidopsis thaliana sphingolipid desaturase sldl protein described in the method of the invention.
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Best Local Similarity
Matches 776; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention.

Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to identifying a stress cell has been exposed, comprising:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1350 BP; 325 A; 359 C; 274 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polynucleotide encoding delta-6 desaturase enzyme useful for producing transgenic plants and for producing antibodies specific to which is useful for screening cDNA expression libraries -
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P-PSDB; AAY71555.
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## ALIGNMENTS

LOCUS  AY103762  AY103762  AY103762  AY103762  AY103762  AY103762  VERSION  AY103762  AY103762  VERSION  AY103762.1 GI:21206840  KEYWORDS  SOURCE  Zea mays  CRGANISM  Zea mays  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Milopsida; Poales; Poaceae; PACCAD  Clade; Panicoideae; Andropogoneae; Zea.  AUTHORS  AUTHORS  ATHUR, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.  Maize Mapping Project/DuPont Consensus Sequences for Design of  Overgo Probes  Ungublished (2002)  AUTHORS  TITLE  JOURNAL  Missouri, Columbia, MO 65211, USA  If you are interested in getting corresponding physical clones, searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the							
AY103762  Zea mays PC0087385 mRNA sequence.  AY103762  AY103762.1 GI:21206840  HTC.  Zea mays  Z	COMMENT	AUTHORS TITLE JOURNAL	JOURNAL	AUTHORS	REFERENCE	VERSION KEYWORDS SOURCE ORGANISM	LOCUS DEFINITION ACCESSION
	If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the	Coe.E.H. Direct Submission Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA	Overgo Probes Unpublished (2002) 2 (bases 1 to 1764)	Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whiteltt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V. Maize Mapping Project/DuPont Consensus Sequences for Design of	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  1 (bases 1 to 1764)	AY103762.1 GI:21206840 HTC. Zea mays Zea mays	1764 bp mRNA linear PCO087385 mRNA sequence.

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/mol_type="mRNA"
/db_xref="MaizeDB:634923"
/db_xref="taxon:4577"
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CRB30001 IIa Fa D04 Cabernet Sauvignon Berry Stage I - CAB3 Vitis vinifera CDNA Clone CAB30001_IIa_Fa_D04 5', mRNA sequence.

CB972537

CB972537.1 GI:30295743
                                                                                                   Seq
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Vitis vinifera
                                                                                                                                   Tel: 530 754 6561
Fax: 530 754 6617
                                                                                                                                                                   UC Davis, Plant Pathology
One Shields Ave, Davis, CA
                                                                                                                                                                                                                                                   Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon' berries at various developmental stages
                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core e
                                                                                                                      Email: drcook@ucdavis.edu
                                                                                                                                                                                                     CAES Genome Facility
                                                                                                                                                                                                                 Contact: Douglas Cook,
                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                    Goes
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                                                                                    primer: ACGGTACCGGACATATGCC.
Location/Qualifiers
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/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCGTCTCTGAGTTTTCTAAGATGGGTTTGTTCAAGACACCAGGCAAAGGGGTCTACTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Cabernet Sauvignon Berry Stage I - CAB3" /note="Organ: Berry; Vector: pDNR; Site 1: Sfi1; Site 2: Sfi1; CAB3 is a CDNA library of Vitis Vinifera 'Cabernet Sauvignon' Clone 8 berries. Samples were collected after berry set from field-grown vines during stage I of berry growth, 17 days after full bloom. The average berry size
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="Berry stage I"
/lab_host="DH5alpha"
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/sex="Hermaphrodite"
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Pred. No. 2.8e-47;
0; Mismatches 246;
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Best Local Similarity
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An integrate
of the cotto
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Gossypium as
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GA_Ed00
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids

; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: rwing@clemson.edu
Total High Quality bases = 563
Total High Quality bases = 563
Seq primer: TAATACGACTCACTATAGGG
High quality sequence stop: 628.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, development, and evolution of the cotton fiber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 864 656 7288
Fax: 864 656 4293
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                                                                                                                                                                                                                                                                                           CAGGAGATTTATGGATCTCTATCAAGGGAAAAGTTTACGATATCTCCAAGTGGACTAAAG 162
                                                                                                                                                                                                                      AGCATCCCGGTGAGCTCCCCATTGTTAAGTTTTTGCCGGCCAAGATGTCACTGATGCGT
TTTCAAAAATGGGTCTTTTTGAAAAGAAGGAACACGGGACAGGCATTTTGCTTTGCATCA
                               TTTCTAAGATGGGTTTGTTCAAGACACCAGGCAAAGGGGTCTACTGCTCAATCTTTTCG
                                                                                      ACGTTCAAGATTACTCTGTCTCTGAGATGTCCAAGGACTACAGAAGGCTCGTCTCTGAGT
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                                                                                                                                                                                                                                                                                                                                                                      CTTCAATGGAAGAGCCAAAGAAGCACATTTCGCAAGCAGACCTTGCAAAGCATAAGCAAC
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_Ed0014D02r Gossypium arboreum 7-10 dpa fiber library
_sreum cDNA clone GA__Ed0014D02r, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cultivar="8400"
/db_xref="taxon:29729"
/clone="GA__Ed0014D02r"
/clssue_type="Fibers isolated from bolls harvested 7-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
    138 c    152 g    191 t
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Pred. No. 1.3e-42;
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QGC27M12.yg.abl QG_ABCDI
QGC27M12, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Department of Vegetable Crops, R.W.Michelmore University of California at Davis (UCD) Asmundson Hall, UCD, Davis, CA 95616, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
Contact: Alexander Kozik [R.W.Michelmore]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cichorieae; Lactuca.

1 (bases 1 to 721)

Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseber Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai Church, S., Jackson, L. and Bradford, K.

Church, S., Jackson, L. and Bradford, K.

Lettuce and Sunflower ESTs from the Compositae Genome Proje
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lactuca sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http:/
                                                                                                                                                                                                                                                                                                                                                                                                                        Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1-(530)-752-9659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1-(530)-742-1742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        //compgenomics.ucdavis.edu,
                                                                                                                                                                                                                                                                                                                                                                                       QGC27 row:
Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/TAG_LIB=QG_ABCDI lettuce salinas
                                                                                                                                                              /clone_lib="QG_ABCDI lettuce salinas"
/note="Vector: pBRcDNASfiAB; The library was constructed
from 10 different sources of RNA from a single genotype.
                                                                                                                                                                                                                                                                                    organism="Lactuca sativa"
/mol_type="mRNA"
/cultivar="Salinas"
                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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egle,J., Ellison
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                        Cramer, G.R. and Cushman, J.C. An expressed sequence tag datal Vitis vinifera var. Chardonnay
                                                                                                                                                                                                                                                             CB002504 674 bp mRNA linear EST 10-JAN-2003 VVB017E10_131866 An expressed sequence tag database for abiotic stressed Teaves of Vitis vinifera var. Chardonnay Vitis vinifera CDNA clone VVB017E10 5, mRNA sequence.
                                                                                                                                                                 Vitis vinifera
Vitis vinifera
                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
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TAG_SEQ=GCTTGACGGG"
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Pred. No. 6.6e-42;
0; Mismatches 224;
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No. 6.6e-42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BACKWARD: T7 21mer
Plate: 0 row: E co
Seq primer: T3 20mer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 775-784-1918
Fax: 775-784-1650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Department of Biochemistry University of Nevada MS200, Reno, NV 89557-0014,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FORWARD: T3 20mer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: jcushman@unr.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Cushman JC
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TCATTTCTCATCCAGTGTTTATGTGGGTCCTCCAAGTGGGAATGATTGGTTTGAGAAGCA
                                  TCACTTTGCTTCTAATGTTTACACTGGTTTGCCTAGCGGTAATGATTGGTTTCACCAGCA 1096
                                                                          GATGTTTGTTGTTCTGAGTTTCTCCTTTACTGGAATCCAGCATGTTCAATTCTGTTTGAA
                                                                                                              CATGIATTICACGICCIGITTAGCAGICGCCGGGITCCAACAITGGCAGITCAGCITGAA 1036
                                                                                                                                                     TGTGTTTTGGATTTGGTACCCTTTACTTGTTTCATGTCTGCCCAATTGGTGGGAAAGAGT
                                                                                                                                                                                                                                                                                                            CTGGACTTTTTATCCTGTGATGTGTTGCTAGATTAAATCTATTTGCTCAGTCCTGGTC
                                                                                                                                                                                                                                                                                                                                              CTGGACATTTTATCCTGCATTGTTAAGCGTTAGGCTCTATCTTTTATTCTGTCTTTTAA 856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="juvenile and adult"
/clone lib="An expressed sequence tag database for abiotic stressed leaves of Vitis vinifers war. Chardonnay"
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1: EcoRI; Site 2: XhoI; Library construction was performed according to Stratagene's recommended protocol for the Lambda UniZapXR vector and cDNA synthesis kit."
a 183 c 125 g 130 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Vitis vinifera"
/mol_type="mRNA"
/db_xref="taxon:29760"
/clone="VVB017E10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="leaf"
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Pred. No. 6.9e-41;
0; Mismatches 232;
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Contact: Cushman JC
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EST
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Tel: 775-784-1918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Department of Biochemistry University of Nevada
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GGAAGTTGGACCATAACACCCATCACTTTGCCTGTAATAGCGCCAATCTGGATCCTGATA
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                   /clone_lib="An expressed sequence tag database for abiotic stressed leaves of Vitis vinifera var. Chardonnay"
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-, Site 1:
ECORI; Site 2: XhoI; Library construction was performed according to Stratagene's recommended protocol for the Lambda Uni-ZapXR vector and cDNA synthesis kit."

182 c 125 g 130 t
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/clone="VVB016E06"
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/dev_stage="juvenile and adult"
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                                                                                                                                           Unpublished
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
                                                                                                                                                                                                                                                               Cichorieae; Lactuca.

1 (bases 1 to 696)

Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Ellison
, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z.,
Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
             Plate: QGC18 row: P column
Location/Qualifiers
                                                                   Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
belongs to contig QG_CA_Contig2376, see http://cgpdb.uc
                                                                                                               Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
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QGC18P18.yg.ab1 QG_ABCDI
QGC18P18, mRNA sequence.
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TAG_TISUSUB-chemical induction
TAG_TGTAGCCGGGG"

87 a 148 c 153 g 208 t
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/note="Vector: pBRcDNASfiAB; The library was constructed
from 10 different sources of RNA from a single genotype
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/cultivar="Salinas"
/db_xref="taxon:4236"
/clone="QGC18P18"
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Pred. No. 2.6e-39;
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                    610
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Complex Carbohydrate Research Center
University of Georgia
220 Riverbend Road, Athens, GA 30602
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available at: www.medicago.com
Seq primer: SKmod (CTA 9AA CTA
Location/Qualifiers
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EST508817 HOGA Medicago truncatula cDNA clone pHOGA-15p24 5' end,
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TTGCATGGTGGAAGTTGGACCATAACACCCATCACTTTGCCTGTAATAGCGCCAATCTGG
                                                                            ACCGTAAGCTTAATCGTCTTTTTCAAATCATTGCAGGAAATGTGATTGCTGGTGTTAGTG
                                                                                                         TGCTATGGATGCAAAGTACTTATATTGGTCATGATTCTGGTCATTATGAGGTTATGTCGA
                                                                                                                                     TGCTATGGCTCCAGAGTGGTTGGGTGGGGCATGATTCTTGTCACTACCAAGTTATGCCTA
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                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                  /clone_lib="MOGA"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in SOLR cells."

a 142 c 169 g 299 t
                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="pHOGA-15924"
/tissue_type="3 day old seedling roots"
/dev_stage="24 hours after treatment in
with 0.5 mg/ml oligogalacturonides (DP 6
presence of 100 ug/ml Gentamicin"
/lab_host="XLOLR"
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/cultivar="A17"
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Utterback,T., Cho,J. and Fraser,C.M.
ESTs from roots of Medicago truncatula treated with
                                                                        TIGR sequence name: MTMDX76TK
More information is available &
Seq primer: SKmod (CTA gAA CTA
Location/Qualifiers
                                                                                                                                                                                                                                                 Complex Carbohydrate Research
University of Georgia
220 Riverbend Road, Athens, GF
                                                                                                                                                                                                                                                                                                                               Unpublished
Contact: Michael G. Hahn
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid
; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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                                                                                                                                                                              Email: hahn@ccrc.uga.edu
                                                                                                                                                                                                          Fax: 706-542-4412
                                                                                                                                                                                                                               Tel: 706-542-4457
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/organism="Medicago truncatula"
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CD005403

VVB047G10 325360 An expressed sequence tag database for abiotic stressed Teaves of Vitis vinifera var. Chardonnay Vitis vinifera
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                                                                                                                                                                                                                                                   TTGTATGACTGGTATAAGTATTGCTTGGTGGAAATGGACTCATAATGCTCATCATATTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in SOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="HOGA-29M7"
/tissue_type="3 day old seedling roots"
/tissue_type="3 hours after treatment in the dark at
/dev_stage="24 hours after treatment in the dark at
with 0.5 mg/ml oligogalacturonides (DP 6-20) in the
presence of 100 ug/ml Gentamicin"
/lab_host="XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         db_xref="taxon:3880"
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Pred. No. 4.2e-39;
0; Mismatches 226;
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Tel: 775-784-1918
Fax: 775-784-1650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 652)
Cramer, G.R. and Cushman, J.C.
An expressed sequence tag data
Vitis vinifera var. Chardonnay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BACKWARD: T7 21mer (backward)
Plate: 0 row: G column: 10
Seq primer: T3 20mer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: jcushman@unr.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Department of Biochemistry University of Nevada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Cushman JC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core e
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                                                                                                                                                                                                                                                          GCCATATCCCCCAAAATTTTTCAACTCCCTTACATCATACTATCACAACTGCAAAATGACC
                                                                             TTAAGCGTTAGGCTCTATCTTTTATTCTGTCTTTTAAGGTGGTGTTTTTCCAACAACAAA 878
                                                                                                                                                               TATGATCGCGCTGCCAGGTTTTTTGTTAGCTTTCAGCACTGGACATTTTATCCTGCATTG
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                                            TGTGTTGCTAGATTAAATCTATTTGCTCAGTCCTGGTCTTTGTTGTTGTC---CAAGAGG
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Location/Qualifiers
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/clone lib="An expressed sequence tag database for abiotic stressed leaves of Vitis vinifera var. Chardonnay"
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1: EcoRI; Site 2: KhoI; Library construction was performed according to Stratagene's recommended protocol for the Lambda UniZapXR vector and cDNA synthesis kit."
a 172 c 124 g 126 t
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/db_xref="taxon:29760"
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/mol_type="mRNA"
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An integrated analysis of the genetics, development, and evolution of the cotton fiber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BF268631 957 bp mRNA linear EST 07-MAR-200: GA Eb0002G08f Gossypium arboreum 7-10 dpa fiber library Gossypium arboreum cDNA clone GA Eb0002G08f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                           Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
High quality sequence stop: 714.
                                                                                                                                                                                                                                                                                                                                                                                                              Clemson University Genomics
Clemson University
100 Jordan Hall, Clemson, SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid; eurosids II, Malvales; Malvaceae; Malvoideae; Gossypium.

1 (bases 1 to 957)
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 AGCAACCAGGAGATTTATGGATCTCTATCAAGGGAAAAGTTTACGATATCTCCAAGTGGA
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                                                                                                                                                    258
                                                                                   Conservative
                                                                                                                                                                                                                                                                         /organism="Gossypium
/mol_type="mRNA"
/strain="AKA"
                                                                                                                                               /lab_host="E. coli"
/Clone_lib="Gossypium arboreum"7-10 dpa fiber library"
/note="Wector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
179 c 233 g 287 t
                                                                                                                                                                                                                 /db_xref="taxon:29729"
/clone="GA_Eb0002G08f"
/tissue_type="Fibers isolated from bolls harvested 7-10
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                                                                                                                         Contact: Michael A. Grusak
                                                                                                                                     Unpublished
                                                                                                                                                                                                      Medicago
                                                                                                                                                                                                                                                                       Medicago truncatula (barrel medic)
                            в398266е
                                       Email: mgrusak@bcm.tmc.edu
TIGR sequence name: More information is
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Medicago truncatula
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid;
eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                 USDA/ARS Children's Nutrition Research Center Baylor College of Medicine 1100 Bates Street, Houston, TX 77030-2600, USJTel: 713-798-7044
                                                                                                                                                                                                                                                                                                                         Grusak,M.A., Samac,D.A., Town,C.D., Van Aken,S., Utterback,T., J. and Fraser,C.M.
                                                                                                                                                                                                                                                                                             ESTs from developing reproductive tissues of Medicago
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 TTTGCCAGAAGCATAATTTGTCCTATGAAAACTGCTACCATGTGGGAGGCCAATAAAATGG
                                                                          ATCTGTTTCCAAGGATGCCTAAGTGCCATTTCAGGAAAATCTCACCCATTGTGAACAAAC
                                                                                                                 TCACTTGTTCAACATGGATGGATTGGTTCTTTGGTGGTTTGCAGTTTCAGCTTGAACATC
                                                                                                                                                 TAACAGCTTCTGCTTGGTGGGATTGGTTTCATGGTGGCCTGCACTTTCAGATTGAGCATC
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                                                                                                                                                                                                                                                                                                                                             CTCTACTCCTTTCTCGCCTACCCAATTGGCCTGAAAGGGTCATGTATTTCACGTCCTGTT
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                                       TTGTTGTTTGTTCCATCCAACATCTTCAATTCTGTTTGAACCATTTCGCTGCAAACGTGT
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B
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/dev_stage="Immature seeds, 1
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/clone="pGESD10F10"
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Gossypium hirsutum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid;

jeurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
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AI729087
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: burr@bnlux1.bnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 516-344-3396
Fax: 516-344-3407
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Upton, NY 11973, USA
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                                                                                                                 CAAAGGTCAAGAAATTTTTGGGATACTTGTTTTTTGGACATGGTATCCATTACTTGTCTC
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                                       TCTCTTACCTAATTGGTACGAAAGAGTAATGTTTGTGGTTGTAAGTTTTTGCTGTGACCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:3635"
/tissue_type="immature fiber"
/dev_stage="Six days post anthesis"
/lab_host="XL1-Blue"
/clone_lib="Six-day Cotton fiber"
/note="Wector: pBluescript II KS+"
a 116 c 137 g 209 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Gossypium hirsutum"
/mol_type="mRNA"
/cultivar="Acala_Maxxa"
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                                                                                                                                                                                                                                                                                                                                           Score 263; DB 9; I
Pred. No. 3.4e-36;
0; Mismatches 215;
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                                 Query Match
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34 TCTGTTGCACTTCAATGGAAGAGCCAAAGAAGCACATTTCGCAAGCAGACCTTGCAAAGC
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Gossypium hirsutum
Gossypium hirsutum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid;
eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
                                                                                                                                                                                                                                                                                                                                                                           Biology Department
Brookhaven National Laboratory
Upton, NY 11973, USA
Tel: 516-344-3396
Fax: 516-344-3407
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1 (bases 1 to 668)
Blewitt,M., Matz,E.C., Davy,D.F. and
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BNLGHi13080 Six-day
to (AF007561) delta
                                                                                                                                                                                                                                                                                                                                           Email: burr@bnlux1.bnl.gov
Seq primer: T3 Primer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
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                                                                                                                            184
                                     Conservative
                                                                                                                       /tissue_type="immature fiber"
/dev stage="Xix days post anthesis"
/lab_host="XI1-Blue"
/clone_lib="Xix-day Cotton fiber"
/note="Vector: pBluescript II KS+"
134 c 131 g 219 t
                                                                                                                                                                                                                                 /mol_type="mRNA"
/cultivar="Acala Maxxa"
/db_xref="taxon:3635"
                                                                                                                                                                                                                                                                              organism="Gossypium hirsutum'
                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                            . 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GI:5048158
                                                    17.6%;
65.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       668 bp mRNA linear EST 11-0
Cotton fiber Gossypium hirsutum cDNA 5'
6-desaturase [Borago officinalis], mRNA
                               Score 259.4; I
Pred. No. 1.4e-
0; Mismatches
                                   0
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                                                    259.4; DB 9;
No. 1.4e-35;
                                   196;
                                                                   Length
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                                 Gaps
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                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticum.

1 (bases 1 to 744)

Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han p.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T., Rausch,C.J., Seaton,C.L., Tong,J.C. and Miller,R., Nguyen,H.T., The structure and function of the expressed portion of the wheat genomes - Normalized shoot cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BQ281359 744 bp mRNA linear EST 13-MAY-2002 MHE3020_D06_H12ZS Wheat unstressed seedling shoot normalized cDNA library Triticum aestivum cDNA clone WHE3020_D06_H12, mRNA
                             Sequences have been trimmed quality sequence with phred Seq primer: SK primer.
                                                                                                                                                          Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
                                                                                                                       800 Buchanan Street,
Tel: 5105595773
                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                              Triticum aestivum
                                                                                     Email: oandersn@pw.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                Triticum aestivum (bread wheat)
                                                                                                      Fax: 5105595818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGACTAAAGAGCATCCCGGTGGTGAGCTCCCCATTGTTAAGTTTTTGCCGGCCAAGATGTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCTCTGAGTTTTCTAAGATGGGTTTGTTCAAGACACCAGGCAAAGGGGTCTACTGCTCAA 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGGGTACTACGTTCAAGATTACTCTGTCTCTGAGATGTCCAAGGACTACAGAAGGCTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AACTTCTTACAGGGAATTGTCTTGCTGGGATCA
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                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GI:20548798
                                                                                                                                           Albany,
                                                    score less than :
                                                                                                                                           CA 94710, USA
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                                                    : sequence
20
                                                                                                                                                                             Service,
                                                                    and
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Query Match
Best Local Similarity
Matches 445; Conserva
                                               1052 TGTTTACACTGGTTTGCCTAGCGGTAATGATTGGTTTCACCAGCAGACAAAGGGCACGCT 1111
                                                                                                                                                                                                                 426
                                                                                                                                                                                                                                                                   932
                                                                                                                                                                                                                                                                                                                           366
                                                                                                                                                                                                                                                                                                                                                                     872 CAACAAAAGGGTATACAAGAGAAGTCAGGAAATTTTAGGCTATGCAGCTTTCTTGACTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              512 GGTGGGGCATGATTCTTGTCACTACCAAGTTATGCCTAACCGTAAGCTTAATCGTCTTTT
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                                                                                                                                        CTGTTTAGCAGTCGCCGGGTTCCAACATTGGCAGTTCAGCTTGAATCACTTTTGCTTCTAA 1051
                                                                                                                                                                                                                 GTACCCCTTGCTGGTCTTGCCTGCCGAATTGGTGGGAGAGGGTTGCTTTTGTGCTTTGC
                                                                                                                                                                                                                                                                GTATTCTCTACTCCTTTCTCGCCTACCCAATTGGCCTGAAAGGGTCATGTATTTCACGTC
                                                                                                                                                                                                                                                                                                                           GCAAAAGAAGGTGCGGCAGCGTTGGCTGGAGATCGCCGGAGTTGCAGCGTTCTGGGTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                               GGTGATGGGATTTGCAAGGATAAATCTTCTTGTGCAGTC---AATCGTGTTCCTGATCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCAGGTGGTCTCCGGGAACTGCCTCACCGGCCTCGGCATCGCCTGGTGGAAGTTCAACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATTGGCCATGACTCCGGCCACCACCAAATCACCAGGCACCCCGCGCTCAACCGCCTCCT
TGTGTATGTTGGGCCACCAAAGGGGAACGACTTGGTTTGAGAGGCCAAACAGCGGGCACACT
                                                                                                       AAGCTTTGTGATCACGGGGATTCAGCATGTTCAGTTCTGCCTGAACCACTTCTCATCCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: Lambda Uni-ZAP XR, excised phagemid phluescript SK; Site 1: EcoRI; Site 2: XhoI; Seeds were surface-sterilized, germinated and grown aseptically in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Roots were harvested. The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. The cDNA clones were in vivo excised to give pBluescript phagemids before normalization was carried out. The mass excision of phagemid library and normalization were done in HT Nguyen lab by D. Zhang at Texas Tech University. Normalization protocol used was that of Soares'. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
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cDNA_library"
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/clone="MHB3020 D06 H12"
/tissue_type="Etiolated shoot"
/dev_stage="Five day old seedling"
/lab_host="E. coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/cultivar="Chinese Spring"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Triticum aestivum"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 257.4; DB 13;
Pred. No. 3e-35;
0; Mismatches 291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      291; Indels
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                         1232 CAAACTTTGCCAGAAGCAT 1250
                                                                                     666 ACACCATTTGTTTCCTCGCCTGCCTCGCTGCCACTATAGGATGGTCGCGCCGATTGTGCG
                                                                                                                                                                          606 TGATATCAAGTGCTCCCCGTGGATGGATTGGTTCCATGGTGGTCTGCAGTTTCCAGGTTGA
726 TGACCTTTGCAAGAAGCAT
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Search completed: December 31, 2003, 23:59:12 Job time : 2246.82 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*
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Query Match 38.0%;
Best Local Similarity 62.8%;
Matches 885; Conservative
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28 48.8 3.3 1843 4 US-09-227-613-7 30 48.8 3.3 1843 4 US-09-227-613-7 31 48.8 3.3 1843 4 US-09-227-613-7 31 48.8 3.3 2257 4 US-09-227-613-8 32 48.8 3.3 2257 4 US-09-227-613-8 43.4 3.3 7218 1 US-08-232-463-14 43.6 3.0 1717 4 US-09-702-705-35-35 42 2.9 347 4 US-09-702-705-35-35 36 42 2.9 347 4 US-09-736-457-355 36 42 2.9 347 4 US-09-736-457-355 37 38.2 2.6 295 4 US-09-736-457-355 38 35 2.4 1677 4 US-09-131-294A-6637 39 34.8 2.4 4350 4 US-09-13-294A-6637 39 34.8 2.4 4350 4 US-09-25-593-37 40 34.2 2.3 1884 1 US-08-307-382-3 41 34.2 2.3 1884 1 US-08-307-382-3 42 34.2 2.3 1884 1 US-08-478-727-3 43 34.2 2.3 1884 1 US-08-478-727-3 44 34.2 2.3 1884 1 US-08-478-936-3 45 34.2 2.3 1884 1 US-08-478-936-3 46 34.2 2.3 1884 1 US-08-478-936-3 47 34.2 2.3 1884 1 US-08-478-936-3 48 34.2 2.3 1884 1 US-08-478-936-3	48.8 3.3 1843 4 US-09 48.8 3.3 1843 4 US-09 48.8 3.3 2257 4 US-09 48.8 3.3 2257 4 US-09 48.4 3.3 7218 1 US-08 48.6 2.9 347 4 US-09 38.2 2.6 295 4 US-09 38.2 2.6 295 4 US-09 38.2 2.6 1677 4 US-09 38.2 2.6 1884 1 US-08 38.2 2.3 1884 1 US-08 38.2 2.3 1884 1 US-08
3.3 1843 4 US-09 3.3 1843 4 US-09 3.3 2257 4 US-09 3.3 2257 4 US-09 3.3 7218 1 US-09 3.3 7218 1 US-09 2.9 347 4 US-09 2.6 29 347 4 US-09 2.4 4350 4 US-09 2.4 4350 4 US-09 2.3 1884 1 US-08	3.3 1843 4 US-09-127-613-7 Sequence 3.3 1843 4 US-09-27-613-7 Sequence 3.3 2257 4 US-09-27-613-8 Sequence 3.3 2257 4 US-09-28-88-2 Sequence 3.3 2257 4 US-09-28-35-5 Sequence 2.9 347 4 US-09-702-705-35-5 Sequence 2.9 347 4 US-09-713-794-75-35-5 Sequence 2.9 347 4 US-09-713-794-75-74 Sequence 2.9 347 4 US-09-313-294A-6637 Sequence 2.0 1884 1 US-08-36-779-3 Sequence 2.1 1884 1 US-08-36-779-3 Sequence 2.3 1884 1 US-08-36-779-3 Sequence 2.3 1884 1 US-08-478-727-3 Sequence 2.3 1884 1 US-08-478-727-3 Sequence 2.3 1884 1 US-08-478-727-3 Sequence 2.3 1884 1 US-08-478-728-3 Sequence 2.3 1884 1 US-08-789-936-3 Sequence 2.3 1884 1 US-08-789-934-254-3 Sequence
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## ALIGNMENTS

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SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/831,570
FILING DATE: 09-APR-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGILO, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10545
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEPHONE: (516) 742-4343
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1684 base pairs
US-08-831-570-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 1, Applic
; Patent No. 5959175
; GENERAL INFORMATI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Thomas, Terry L.
APPLICANT: Nunberg, Andrew N.
APPLICANT: Beremand, Phillip D.
TITLE OF INVENTION: A SUMPLOWER ALBUMIN 5' REGULATORY REGION
TITLE OF INVENTION: FOR THE MODIFICATION OF PLANT SEED LIPID
TITLE OF INVENTION: COMPOSITION
                                                             MOLECULE TYPE: FEATURE:
                 NAME/KEY:
                                                                                                    LENGTH: 1684 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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Score 559.4; DB 2; Pred. No. 1.6e-164; 0; Mismatches 522;

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GATTGGTTTCACCAGCAGACAAAGGGCACGCTCAACATAACAGCTTCTGCTTGGTGGGAT 1139
                                                                                                                                        TGGCAGTTCAGCTTGAATCACTTTGCTTCTAATGTTTACACTGGTTTGCCTAGCGGTAAT
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US-08-831-575-1
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                                                                                                                                                                                         TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1684 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
Query Match 38.0%;
Best Local Similarity 62.8%;
Matches 885; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Thomas, Terry L.

APPLICANT: Li, Zhongsen
TITLE OF INVENTION: AN OLEOSIN 5'REGULATORY REGION FOR THE
TITLE OF INVENTION: MODIFICATION OF PLANT SEED LIPID COMPOSITION
                                                                                                                                                       TOPOLOGY: 1
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,
REFERENCE/DOCKET NUMBER:
                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (516) 742-4343
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 400 Garden
CITY: Garden City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/831,575 FILING DATE: 09-APR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
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400 Garden City Plaza
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43..1387
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   Score 559.4; DB 2;
Pred. No. 1.6e-164;
0; Mismatches 522;
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Query Match Best Local Similarity

38.0%;

Score 559.4; DB 1; Pred. No. 1.6e-164;

Length 1685;

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; TOPOLOGY: 1; MOLECULE TYPE: US-08-366-779-4
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US-08-366-779-4
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                                            TELEPHONE: (516) 742-4343
TELEPAX: (516) 742-4366
TELEFAX: (516) 742-4366
TELEFAX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1685 base pairs
TYPE: nucleic acid
STEANDENESS: both
                                                                                                                                                                                                             Sequence 4, Application US/08366779 Patent No. 5614393
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APPLICANT: Thomas
APPLICANT: Reddy,
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                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 83
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
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CORRESPONDENCE ADDRESS:
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CITY: Garden Cit
STATE: New York
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Freyssinet, Georges L.
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                                                                                   GTTCAGTTCTCCTTGAACCACTTCTCTTCAAGTGTTTATGTTGGAAAGCCTAAAGGGAAT
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                                                                                                                                                                            APPLICATION NUMBER: US/08/789,931
FILING DATE: 28-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/366,779
FILING DATE: 30-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGESTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 8383ZYX
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1742-4343
                                                                                                                        TELEFAX: (516) 742-43
TELEX: 230 901 SANS U
INFORMATION FOR SEQ ID NO:
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LENGTH: 1685 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: DEPODUCTION OF GAMMA LINO
TITLE OF INVENTION: DELTA 6-DESATURASE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
                                                                                                     SEQUENCE CHARACTERISTICS:
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STATE: New York
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                                                                                                                                                                     GAAATTTTAGGCTATGCAGCTTTCTTGACTTGGTATTCTCTACTCCTTTCTCGCCTACCC
 GTTCAGTTCTCCTTGAACCACTTCTCTTCAAGTGTTTATGTTGGAAAGCCCTAAAGGGAAT
                      TGGCAGTTCAGCTTGAATCACTTTGCTTCTAATGTTTACACTGGTTTGCCTAGCGGTAAT 1079
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                                                                       AATTGGGGTGAAAGAATTATGTTTGTTATTGCAAGTTTATCAGTGACTGGAATGCAACAA 1015
                                                                                                  AATTGGCCTGAAAGGGTCATGTATTTCACGTCCTGTTTAGCAGTCGCCGGGTTCCAACAT 1019
                                                                                                                                             GAACTCTTGGGATGCCTAGTGTTCTCGATTTGGTACCCGTTGCTTGTTTCTTTGCCT
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Pred. No. 1.6e-164;
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                                                 Sequence 4, Application Patent No. 6355861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (516) 742-4343
                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSZE: SCully, Scott, Murj
STREET: 400 Garden City Plaza
CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                     NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 83
                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1316
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APPLICANT: Thomas, Terry L.

TITLE OF INVENTION: PRODUCTION OF GAMMA
TITLE OF INVENTION: DELTA 6-DESATURASE
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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Best Local Similarity Matches 885; Conserv
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                                                                                    TGGCAGTTCAGCTTGAATCACTTTGCTTCTAATGTTTTACACTGGTTTTGCCTAGCGGTAAT
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                                                             GTTCAGTTCTCCTTGAACCACTTCTCTTCAAGTGTTTATGTTGGAAAGCCTAAAGGGAAT
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US-08-934-254-26
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TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 1702 base pairs
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Patent No. 6355861
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APPLICANT: Thomas
                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION UNMER: 19,827
REFERENCE/DOCKET NUMBER: 8383
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Thomas, TO TITLE OF INVENTION: IT TITLE OF INVENTION: IT TITLE OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,254
                    FEATURE:
NAME/KEY:
                                                                                                  MOLECULE TYPE:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
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STREET: 400 Garden City Plaza
CITY: Garden City
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; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; NAME/KEY: misc feature
; NAME/KEY: unsure
; NAME/KEY: unsure
; LOCATION: 256
; OTHER INFORMATION: a, t, c, g, or c
US-09-313-294A-1966
RESULT 8
US-09-313-294A-3256
; Sequence 3256, Application
; Patent No. 6476212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lalgudi, Raghunath APPLICANT: Ito, Laura Y.
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                                                                                                                                   TGTTTCCCCNCCTACCTAGGTGCCACCTCCGTAA
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                      US/09313294A
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Pred. No. 1.8e-28;
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APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
APPLICANT: Sherman, Bradley K.
TITLE OP INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999.05-14
                                                                                                                                                                                                                                                                                            1000 CAGTCGCCGGGTTCCAACATTGGCAGTTCAGCTTGAATCACCTTTGCTTCTAATGTTTACA 1059
                                                                                                                                                                                                                                                                                                                                                                                                             940 TACTCCTTTCTCGCCTACCCAATTGGCCTGAAAGGGTCATGTATTTCACGTCCTGTTTAG
                                                                                                                                                          CTGGTTTGCCTAGCGGTAATGATTGGTTTCACCAGCAGACAAAGGGCACGCTCAACATAA 1119
                                                CAGCTTCTGCTTGGTGGGATTGGTTTCATGGTGGCCTGCACTTTCAGATTGAGCATCATC 1179
                                                                                                                                                                                                                                                                                                                                                                         TGCTGGTGGCTTCCCTGCCGAATTGGTGGGAGAGGGTCGCGTTTGTGCTTTTCAGCTTCA
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TGTGCTCTCCTTGGATGGATTGGTTCCACGGTGGCCTGCAGTTCCAGATTGAGCACCATC
                                                                                                                          TCGGGCCACCCAAGGGCAATGACTGGTTTGAGAAGCAGACGCCAGGCACGCTCGACATCC
                                                                                                                                                                                                                                                     CCATCTGCGGGATTCAGCACGTCCAATTCTGCCTGAACCACTTCTCGTCCGACGTGTATG
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RESULT 9
US-08-834-655-1
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LENGTH: 266
; TYPE: DNA
ORGANISM: Zea mays
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08834655 Patent No. 5968809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 162; Conserv
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APPLICANT:
APPLICANT:
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APPLICANT: KNUTZOI
APPLICANT: MURKER
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APPLICANT: Sherman, Bradley K.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No.
NAME/KEY: unsure
LOCATION: 262
                                                              ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                      TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                APPLICANT:
SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                            STREET: Zou ______
           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin policy
                                                                                                                           COUNTRY:
                                                                                                                                                                                                 ADDRESSEE:
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                                                                                                                                                                                3: RAE-VENTER LAW GROUP, P.C. 260 SHERIDAN AVENUE, P.O. BOX 60039
                                                                                                                             USA
                                                                                                                                                                                                                                                                                          THURMOND, JENNIFER CHAUDHARY, SUNITA
                                                                                                                                                                                                                                                                                                                            MURKERJI, PRADIP
HUANG, YUNG-SHENG
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ilarity 62.5%;
Conservative
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Pred. No. 2.2e-19;
0; Mismatches 96;
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                 Version
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TELEX: N/A
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
SEQUENCE HARACTERISTICS:
SEQUENCE HARACTERISTICS:
SEQUENCE HARACTERISTICS:
SEQUENCE HARACTERISTICS:
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SEQUENCE HARACTERIS
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GENERAL INFORMATION:
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Best Local Similarity
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                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,033.
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY AC NUMBER OF SEQUENCES: 26
CORRESPONDENCE TADDRESS:
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                              COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                    STATE:
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FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                     CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: LIMBACH AND LIMBACH, L.L.P STREET: 2001 FERRY BUILDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
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REFERENCE/DOCKET NUMBER: CGNE.124.00US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          518 ACCCTCGCCAACGTGCTCTCGGCTGCGCTTTTGGGTCTGTTCTGGCAGCAGTGCGGATGG
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: HUANG, YUNG-SHENG
: THURMOND, JENNIFER
: CHAUDHARY, SUNITA
                                                                                                                                                                                                                                                                                                                   USA
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Pred. No. 4.8e-08;
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SEQUENCE CHARACTERISTICS:
LENGTH: 1617 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEPAX: (415) 433-8716
                                                   SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                 ADDRESSEE: LIMBACH AND LIMBACH L.L.P. STREET: 2001 FERRY BUILDING CITY: SAN FRANCISCO
                 FILING DATE:
CLASSIFICATION:
                                                                                                                                                                               COUNTRY: U
                                                                                                                                                                                                                       STATE:
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MURKERJI, PRADIP
HUANG, YUNG-SHENG
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                                                                                     Release #1.0, Version #1.30
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
SEQUENCE 1617 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1
Patent No.
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Best Local Similarity
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REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,
                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                             APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
STREET: 2001 FERRY BUILDING
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                                                APPLICATION NUMBER: FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                           CITY: SAN FRANCISCO
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TOPOLOGY: lir
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                                                                                     US/09/363,526
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Pred. No. 4.8e-08;
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                                                                                                                       #1.30
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: KNUTZON, Debbie
TITLE OF INVENTION: POLYUNGATURATED FATTY ACIDS
FILE REFERENCE: MOCO.156.00US
CURRENT APPLICATION NUMBER: US/09/330,235
CURRENT FILING DATE: 1999-06-10
PRIOR APPLICATION NUMBER: 60/089,043
PRIOR FILING DATE: 1998-06-12
                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.0
SEQ ID NO 17
LENGTH: 1617
                                                                                                                                                                                      Matches 130;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Mortierella alpina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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TOPOLOGY: 1ir
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STRANDEDNESS: single
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CAAATCATTGCAGGAAATGTGATTGCTGGTGTTAGTGTTGCATGGAGGTGGAAGTTGGACCAT 632
                                                                                 GTGGGGCATGATTCTTGTCACTACCAAGTTATGCCTAACCGTAAGCTTAATCGTCTTTTT
                                                                                                                    ACCCTCGCCAACGTGCTCTCGGCTGCGCTTTTGGGTCTGTTCTGGCAGCAGCAGTGCGGATGG
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                                                  TTGGCTCACGACTTTTTGCATCACCAGGTCTTCCAGGACCGTTTCTGGGGTGATCTTTTC
                                                                                                                                                   ACCTGGGCTCATCTTTGCTCTGGTTTGCTAATGGGTATGCTATGGCTCCAGAGTGGTTGG
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52.2%;
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Pred. No. 4.8e-08;
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Pred. No. 4.8e-08;
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RESULT 15 US-09-227-613-37

GENERAL INFORMATION:

APPLICANT: MUKERJI, Pradip APPLICANT: LEONARD, Amanda E. APPLICANT: HUANG, Yung-Sheng

TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF FILE REFERENCE: 6295.US.P1

CURRENT APPLICATION NUMBER: US/09/227,613A

Sequence 37, Application US/09227613A Patent No. 6432684

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NAME/KEY: misc_feature

COTHER INFORMATION: (5)

NAME/KEY: misc_feature

COTHER INFORMATION: (6)

COTHER INFORMATION: m = a or c at

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Best Local Similarity
Matches 100; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence 38, Application US/09439261
Patent No. 6428990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR AFFILING DATE: 1998-04-10 PRIOR APPLICATION NUMBER: US (PRIOR APPLICATION DATE: 1999-01-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/439,261
CURRENT FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: US 08/833,610
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: PCT/US98/07422
PRIOR FILING DATE: 1998-04-10
PRIOR APPLICATION NUMBER: PCT/US98/07422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 1
NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Huang, Yung-Sheng
TITLE OF INVENTION: HUMAN DESATURASE GENE
FILE REFERENCE: 6295.US.P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Abbott Laboratories APPLICANT: Mukerji, Pardip APPLICANT: Leonard, Amanda E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 449
                                                                                                         1140 TGGTTTCATGGTGGCCTGCACTTTCAGATTGAGCATCATCTGTTTTCCAAGGATGCCTAAG 1199
                                      1200 TGCCATTTCAGGAAAATCTCACCCATTGTGAACAAACTTTGCCAGAAGCAT 1250
                                                                                                                                                                                                     1080 GATTGGTTTCACCAGCAGACAAAGGGCACGCTCAACATAACAGCTTCTGCTTGGTGGGAT 1139
                                                                                                                                                                 167 GACTGGGTTTCCACCCAGCTCCAGGCCACATGCAATGTCCACAAGTCTGCCTTCAATGAC 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               638 GGCGCCTTCTTGGGAGGTGTCTGCCAGGGCTTCTCGTCCTCGTGGTGGAAGGACAAGCAC 697
CACAATTACCACAAAGTGGCTCCCCTGGTGCAGTCCTTGTGTGCCAAGCAT 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FastSEQ for Windows Version 4.0
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                                                                               TGGTTCAGTGGACACCTCAACTTCCAGATTGAGCACCATCTTTTTCCCACGATGCCTCGA
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Pred. No. 5.4e-08;
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OM nucleic - nucleic search, using sw model
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                                                                                                                                                                                                                                                                                                                          No.
        1121098
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Match
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
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Cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
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_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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US-09-770-149-494
US-09-770-444-39
US-09-770-444-3260
US-09-9878-574-3260
US-09-924-035A-370
US-09-923-876-5116
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US-10-029-756-26
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13877.414 Million cell updates/sec
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                                                        Sequence 4, Appli
Sequence 558, App
Sequence 26, Appl
Sequence 39, Appl
Sequence 39, Appl
Sequence 370, App
Sequence 370, App
Sequence 27824, A
Sequence 5116, Ap
Sequence 5116, Ap
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                                         Sequence
                    3, Appli
37, Appl
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2710 473 363 1335 1363 1366 11474 11686 2257 2257 2253 12413 1413 1413 1413 1413 1344 405 1336 376 376 3778 3788	864 1928 1972 4213 2710
13 13 13 13 13 13 13 13 13 13 13 13 13 1	15 15 13
US-10-400-902-4 US-10-191-513A-1 US-10-191-513A-1 US-10-191-513A-1 US-10-19-806-232 US-99-967-477B-7 US-10-191-513A-6 US-10-191-513A-7 US-10-191-513A-7 US-10-191-513A-7 US-10-191-513A-7 US-10-191-513A-7 US-10-98-78-574-11074 US-09-878-574-11074 US-09-878-574-119 US-10-060-793-27 US-10-060-793-27 US-10-54-534B-34 US-09-878-574-5819 US-10-340-779A-2 US-10-340-779A-2 US-10-340-779A-2 US-09-878-574-13904 US-09-878-574-13904 US-09-981-876-63 US-09-981-876-63 US-09-981-876-63 US-09-981-876-63 US-09-981-876-63 US-09-981-876-63 US-09-981-876-63	US-10-191-513A-13 US-10-262-617-4 US-09-822-649A-485 US-10-133-937-7 US-09-911-781-4
	Sequence 13, Appl Sequence 4, Appli Sequence 485, Appli Sequence 7, Appli Sequence 4, Appli

## ALIGNMENTS

RESULT 1 US-10-029-756-4

Sequence 4, Application US/10029756
Publication No. US20020108147A1
GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
TITLE OF INVENTION: DETA 6-DESATURASE
NUMBER OF SEQUENCES: 27
CORESSONDENCE ADDRESS:
ADDRESSES: Scully, Scott, Murphy & Presser
STREET: 400 Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COUNTRY: United States
ZIP: 11530
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
PRIOR APPLICATION NUMBER: US/10/029,756
FILING DATE: 21-Dec-2001
CLASSIFICATION NUMBER: 08/934,254
FILING DATE: CUNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/934,254
REFERENCE/DOCKET NUMBER: 8383ZYXWVU
TELEPAX: (516) 742-4343
TELEFAX: (516) 742-4343
TELEFAX: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 23 901 SANS UR
INFORMATION FOR SEQUENCE CHARACTERISTICS:

LENGTH: 1685 base

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Best Local Similarity
Matches 885; Conserv
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STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID
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AATTGGCCTGAAAGGGTCATGTATTTCACGTCCTGTTTTAGCAGTCGCCGGGTTCCAACAT 1019
                             GAACTCTTGGGATGCCTAGTGTTCTCGATTTGGTACCCGTTGCTTGTTTCTTTGTCTTGCCT
                                                          GAAATTTTAGGCTATGCAGCTTTCTTGACTTGGTATTCTCTACTCCTTTCTCGCCTACCC
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US-09-938-842A-558
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GENERAL INFORMATION:
APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-06-22
PRIOR FILING DATE: 2001-06-22
                                                                                                                                                                        Query Match
Best Local Similarity
Matches 776; Conserv
                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 558
LENGTH: 1350
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                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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Pred. No. 2.7e-123;
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                                                                                                                                                                                                                                                                                                                       TGGCAGTTCAGCTTGAATCACTTTGCTTCTAATGTTTTACACTGGTTTGCCCTAGCGGTAAT 1079
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                                                                                                                                                                                                                                                                                                                                                                                                                             AATTGGCCTGAAAGGGTCATGTATTTCACGTCCTGTTTAGCAGTCGCCGGGTTCCAACAT 1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACTTCGCCGGAATCTTAGTCTTCTGGACTTGGTTCCCACTCTTAGTCTCATGTCTACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAAATTTTAGGCTATGCAGCTTTCTTGACTTGGTATTCTCTACTCCTTTCTCGCCTACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTAATGGGTATGCTATGGCTCCAGAGTGGTTGGGTGGGGCATGATTCTTGTCACTACCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTCTCTGAGATGTCCAAGGACTACAGAAGGCTCGTCTCTGAGTTTTCTAAGATGGGTTTG
                                                                                                                                                                                                                                    GATTGGTTTCACCAGCAGACAAAGGGCACGCTCAACATAACAGCTTCTGCTTGGTGGGAT 1139
                                                                                                                                                                                                                                                                                      AACTGGCCTGAGAGATTCTTCCTCCTCTTCACAAGCTTCACCGTCACGGCGCTTCAACAC 975
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TGCCATCTCCGGAAAGTTTCTCCGGTGGTTCAAGAGCTTTGCAAGAAGCATAATCTTCCG 1215
                                     TGCCATTTCAGGAAAATCTCACCCATTGTGAACAAACTTTGCCAGAAGCATAATTTGTCC 1259
                                                                                          TGGTTCTTTGGTGGATTACAGTTTCAGCTTGAGCATCATTTGTTCCCTCGCTTACCTCGT 1155
                                                                                                                                       TGGTTTCATGGTGGCCTGCACTTTCAGATTGAGCATCATCTGTTTCCAAGGATGCCTAAG 1199
                                                                                                                                                                                       GACTGGTTCGAGAAGCAAGCGGCGGGAACAATCGATATCTCTTGTAGATCATACATGGAT
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RESULT 3
US-10-029-756-26
; Sequence 26, Application US/10029756
; Publication No. US20020108147A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; APPLICANT: Thomas, TERDUCTION
PRIMA 6-DE
                                                                                                                          NAME/KEY: CDS
LOCATION: 48..1406
SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-029-756-26
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                                                                 Query Match
Best Local S
Matches 717
                                                                                                                                                                                                                                                                                                                                                              TELEX: 230 901 SANS UR INFORMATION FOR SEQ ID NO: 26: SEQUENCE CHARACTERISTICS:
                                                                  Local Similarity
nes 717; Conserv
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APPLICATION DATA:
APPLICATION NUMBER: US/10/029,756
FILING DATE: 21-Dec-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (516) 742-4343
TELEPAX: (516) 742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/934,254
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
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CITY: Garden City
STATE: New Your
GGGCGAAGCTAAGAAGTATATCACGGCGGAGGACCTCCGCCGCCACAACAAGTCCGGCGA
                                GGAAGAGCCAAAAGAAGCACATTTCGCAAGCAGACCTTGCAAAGCATAAGCAACCAGGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCTATGGAAGCTAAGGATGTTACCAAGCCAGTTCCCAAGAACATGGTCTGGGAAGCAATG 1379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TATGAAACTGCTACCATGTGGGAGGCCAATAAAATGGTATACTCCACCCTGCGTGCTGTG 1319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Presser, Leopold REGISTRATION NUMBER: 19,827 REFERENCE/DOCKET NUMBER: 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AACACTTTCGGGTGA 1394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATAGGAGTATGTCGTGGTTTGAAGCAAATGTGTTGACCATTAACACTTTGAAGACAGCA 1275
                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: United States
                                                                                                                                                                                                                        LOCATION:
                                                                                                                                                                                                                                                                                                                                            LENGTH: 1702 base pairs
                                                                  Conservative
                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                       CDS
48..1406
                                                                                 25.7%;
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                                                                 Score 377.8; DB 14;
Pred. No. 4.8e-107;
O; Mismatches 522;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                593 CAACATCCTAACCGGAATCAGCATCGCGTGGTGGAAGTGGACCCACAACGCCCACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    353 GCGGTCCGGGATCTTCGAGAAGAAGGGCCACCACATCATGTGGACGTTCGTCGGCGTTGC
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                                                                                         GCCTAGCGGTAATGATTGGTTTCACCAGCAGACAAAGGGCCACGCTCAACATAACAGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAGGCTCTATCTTTTATTCTGTCTTTTAAGGTGGTGTTTTTCCAACAACAAAAGGGTATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A GTO GEAC GETT CETA GTO A GETA CEA GEAC TO GA CETA CTA CE CE GTO A TEAT CTT C GE
                                                                                                                                                                                                                                                                                                                                                                      CAAGAGAAGTCAGGAAATTTTAGGCTATGCAGCTTTCTTGACTTGGTATTCTCTACTCCT
TGCTTGGTGGGATTGGTTTCATGGTGGCCTGCACTTTCAGATTTGAGCATCATCTGTTTCC
                                                                                                                                                       GGCGATCCAGCACGTCCAGTTCACGCTCAACCACTTCTCCGGCGACACATACGTGGGCCC
                                                                                                                                                                                                  CGGGTTCCAACATTGGCAGTTCAGCTTGAATCACTTTGCTTCTAATGTTTACACTGGTTT
                                                                                                                                                                                                                                                                                    TTCTCGCCTACCCAATTGGCCTGAAAGGGTCATGTATTTCACGTCCTGTTTAGCAGTCGC
                                                                                                                                                                                                                                                                                                                                              TGACCGCGCTCTAAACTTAATGGGTATCGCGGTTTTCTGGACGTGGTTCCCCGCTCTTCGT
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APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2024 (PARA-013PRV)
CURRENT APPLICATION NUMBER: US/09/770,149
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,506
PRIOR APPLICATION NUMBER: 60/178,506
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 494
LENGTH: 657
TYPE: DNA
CORGANISM: Arabidopsis thaliana
US-09-770-149-494
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Best Local Similarity 59.9%;
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 1217 CTCACCCATTGTGAACAAACTTTGCCAGAAGCATAATTTGTCCTATGAAACTGCTACCAT 1276
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Kricker, Maja
Slader, Ted
Davis, Keith R.
Allen, Keith
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                                        ACAGTTTCAGCTTGAGCATCATTTGTTCCCTCGCTTACCTCGTTGCCATCTCCGGAAAGT
                                                                                                               AGCGGCGGGAACAATCGATATCTCTTGTAGATCATACATGGATTGGTTCTTTGGTGGATT
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Hamilton, Carol
Price, Jennifer
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Rameaka, Joshua G.
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Pred. No. 3.7e-44;
0; Mismatches 197;
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APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2027 (PARA-016PRV)
CURRENT APPLICATION NUMBER: US/09/770,444
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,502
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 39
LENGTH: 476
TYPE: DNA
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, NAME/KEY: misc_feature
; LOCATION: (1)...(476)
; OTHER INFORMATION: n = A,T,C
US-09-770-444-39
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US-09-770-444-39
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Best Local Similarity 55.4
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                                                                                         250 GGCAATACCTTGACAGGTTCTTTACTGGGTACTACGTTCAAGATTACTCTGTCTCTGAGA 309
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                                                        GGCACCATCTCGACCATCTCTTCACCGGTTACCACATCAGAGATTTCCAAGTCTCCGAAG
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Davis, Keith R.
Allen, Keith
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Ledford, Brooke L.
Woessner, Jeffrey P.
Haas, William David
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Kricker, Maja
Slader, Ted
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Raines, Tracy M.
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Hamilton, Carol M.
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                                                                                                                                                                                                                                                                                                      or G
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (13401) B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 3260
LENGTH: 287
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                                                                                                                                                                                                                                                                                                                                                                            Matches 180;
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEATURE:
NAME/KEY: unsure
LOCATION: (1)..(287)
COTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: LIB3028-013-Q1-B1-H6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
                                      1161
                                                                                                                                                                                        1041
   242
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                                                                                                                                                                                                                                                                                                                          921 TTCTTGACTTGGTATTCTCTACTCCTTTCTCGCCTACCCAATTGGCCTGAAAGGGTCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136 TCTCACGCGATTACCGTCGTATGGCTGCCGAGTTTCGTAAACTCGGTCTCTTCGAAAACA 195
                                                                                                                                                                                                                             62
                                                                                                                                                                                                                                                    TATTTCACGTCCTGTTTAGCAGTCGCCGGGTTCCAACATTGGCAGTTCAGCTTGAATCAC 1040
                                TTTCAGATTGAGCATCATCTGTTTCCAAGGATGCCTAAGTGCCATT 1206
                                                                                                              AAGGGCACGCTCAACATAACAGCTTCTGCTTGGTGGGATTGGTTTCATGGTGGCCTGCAC 1160
                                                                                                                                                                                    TTTGCTTCTAATGTTTACACTGGTTTGCCTAGCGGTAATGATTGGTTTCACCAGCAGACA 1100
                                                                                                                                                                                                                                                                                                     TTTTGGATTTGGTTCCCTCTATTGATCTCATCCCTGCCAAATTGGGGAGAAAGGGTCATG
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   TTCCAACTTGAGCACCATTTGTTCCCTANGCTCCCAAAGGCACAAT 287
                                                                                                                                                                                                                             TCGCGTGGTGGAAATGGACTCACAATGCTCATCATCTAGC 475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCCTCTGGATCCAGAGCGCTTACATAGGTCACGATTCTGGTCATTACGTTATCATGTCGA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACGGTGTTCTCTACTGCAAGAGCACCTGGGCTCATCTTTGCTCTGGTTTGCTAATGGGTA 489
                                                                                                                                                   TTCGCAGCAGATGTGTATGAGGGCCCACCAAATGGCAATGACTGGTTTGAGAAGCAAACT
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                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                              8.0%;
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                                                                                                                                                                                                                                                                                                                                                                        Score 117; DB 10; Length;
Pred. No. 9e-26;
0; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             Length 287;
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NUMBER OF SEQ ID NOS: 15
; SEQ ID NO 9255
; LENGTH: 263
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clor
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; ORGANISM: Arabidopsis
US-09-924-035A-370
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                                                                                                                                                               Sequence 9255, Application US/09878574
Patent No. US20020110548A1
GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT ELING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 1999-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 370, Application Patent No. US20020142319A1 GENERAL INFORMATION: APPLICANT: Grlach, Jrn
Query Match
Best Local Similarity
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Best Local Similarity
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LENGTH: 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 900 SOFTWARE: FastSEQ for Windows Version 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1136 GGATTGGTTTCATGGTGGCCTGCACTTTCAGATTGAGCATCATCTGTTTCCAAGGATGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1256 GTCCTATGAAACTGCTACCATGTGGGAGGCCAATAAAATGGTATACTCCACCCTGCGTGC
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                                                                                                                                                    ID NOS: 15775
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                                                                   Clone ID: 701102270H1
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5.5%;
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Score 81.4; DB 10 Pred. No. 1.2e-14;
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               DB 10;
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                 Length 263;
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US-10-369-493-27824
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Best Local
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                                                                                                                                                                                                                                                                                                                     179
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793 AGCACTGGACATTTTATCCTGCATTGTTAAGCGTTAGGCTCTATCTTTTATTCTGTCTT
                                                                                 733
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
ITILE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
ITILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 27824
LENGTH: 1098
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                                                                                                                                                                                                       299 GTTGGTGGAAGCGAACCACAACGTTCACCATATCATCACCAACAGCCCTGAGCACGATC
                                                                                                                                                                                                                                                                                                            239 TCCATGTCGATACTGTCATCGGCATCATTGCCGACTTCATCGGTGGTCTCAGTCTAG
                                                                                                                                                                                                                                                                                                                                                            553 GTAAGCTTAATCGTCTTTTTCAAATCATTGCAGGAAATGTGATTGCTGGTGTTAGTGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 493 TATGGCTCCAGAGTGGTTGGGTGGGGCATGATTCTTGTCACTACCAAGTTATGCCTAACC
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                                                                                                                                                                                                                                                       CATGGTGGAAGTTGGACCATAACACCCATCACTTTGCCTGTAATAGCGCCAATCTGGATC
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CTGATATTCAGCACCTTCCTATAATTGCCATATCCCCAAAATTTTTCAACTCCCTTACAT
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49.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 69; DB 12;
Pred. No. 2.4e-10;
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; NAME/KBY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020013958A1 700456385H1
US-09-923-876-5116
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SEQ ID NO 5116
LENGTH: 265
                                                                                                                                                                                                                                                                      Sequence 5116, Application US/09923876 Publication No. US20030237110A9 GENERAL INFORMATION:
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Patent No. US20020013958A1
GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: Kamigaki, Laura Y. (Ito)
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: PL-0012-1 CON
CURRENT APPLICATION NUMBER: US/09/923,876
CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/298,329
PRIOR FILING DATE: 1999-04-21
PRIOR PILICATION NUMBER: 60/085,331
PRIOR PILING DATE: 1998-05-05
NUMBER OF SEQ ID NOS: 6332
                                                                            FILE REPERENCE: PL-0012-1 CON
CURRENT APPLICATION NUMBER: US/09/923,876
CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/298,329
PRIOR FILING DATE: 1999-04-21
                                                                                                                                                                             APPLICANT: Lalgudi, Raghunath V.

APPLICANT: Kamigaki, Laura Y. (Ito)

APPLICANT: Sherman, Bradley K.

TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
PRIOR APPLICATION NUMBER: 60/085,331
PRIOR FILING DATE: 1998-05-05
NUMBER OF SEQ ID NOS: 6332
SOFTWARE: PERL Program
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Pred. No. 7.2e-10;
0; Mismatches 103
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; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1200
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SEQ ID NO 1200
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Best Local Similarity
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LENGTH: 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: misc_feature
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20030237110A9 700456385H1
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                                                            CCCGGTGGTGAGCTCCCATTGTTAAGTTTTGCCGGCCAAGATGTCACTGATGCGTT 223
                                                                                                      GACTGTTGGATTGTCATCAATGGAAAGGTGTACAATGTGACCAAGTTTCTTGAAGACCAT
                                                                                                                                           GATTTATGGATCTCTATCAAGGGAAAAGTTTACGATATCTCCAAGTGGACTAAAGAGCAT 167
                                                                                                                                                                                      ATGGGAGACGAAGCAAAGATCTTCACTCTTTCAGAAGTTTCAGAGCATAATCAAGCTCAT 60
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                     CCAGGTGGGGACGATGTTCTCTTGTCTTCAACAGGTAAGGATGCAACGGATGATTT
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; Pred. No. 4.7e
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Pred. No. 7.2e-10;
0; Mismatches 103;
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4.7e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 4.0%;
Best Local Similarity 52.2%;
Matches 130; Conservative
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Publication No. US20030159164A1
GENERAL INFORMATION:
APPLICANT: KOPCHIK, JOHN J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPACTIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,391
FILING DATE: 23-Oct-2002
CLASSIFICATION BOO
PRIOR APPLICATION NUMBER: US/09/087,578
FILING DATE: 29-MAY-1998
APPLICATION NUMBER: US/09/087,578
FILING DATE: 29-MAY-1998
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OHU-03348
TELEPHONE: (415) 705-8410
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 MONTCOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
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693 ATAATTGCC 701
                                                                                        633 AACACCCATCACTTTGCCTGTAATAGCGCCAATCTGGATCCTGATATTCAGCACCTTCCT
                                                                                                                                       568 GGCGCCTTCTTGGGAGGTGTCTGCCAGGGCTTCTCGTCCTCGTGGTGGAAGGACAAGCAC
                                                                                                                                                                                  573 CAAATCATTGCAGGAAATGTGATTGCTGGTGTTAGTGTTGCATGGTGGAAGTTGGACCAT
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                                             TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (415) 397-8338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KOPCHIK, JOHN J.
KELDER, BRUCE
HUANG, YUNG-SHENG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KIRCHNER, STEPHEN J.
MUKERJI, PRADIP
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; NAME/KEY: misc feature
; LOCATION: (6)...(6)
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US-10-191-513A-37
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US-10-191-513A-37
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                                                                                                                                                                       Sequence 3, Application US/10191513A
Publication No. US20030104596A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pardip
APPLICANT: Leonard, Amanda E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 37
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Best Local Similarity
APPLICANT: Huang, Yung-Sheng
APPLICANT: Tapas, Das
TITLE OF INVENTION: HUMAN DESATURASE GENE AND
FILE REFERENCE: 6295.US.D3
CURRENT APPLICATION NUMBER: US/10/191,513A
CURRENT FILING ADTE: 2002-09-25
PRIOR APPLICATION NUMBER: US 09/227,613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 08/833,610
PRIOR FILING DATE: 1997-04-11
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FASTSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2002-09-25
PRIOR APPLICATION NUMBER: US 09/227,613
PRIOR FILING DATE: 1999-01-08
PRIOR APPLICATION NUMBER: PCT/US98/07422
PRIOR FILING DATE: 1998-04-10
PRIOR FILING DATE: 1998-04-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pardip
APPLICANT: Leonard, Amanda E.
APPLICANT: Huang, Yung-Sheng
APPLICANT: Tapas, Das
TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
FILE REFERENCE: 6295.US.D3
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LOCATION: (5)...(5)
OTHER_INFORMATION: k = g or t/u at position 5
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ORGANISM: Homo sapiens
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No. US20030104596A1
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58.58;
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Pred. No. 5.9e-07;
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2470
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Florida bitterbush
Borage delta-6 des
Borage delta-6 des
Borage delta-6 des
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Sunflower HADES pr
Borago officinalis
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AAY56045	AAY92599	AAW95504	AAW84137	ABB98277	73	ABG73607	73	AAB46810	AAY51354	AAE22063	AAB46440	VAY71553	AAB46436	VAB46435	\AY51350	VAY51352	AW84141	AAY51351	\AG53863	\AG29291	VAG53862	VAG07393	AAY71555	VAY71552	ABG73418	\BG73416	AU79851	AAG07391	w	AAG53861	739	34	133	2929	ABG73417
lta6-de	ina de	_	6 desat	rella pa	delta6	delta6	ens	delta6-	tein b5pp with	irr	C. purpureus delta	Soybean sphingolip	C. purpureus delta	C. purpureus delta	Protein d51pu with	Protein d52pu with	Desaturase enzyme	Protein b51bo with	_	8				ningo:	Evening primrose d	prim	prim	818	_	18	_	þ	s sld1 pro	rabidopsis thali	Borage delta-6-des

## ALIGNMENTS

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Polynucleotide encoding delta-6 desaturase enzyme useful for producing transgenic plants and for producing antibodies specific to which is

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Best Local
          Key
Region
                                                             Delta-6-desaturase; gamma-linolenic acid; transgenic plant; polyunsaturated fatty acid; octadecatetraeonic acid; chilling resistance; oilseed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from clone pps.pk0011.d5:fis isolated from Florida bitterbush developing seed cDNA library, pps. The delta-6 desaturase enzyme catalyses the formation of tarriric acid, a fatty acid that has a triple bond at the delta-6 carbon. The present sequence is useful for producing transgenic plants having altered levels of delta-6 desaturase which in turn would alter the fatty acid composition. The enzyme is also useful for producing polyclonal or monoclonal antibodies. The polynucleotide is useful as primer or probe for screening cDNA libraries to isolate desired full-length cDNA clones.
                                           Borago
                                                                                                         Borage
                                                                                                                                                                     AAR98455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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m clone pps.pk0011.d5:fis isolated from Florida bitterbush developing
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                                            officinalis.
                                                                                                         delta-6-desaturase
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                                                                                                                                                                                                                                                                           AWWDWFHGGLHFQIEHHLFPRMPKCHFRKISPIVNKLCQKHNLSYETATMWEANKMYYST
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                                                                                                                                                                                                                                                                                                                                                              AARFFVSFQHWTFYPALLSVRLYLFILSFKVVFSNNKRVYKRSQBILGYAAFLTWYSLLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                              VLFALSVYGVLYCKSTWAHLCSGLLMGMLWLQSGWVGHDSCHYQVMPNRKLNRLFQIIAG
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                                                                                                                                                                                                                                                                                                       SRLPNWPERVMYFTSCLAVAGFQHWQFSLNHFASNVYTGLPSGNDWFHQQTKGTLNITAS
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 Location/Qualifiers
156..163
/label= Lipid_box
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Lipid_box
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Borage delta-6-desaturase (AAR98455) catalyses the conversion of linoleic acid to gamma-linolenic acid (GLA). Its sequence was deduced from that of the delta-6-desaturase gene (AAR30395) isolate from a borage membrane-bound polysomal library. The sequence is distinct from that of Synechocystis delta-6-desaturase (AAR98456).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Expression of the desaturase in transgenic plants, esp. sunflower, soybean, maize, tobacco, peanut, carrot or oilseed rape, results in increased GIA prodn. Alteration of the plant membrane lipids as a result of expression of the desaturase may also result in increased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transgenic plants comprising the borage delta-6-desaturase gene show increased production of gamma linolenic acid and having increased resistance to chilling
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DB; AAT30395.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 LSVYGVLYCKSTWAHLCSGLLMGMLWLQSGWVGHDSCHYQVMPNRKLNRLFQIIAGNVIA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Page 52-53; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                   GVSVAWWKLDHNTHHFACNSANLDPDIQHLPIIAISPKFFNSLTSYYHNCKMTYDRAARF
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                            WFHGGLHFQIEHHLFPRMFKCHFRKISFIVNKLCQKHNLSYETATMWEANKMVYSTLRAV
                                                                                                 NWPERVMYFTSCLAVAGFQHWQFSLNHFASNVYTGLPSGNDWFHQQTKGTLNITASAWWD
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WFHGGLQFQIEHHLFPKMPRCNLRKISPYVIELCKKHNLPYNYASFSKANEMTLRTLRNT
                                                                                                                                                                                                        FVSYQHWTFYPIMCAARLNMYVQSL-IMLLTKRNVSYRAQELLGCLVFSIWYPLLVSCLP
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372..377
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55.4%; Pred. No. 1.7e-146;
Mismatches 107;
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Best Local Similarity
Matches 246; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence corresponds to the borage (Borago officinalis) delta-6 desaturase enzyme. The encoding lipid metabolism gene is an example of a heterologous gene which can be expressed at high levels in a seed-specific manner in transgenic plants, when placed under control of the sunflower albumin gene 5' regulatory region (AAV34397).
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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lipid metabolism; delta-6 desaturase; transgenic plant.
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                                                                        LSVYGVLYCKSTWAHLCSGLLMGMLWLQSGWVGHDSCHYQVMPNRKLNRLFQIIAGNVIA 184
                                                                                                                                                                       GTAWQYLDRFFTGYYVQDYSVSEMSKDYRRLVSEFSKWGLFKTPGKGVYCSIFFVSVLFA
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GVSVAWWKLDHNTHHFACNSANLDPDIQHLPIIAISPKFFNSLTSYYHNCKMTYDRAARF
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156..163
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Pred. No. 1.7e-146;
0; Mismatches 107;
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The present sequence is borage delta-6 desaturase, an enzyme that catalyses the conversion of linoleic acid to gamma-linolenic acid (GLA). Delta-6 desaturase cDNA (see ANX24917) was isolated from a borage membrane-bound polysomal cDNA library using a partial clone, obtained from an EST database search, as probe. The borage delta-6 desaturase nucleic acid can be operably linked to the seed-specific
                                                                                                                                                                                                                             Nucleic acid containing oleosin 5'-regulatory region - umodulating fatty acid synthesis and lipid metabolism in particularly to increase content of gamma-linolenic acid
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                                                                                                                                                                                Example 2; Page 61; 101pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
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                                                                                                                                                                                                                                                                                                                                                                        desaturase; membrane-bound
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Pred. No. 1.7e
90; Mismatches
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Kinney
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No. 1.7e-146;
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                                                                                                                                                                                                                                                                                                                                                                        desaturase;
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RESULT 6
AAY51349
ID AAY5
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AC AAY5
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Z7-A
DT 27-A
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DE Sunf
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KW Sphi
KW tran
KW tran
KW cold
KW phax

AAY51349 st AAY51349; 27-APR-2000

(first

standard;

Protein;

448 AA

Sunflower HADES protein.

Sphingolipid desaturase; sld1; sphingobase; ceramide; capnoid; transgenic plant; crop plant; delta-8-unsaturated long-chain base; tolerance; resistance; soil salinity; ion stress; toxicity; drought; cold; frost; phytopathogenic microorganism; flowering time; cosmetic pharmaceutical; food; chemical raw material.

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Best Local S
Matches 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is a sphingolipid desaturase from clone sal.pk0017.b4:fis isolated from soybean seedling cDNA library, sal. The present sequence is useful for producing transgenic plants having altered levels of sphingolipid desaturase whin turn would alter the fatty acid composition. The enzyme is also use for producing polyclonal or monoclonal antibodies. The polynucleotide is useful as primer or probe for screening cDNA libraries to isolate desired full-length cDNA clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polynucleotide encoding delta-6 desaturase enzyme useful for producing transgenic plants and for producing antibodies specific to which is useful for screening cDNA expression libraries .
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N-PSDB; AAD01352.
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423
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                        AARFFVSFQHWTFYPALLSVRLYLFILSFKVVFSNNKRVYKRSQBILGYAAFLTWYSLLL
                                                                                                                                                                                                            VLFALSVYGVLYCKSTWAHLCSGLLMGMLWLQSGWVGHDSCHYQVMPNRKLNRLFQIIAG
                                                                                                                                                                                                                                                                                                                    AYHPGTAWSHLEKFFTGYHLSDFKVSEVSKDYRKLASEFSKLGLFDTKGHVTSCTLASVA
                                                                                                                                                                                                                                                                                                                                  AYHPGTAWQYLDRFFTGYYVQDYSVSEMSKDYRRLVSEFSKMGLFKTPGKGVYCSIFFVS
                LRAVAMEAKDVTKPVPKNMVWEAMNTFG 448
                                                  SSMDWFFGGLQFQLEHHLFPRLPRCQLRKISPLVSDLCKKHNLPYRSLSFWEANQWTIRT
                                                                                                                              SRLPNWPERVMYFTSCLAVAGFQHWQFSLNHFASNVYTGLPSGNDWFHQQTKGTLNITAS
                                                                                                                                                         TARFLICYOHFTFYPVMCVARVNLYLQTILLLFSRRK-VQDRALNIMGILVFWTWFPLLV
                                                                                                                                                                                                                                                               VEKEKKY ITSEELKGHNKEGDLWISIQGKVYNVSDWVKEHPGGDVPISNLAGQDVTDAFI
LRTAALQARDLTNPAPKNLLWEAVNTHG
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                                                                                                                                                                                                                                                                                                                                                                                                                          90;
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1465.5;
Pred. No. 1.8e.
90; Mismatches
 450
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This invention describes a novel sphingolipid desaturase that selectively clintroduces a double bond into the sphingobase of the ceramide residue of sphingolipids and capnoids. A DNA sequence encoding the sphingolipid cc sphingolipid and capnoids. A DNA sequence, can be used to produce transgenic plants, especially crop plants, with an increased or ceramide created long-chain base content or an altered conditate. S-unsaturated long-chain base content or an altered cc compensate for a delta-S-unsaturated long-chain base deficiency, to exclude production of delta-S-unsaturated bases, to increase tolerance conditions, cold or frost and/or phytopathogenic microorganisms, or to conditions, cold or frost and/or phytopathogenic microorganisms or to calter size growth and flowering time. Cells, transgenic organisms or cc plants containing the DNA sequence can be used to produce sphingolipids or capnoids can be used in cosmetics, pharmaceuticals and foods and as chemical raw materials. This sequence represents a desaturase protein, HADES, isolated considerable and sandurase protein, solated considerable and solated sequence capters which is used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 33-34; 62pp; German.
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WFHGGLHFQIEHHLFPRMPKCHFRKISPIVNKLCQKHNLSYETATMWEANXMVYSTLRAV
                                                                                                                                                                                                                   FVSFQHWTFYPALLSVRLYLFILSFKVVFSNNKRVYKRSQEILGYAAFLTWYSLLLSRLP
                                                                                                                                                                                                                                                                                                                       GVSVAWWKLDHNTHHFACNSANLDPDIQHLPIIAISPKFFNSLTSYYHNCKMTYDRAARF
                                                                                                                                                                                                                                                                                                                                                                                                                                              LSVYGVLYCKSTWAHLCSGLLMGMLWLQSGWVGHDSCHYQVMPNRKLNRLFQIIAGNVIA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASTWKNIDKFFTGYYLKDYSVSEVSKDYRKLVFEFSKMGLYDKKGHIMFATLCFIAMLFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KKHISQADLAKHKQPGDLWISIKGKVYDISKWTKEHPGGELPLLSFAGQDVTDAFIAYHP
                                                                                 NWGERIMFVIASLSVTGMQQVQFSLNHFSSSVYVGKPKGNNWFEKQTDGTLDISCPPWMD
                                                                                                                       NWPERVMYFTSCLAVAGFQHWQFSLNHFASNVYTGLPSGNDWFHQQTKGTLNITASAWWD
                                                                                                                                                                                                                                                                                         GISIGWWKWNHNAHHIACNSLEYDPDLQYIPFLVVSCKFFGSLTSHFYEKRLTFDSLSRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KKYITSDELKNHDKPGDLWISIQGKAYDVSDWVKDHPGGSFPLKSLAGQEVTDAFVAFHP
                                                                                                                                                                                        FVSYQHWTFYPIMCAARLNMYVQSL-IMLLTKRNVSYRAQELLGCLVFSIWYPLLVSCLP
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Pred. No. 2.9e-146;
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Query Match
Best Local Similarity
Matches 245; Conserv

Conservative

90;

Mismatches

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Gaps

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.6e-146;

DB 23; Length 448; Indels

59.1%; Score 1459.5; 55.2%; Pred. No. 7.6e

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                                                                                                                                                                                                                                                                                                                                                           10-OCT-1991;
08-JAN-1992;
14-SEP-1994;
                        The invention describes an isolated nucleic acid encoding an evening primrose Delta6-desaturase. The nucleic acid and a vector expressing the nucleic acid are useful for producing a plant such as sunflower, soybean, maize, tobacco, peanut, carrot or oil seed rape plant, with increased gamma linolenic acid (GLA) content, and also for inducing or increasing production of GLA in a bacteria or plant deficient, lacking in or producing low levels of GLA. The nucleic acid is also useful for inducing chilling tolerance in plants. This is the amino acid sequence of the borage delta6 desaturase involved in the production of gamma linoleic acid.
                                                                                                                                                                                                Novel nucleic acid encoding evening primrose delta6-desaturase which converts linoleic acid to gamma linolenic acid useful for producing gamma linolenic acid in transgenic plant or bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          delta6-desaturase; sunflower; soybean; maize; t
peanut; carrot; oil seed rape; gamma linolenic
chilling tolerance; borage.
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  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Borago officinalis delta6-desaturase
                                                                                                                                                                       Example 9; Column 31-34; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                   13-OCT-1992;
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                                                                                                                                                                                                                                                                                                                      (RHON ) RHONE-POULENC AGROCHIMIE
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91US-0774475.
92US-0817919.
94US-0307382.
97US-0789936.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   label= Metal_box_1
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ARESULT 8
AREGAIN AREG
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19-SEP-1997;
10-OCT-1991;
08-JAN-1992;
14-SEP-1994;
28-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Delta-6-desaturase; enzyme; delta-12-desaturase; sunflower; soybean; maize; tobacco; peanut; carrot; oil seed rape; gamma-linolenic acid; octadecatetraenoic acid; alpha-linolenic acid; delta-15-desaturase;
WPI; 2003-066659/06
N-PSDB; ABX15366.
                                                                            Thomas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NWPERVMYFTSCLAVAGFQHWQFSLNHFASNVYTGLPSGNDWFHQQTKGTLNITASAWWD
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97US-0934254.
91US-0774475.
92US-0817919.
94US-0307382.
97US-0789936.
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RESULT 9
AAW85122
ID AAW8
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AC AAW8
XX
DT 11-F
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DE A de
XX
KW Fatt
KW maln

AAW85122; 11-FEB-1999

(first

entry)

delta-6

desaturase

enzyme

amino acid sequence

AAW85122 standard;

Protein;

446

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Fatty acid; delta-6 desaturase; polyunsaturated fatty acid
malnutrition; inflammation; rheumatoid arthritis; asthma;

psoriasis;

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Best Local Similarity
Matches 245; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a nucleic acid encoding an evening primrose delta-6-desaturase polypeptide. The nucleic acid, a vector comprising nucleic acid or a nucleic acid encoding delta-12-desaturase, is useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acid encoding evening primrose delta-6-desaturase, for producing plant with increased gamma linolenic acid content, for inducing octadecatetraenoic acid production in plant
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                                                                                                                                                                                                                                                                                                                                                                                 MSVYGVLFCEGVLVHLFSGCLMGFLWIQSGWIGHDAGHYMVVSDSRLNKFMGIFAANCLS
                                                                                                                                                                                                                                                                                                                                                                                                     LSVYGVLYCKSTWAHLCSGLLMGMLWLQSGWVGHDSCHYQVMPNRKLNRLFQIIAGNVIA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTAWQYLDRFFTGYYVQDYSVSEMSKDYRRLVSEFSKWGLFKTPGKGVYCSIFFVSVLFA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KKYITSDELKNHDKPGDLWISIQGKAYDVSDWVKDHPGGSPPLKSLAGQEVTDAFVAFHP
                                                                                                      WFHGGLHFQIEHHLFPRMPKCHFRKISPIVNKLCQKHNLSYETATMWEANKMVYSTLRAV
                                                                                                                                                                                                                                                                                                      GISIGWWKWNHNAHHIACNSLEYDPDLQYIPFLVVSSKFFGSLTSHFYEKRLTFDSLSRF
                                                                                                                                                                                                                                                                                                                        GVSVAMWKLDHNTHHFACNSANLDPDIQHLPIIAISPKFFNSLTSYYHNCKMTYDRAARF
ALQARDITKPLPKNLVWEALHTHG
                     AMEAKDVTKPVPKNMVWEAMNTFG
                                                                       WFHGGSQFQIEHHLFPKMPRCNLRKISPYVIELCKKHNLPYNYASFSKANEMTLRTLRNT
                                                                                                                                                                                                                           FVSYQHWTFYPIMCAARLNMYVQSL-IMLLTKRNVSYRAQELLGCLVFSIWYPLLVSCLP
                                                                                                                                                                                                                                                               FVSFOHWTFYPALLSVRLYLFILSFKVVFSNNKRVYKRSQEILGYAAFLTWYSLLLSRLP
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                                                                                                                                                  NWGERIMFVIASLSVTGMQQVQFSLNHFSSSVYVGKPKGNNWFEKQTDGTLDISCPPWMD
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Pred. No. 7.6e-146;
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                                   448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24; Length
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and
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid encoding delta5 and other desaturase enzymes - useful in production of oils of increased arachidonic acid cont used, e.g. for treating cancer, as foods, animal feeds and cosm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-APR-1998;
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cholesterol level; endometriosis; premenstrual syndrome;
myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Pages 96-98; 153pp; English.
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FVSFQHWTFYPALLSVRLYLFILSFKVVFSNNKRVYKRSQEILGYAAFLTWYSLLLSRLP
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55.2%; Pred. No. 5.3e-145;
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14-SEP-1994;
28-JAN-1997;
                                                  The invention relates to a nucleic acid encoding an evening primrose delta-6-desaturase polypeptide. The nucleic acid, a vector comprising the nucleic acid or a nucleic acid encoding delta-12-desaturase, is useful for producing a plant (such as sunflower, soybean, maize, tobacco, peanut, carrot or oil seed rape plant) with increased gamma-linolenic acid (GLA) content by transforming a plant cell with the nucleic acid or vector and regenerating a plant with increased GLA content from the plant cell, for inducing or increasing production of GLA in an organism lacking in or producing low levels of GLA and for inducing production of octadecatetraenoic acid in at least one of a plant deficient or lacking in or producing low levels of octadecatetraenoic acid, a bacterium which produces alpha-linolenic acid or a bacterium which exhibits a delta-15-desaturase activity on a GLA substrate. This sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel nucleic acid encoding evening primrose delta-6-desaturase, for producing plant with increased gamma linolenic acid content, for inducing octadecatetraenoic acid production in plant -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 15; Fig 11; 55pp; English.
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L0-OCT-1991;
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94US-0307382.
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09-MAR-1999

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21-APR-1999
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99US-0121825

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99US-0125788

99US-0126264

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Matches 242
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Sphingolipid desaturase; sld1; sphingobase; ceramide; capnoid; transgenic plant; crop plant; delta-8-unsaturated long-chain base; tolerance; resistance; soil salinity; ion stress; toxicity; drought;
                              B. napus sldl
                                              27-APR-2000
                                                              AAY51333;
                                                                             AAY51333
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                                                                                                                  AMEAKDVTKPVPKNMVWEAMNTFG
|::|:| | | | | | ::|| | | | |
AIQARDATNPVLKNLLWEAVNTHG
                                                                                                                                                                                        NWPERVMYFTSCLAVAGFQHWQFSLNHFASNVYTGLPSGNDWFHQQTKGTLNITASAWWD
                                                                                                                                                                                NWQERF1FVFVSFAVTA1QHVQFCLNHFAADVYTGPPNGNDWFEKQTAGTLD1SCRSFMD
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                              protein.
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54.5%;
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Pred. No. 2.5e-140;
2; Mismatches 119;
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3-0145088 3-0145085 3-0145089 3-0145192 3-014518 3-014518 3-0145218 3-0145213 3-0145213 3-0145213 3-0145218 3-0145218 3-0145218 3-0145218 3-0145218 3-0145218 3-0145218 3-0145218 3-0145218 3-0145218 3-0145218 3-0145218 3-0145218 3-0147308 3-0147308 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-0147303 3-014730 3-014730 3-014730 3-014730 3-014730 3-014730 3-014730 3-014730 3-014730 3-014730 3-014730 3-014730 3-014730 3-014730 3-014730 3-014730 3-014730 3-014730 3-014730 3-014730 3-014730 3-014730 3-014730 3-014730 3-014730 3-014730 3-014730 3-014730 3-014730 3-014730 3-014730 3-014730 3-014730 3-014730 3-014730 3-014730 3-014730 3-014730 3-01473

3-0158029 3-0158232 3-0158369 3-0159293 3-0159294 3-0159239 3-0159329 3-0159330

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CC introduces a double bond into the sphingobase of the ceramide residue of CC sphingolipids and capnoids. A DNA sequence encoding the sphingolipid CC desaturase, or a vector containing the DNA sequence, can be used to CC produce transgenic plants, especially crop plants, with an increased or decreased delta-8-unsaturated long-chain base content or an altered CC delta-8-unsaturated long-chain base deficiency, to CC compensate for a delta-8-unsaturated long-chain base deficiency, to CC exclude production of delta-8-unsaturated bases, to increase tolerance CC or resistance to soil salinity, ion stress or toxicity, drought, wet CC conditions, cold or frost and/or phytopathogenic microorganisms, or to CC alter size growth and flowering time. Cells, transgenic organisms or CC plants containing the DNA sequence can be used to produce sphingolipids CC and capnoids with unsaturated sphingobases. The sphingolipids or capnoids with unsaturated sphingobases. The sphingolipids or capnoids can be used in cosmetics, pharmaceuticals and foods and as chemical raw CC materials. This sequence represents the Brassica napus sphingolipid desaturase sldl protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 240; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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pharmaceutical; food; chemical raw material.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New sphingolipid desaturase that selectively introduces double into sphingolipids and capnoids -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-DEC-1999
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)B; AAZ44832.
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                                                                                                                                                                                                                                                                                 GVSVAWWKLDHNTHHFACNSANLDPDIQHLPIIAISPKFFNSLTSYYHNCKWTYDRAARF
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                                                          NWPERVMYFTSCLAVAGFQHWQFSLNHFASNVYTGLPSGNDWFHQQTKGTLNITASAWWD
                                                                                                                                                                                      FVSFQHWTFYPALLSVRLYLFILSFKVVFSNNKRVYKRSQEILGYAAFLTWYSLLLSRLP
                                                                                                                                                                                                                                                                                                                                                                            AVVYGVVACTSIWAHLISAVLLGLLWIQSAYVGHDSGHYNVTSTKPCNKLVQLLSGNCIT
NWQERIIFVFLSMAVTAIQHVQFCLNHFAADVYTGPPNGNDWFEKQTAGTLDISCRSYMD
                                                                                                                                                                                                                                                       GISIAWWKWTHNAHHISCNSLDHDPDLQHIPVLAVSNKFFKSMTSRFYGRKLTFDPLARF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTAWRHLENLHNGYHVKDHHVSDVSRDYRRLAAEFSKRGLFDKKGHVTLYTLTCVAAMLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KRFITSDDLKKHNQPGDLWISIQGKVYDVSHWVKSHPGGEAAILNLAGQDVTDAFIAYHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KKHISQADLAKHKQPGDLWISIKGKVYDISKWTKEHPGGELPLLSFAGQDVTDAFIAYHP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a novel sphingolipid desaturase that selectively into the sphingobase of the ceramide residue of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schmidt H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1395.5; DB 2
Pred. No. 4.8e-139;
5; Mismatches 118;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 449;
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KKHISQADLAKHKQPGDLWISIKGKVYDISKWTKEHPGGELFLLSFAGQDVTDAFIAYHP

Query Match Best Local S Matches 234

Similarity

56.3%; Score 1391.5; 52.7%; Pred. No. 1.3

234; ഗ

Conservative

90;

Mismatches

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Indels Length

1;

Gaps

64

Sequence

458

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RESULT 13
AAY51348
ID AAY51
XX AY51
XX Sphin
XX Cold;
XW Cold;
XW Cold;
XW Dharm
XX Unide
XX Inide
XX 
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                                                               This invention describes a novel sphingolipid desaturase that selectively controduces a double bond into the sphingolase of the ceramide residue of sphingolipids and capnoids. A DNA sequence encoding the sphingolipid desaturase, or a vector containing the DNA sequence, can be used to produce transgenic plants, especially crop plants, with an increased or decreased delta-8-unsaturated long-chain base content or an altered delta-8-unsaturated long-chain base content or an altered delta-8-unsaturated long-chain base deficiency, to compensate for a delta-8-unsaturated long-chain base deficiency, to compensate for a delta-8-unsaturated bases, to increase tolerance or resistance to soil salinity, ion stress or toxicity, drought, wet conditions, cold or frost and/or phytopathogenic microorganisms, or to alter size growth and flowering time. Cells, transgenic organisms, or plants containing the DNA sequence can be used to produce sphingolipids and capnoids with unsaturated sphingobases. The sphingolipids or capnoids can be used in cosmetics, pharmaceuticals and foods and as chemical raw materials. This sequence represents a sphingolipid desaturase protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sphingolipid desaturase; sld1; sphingobase; ceramide; capnoid; transgenic plant; crop plant; delta-8-unsaturated long-chain base; tolerance; resistance; soil salinity; ion stress; toxicity; drought; cold; frost; phytopathogenic microorganism; flowering time; cosmetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New sphingolipid desaturase that selectively introduces double bond into sphingolipids and capnoids -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-JUN-1998;
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RESULT 14
AAG07392
ID AAG077392
XX AAG077
XX AAG07
XX Arabi
XX Prote
XW Prote
XW Cermi
XX Cer
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05-MAR 1999

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23-MAR-1999

25-MAR-1999

26-MAR-1999

01-APR-1999

01-APR-1999

16-APR-1999

11-APR-1999

21-APR-1999

23-APR-1999

30-APR-1999

30-APR-1999

05-MAY-1999

06-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                              06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana protein fragment SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG07392;
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99US-0123548
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99US-0126785
99US-01267462
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99US-0132863.
99US-0134256.
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RESULT 15
AAG53861
ID AAG53
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XX AAG53
XX AAG53
XX AAG53
XX Arabi
XX Prote
XW Prote
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25-FEB-2000; 2000EP-0301439.
               06-SEP-2000
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                                            Arabidopsis
                                                          termination
                                                               Protein identification; signal transduction pathway; metabolic pathway; hybridiaation assay; genetic mapping; gene expression control; promoter;
                                                                                       Arabidopsis
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                                                                                                                     AAG53861;
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                                                                                       thaliana protein fragment SEQ
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Matches 231;
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               RAVAMEAKDVTKPVPKNMVWEAMNTFG
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Search completed: January 1, 2004, 06:36:51 Job time: 43.2461 secs

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Result
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 MEEPKKHISQADLAKHKQPG.....KDVTKPVPKNMVWEAMNTFG
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Delta5 fatty acid
protein T13F2.1 [i
probable Delta6 fa
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probable heme bind
omega-3 fatty acid
conserved hypothet
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probable fatty aci
omega-6 desaturase
          cytochrome b5 probable desA3
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: A84900
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N.M.; Koo, H.; Moffat, K.S.; CITONIN, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L., euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: A84900
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-449 <STO>
A;Cross-references: GB:AE002093; NID:g3702328; PIDN:AAC62885.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g46210
A;Map position: 2
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A84900
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<b>4</b> 5	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
137.5	137.5	138.5	139	139	139.5	139.5	140.5	140.5	140.5	141.5	141.5	141.5	142	142.5	142.5
5.6	5.6	5.6	5.6	5.6	5. 6	5.6	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.8	5.8
431	129	359	380	132	135	134	904	591	446	904	453	352	881	900	890
N	N	N	ນ	N	ผ	N	<u>ب</u>	<u>,                                    </u>	۲	ب	$\vdash$	N	N	N	N
T07685	T41083	AG2005	JQ2338	E84905	S49200	T14454	RDNTNS	CBBY2	JQ2336	RDNTNT	JQ2339	B69901	S25445	S47029	T11805
omega-3 fatty acid	probable cytochrom	omega-3 fatty acid	omega-3 fatty acid	probable cytochrom	cytochrome b5 - co	cytochrome b5 - wi	nitrate reductase	L-lactate dehydrog	omega-3 fatty acid	nitrate reductase	omega-3 fatty acid	fatty-acid desatur	nitrate reductase	nitrate reductase	nitrate reductase

## ALIGNMENTS

Query Match 57.0 Best Local Similarity 54.9 Matches 242; Conservative 366 365 306 305 187 247 245 185 67 65 ഗ FVSFQHWTFYPALLSVRLYLFILSFKVVFSNNKRVYKRSQEILGYAAFLTWYSLLLSRLP GVSVAWWKLDHNTHHFACNSANLDPDIQHLPIIAISPKFFNSLTSYYHNCKWTYDRAARF GTAWHHLEKLHNGYHVRDHHVSDVSRDYRRLAAEFSKRGLFDKKGHVTLYTLTCVGVMLA GTAWQYLDRFFTGYYVQDYSVSEMSKDYRRLVSEFSKMGLFKTPGKGVYCSIFFVSVLFA KRYVTSEDLKKHNKPGDLWISIQGKVYDVSDWVKSHPGGEAAILNLAGQDVTDAFIAYHP KKHISQADLAKHKQPGDLWISIKGKVYDISKWTKEHPGGELPLLSFAGQDVTDAFIAYHP WFHGGLHFQIEHHLFPRMPKCHFRKISPIVNKLCQKHNLSYETATMWEANKMVYSTLRAV NWPERVMYFTSCLAVAGFQHWQFSLNHFASNVYTGLPSGNDWFHQQTKGTLNITASAWWD LISYQHWTFYPVMCVGRINLFIQTFLLLFS-KRHVPDRALNIAGILVFWTWFPLLVSFLP GISIAWWKWTHNAHHIACNSLDHDPDLQHIPIFAVSTKFFNSMTSRFYGRKLTFDPLARF WFFGGLQFQLEHHLFPRLPRCHLRTVSPVVKELCKKHNLPYRSLSWWEANVWTIRTLKNA 425 57.0%; Score 1407.5; DB 2; 54.5%; Pred. No. 1.2e-110; tive 82; Mismatches 119; Indels Length 449; Gaps 424 364 304 126 305 246 244 124 66 64

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RESULT 3
S68358
Delta8 sphingolipid desaturase (EC 1.14.99.-) [similarity] - c. C. Species: Helianthus annuus (common sunflower)
C. C. Species: Helianthus annuus (common sunflower)
C. Accession: S68358
R.; Eur. J. Biochem. 232, 798-805, 1995
A.; Title: A cytochrome-b(5)-containing fusion protein similar
A. Reference number: S68358; MUID: 96028121; PMID: 7588718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Brassica napus (rape)
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 15-Sep
C;Accession: T50555
R;Sperling, P; Zaehringer, U; Heinz, E.
J. Biol. Chem. 273, 28590-28596, 1998
A;Title: A sphingolipid desaturase from higher plants. Identification A;Reference number: Z22986; MUJD:99003197; PMID:9786850
A;Accession: T50555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      delta-8 sphingolipid desaturase [imported] - rape C;Species: Brassica napus (rape) C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000
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A;Gene: sld1
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A;Experimental source: cultivar Drakkar
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                               NWPERVMYFTSCLAVAGFQHWQFSLNHFASNVYTGLPSGNDWFHQQTKGTLNITASAWWD
                                                                                                                                                                                                                                                                                                                                                                                                                           GVSVAWWKLDHNTHHFACNSANLDPDIQHLPIIAISPKFFNSLTSYYHNCKMTYDRAARF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KKHISQADLAKHKQPGDLWISIKGKVYDISKWTKEHPGGELPLLSFAGQDVTDAFIAYHP
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Pred. No. 1.2e-109;
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A;Molecule type: mRNA
A;Residues: 1-458 <SPB>
A;Residues: 1-458 <SPB>
A;Cross-references: EMBL:X87143; NID:g1040728; PIDN:CAA60621.1;
C;Superfamily: cytochrome b5 core homology
C;Keywords: heme; iron; metalloprotein; oxidoreductase
F;16-90/Domain: cytochrome b5 core homology <CB5>
F;51,74/Binding site: heme iron (His) (axial ligands) #status pr
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                                                                                                                                                                                                                                                                                                                           GTAWKHLDKLFTGYHLKDYOVSDISRDYRKLASBFAKAGMFEKKGHGVIYSLCFVSLLLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KKHISQADLAKHKQPGDLMISIKGKVYDISKWTKEHPGGELPLLSFAGQDVTDAFIAYHP
                                                              WFFGGLQFQLEHHLFPRLPRCHLRSISPICRELCKKYNLPYVSLSFYDANVTTLKTLRTA
                                                                                             WFHGGLHFQIEHHLFPRMPKCHFRKISPIVNKLCQKHNLSYETATMWEANKMVYSTLRAV
                                                                                                                                                                                                                            FVSFQHWTFYPALLSVRLYLFILSFKVVFSNNKRVYKRSQEILGYAAFLTWYSLLLSRLP
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ALQARDLTNPAPONLAWEAFNTHG
                              AMEAKDVTKPVPKNMVWEAMNTFG 448
                                                                                                                               NWPERVAFVLVSFCVTGIQHIQFTLNHFSGDVYVGPPKGDNWFEKQTRGTIDIACSSWMD
                                                                                                                                                          NWPERVMYFTSCLAVAGFQHWQFSLNHFASNVYTGLPSGNDWFHQQTKGTLNITASAWWD
                                                                                                                                                                                              FVSYQHYLYYPIMCVARVNLYLQTILLLISKRK-IPDRGLNILGTLIFWTWFPLLVSRLP
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52.7%;
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Pred. No. 2.7e-109;
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A; Molecule type: mtNA
A; Residues: 1-449 cSPE>
A; Cross-references: EMBL: AJ224161; PIDN: CAA11858.1
A; Experimental source: cultivar Columbia; mainly g: C; Genetics: A;Residues: 1-449 <DEH>
A,Cross-references: EMBL.AL132962; PIDN:CAB71088.1
A;Experimental source: cultivar Columbia; BAC clone F2.
R.Sperling, P.; Zaehringer, U.; Heinz, E.
J. Biol. Chem. 273, 28590-28596, 1998
A;Title: A sphingolipid desaturase from higher plants.
A,Reference number: Z22986; MUID:99003197; PMID:978685.
A;Accession: T51848 delta-8 sphingolipid desaturase (EC 1.14.99.-) [validated]
N;Alternate names: protein F2A19.180
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_c)
C;Accession: T47950; T51848 R;De Haan, M.; Maarse, A.C.; Grivell, L.A.; submitted to the Protein Sequence Database, A; Status: preliminary; translated A; Molecule type: DNA A; Accession: T47950 A; Reference number: Z24480 Status: preliminary from GB/EMBL/DDBJ PMID: 9786850 January Mewes, H.W.; green #text_change F2A19 2000 parts, Identification Lemcke, - Arabidopsis thalians some 02-Sep-2000 flowers, Mayer, 0f ĝ new K.F.X.; few cytochrone Que

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R;Laoteng, K.; Mannontarat, R.; Tanticharoen, M.; Cheevadhanarak, S.
Biochem. Biophys. Res. Commun. 279, 17-22, 2000
A;Title: Delta6-desaturase of Mucor rouxii with high similarity to plant delta6-desatura A;Reference number: JC7556; MUID: 20563795; pMID:11112411
A;Accession: JC7556
A;Molecule type: DNA
A;Residues: 1-523 <LAO>
A;Residues: 1-523 <LAO>
                                                                                                                                                                                                                                                                                                                                       C;Species: Mucor rou
C;Date: 30-Jun-2001
C;Accession: JC7556
                                                                                                                                                                       A;Cross-references: GB:AF290983
A;Experimental source: strain ATCC 24905
C;Comment: This enzyme, a membrane-bound key enzyme,
C;Keywords: oxidoreductase; transformation
                                                                                                                                                                                                                                                                                                                                                                                           N;Alternate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Note: F2A19.180
C; Function:
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N;Alternate names: delta6-desaturase
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Matches 146
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Matches
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                                                                                                                                                                      Keywords: oxidoreductase; transformation
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                                              GDSVFIYEQKVYRVNNFMAKHPGGEAALRSALGRDVTDEIRTMHPPQVYEKLINLYCIGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RLPNWPERVMYFTSCLAVAGFQHWQFSLNHFASNVYTGLPSGNDWFHQQTKGTLNITASA
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                                                              GDLWISIKGKVYDISKWTKEHPGGELPLLSFAGQDVTDAFIAYHPGTAWQYL------
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                                                                                                                        25.2%;
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                                                                                                        Score 622; DB 2;
Pred. No. 1.9e-44;
6; Mismatches 191
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5; Mismatches 12
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                                                                                                                                     Length 523;
                                                                                                                                                                                      is responsible
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A;Reference number: 216471
A;Reference number: 216471
A;Reference number: 216471
A;Rolecule type: mRNA
A;Rolecule type: mRNA
A;Residues: 'RTRG',138-428,'D',430,'M',432-444 <WAM>
A;Residues: 'RTRG',138-428,'D',430,'M',432-444 <WAM>
A;Residues: 'RTRG',138-428,'D',430,'M',432-444 <WAM>
A;Ross-references: RMBL:ALD50118
A;Experimental source: adult uterus; clone DKFZp586C201
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Gross-references: GDB:9956652
A;Cross-references: GDB:9956652
A;Cross-references: GDB:956652
A;Note: DKFZp586C201.1
C;Superfamily: cytochrome b5 core homology
C;Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase; unsaturated
F;18-94/Domain: cytochrome b5 core homology <CB5>
F;153,76/Binding site: heme iron (His) (axial ligands) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N;Alternate names: Delta6 fatty acid desaturase; protein DKFZp58 (;Species: Homo sapiens (man) C;Species: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change C;Accession: T13155; T08765 R;Cho, H.P.; Nakamura, M.T.; Clarke, S.D. J. Biol. Chem. 274, 471-477, 1999 A;Title: Cloning, expression, and nutritional regulation of the A;Reference number: Z17612; MUID:99085046; PMID:9867867 A;Accession: T13155 A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:AF126799; NID:g4406527; PID:g4406528; PIDN:AAD20018.1 R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, March 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-444 < CHO>
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N;Alternate names: Delta6 fatty acid desaturase; protein DK
                                                                                                                      Query Match
Best Local Similarity
Matches 124; Conserv
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                                                              SQADLAKHKQPGDLWISIKGKVYDISKWTKEHPGGELPLLSFAGQDVTDAFIAYHPGTAW
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                                                                                                                                                        18.4%; Score 454; DB 2;
28.7%; Pred. No. 2.1e-30;
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                                                                                                                             Mismatches 185;
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QYLDRFFTGYYV-----

-QDYSV-SEMSKDYRRLVSEFSKMGLFKTPGKGVY 113

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R;Aki, T.; Shimada, Y.; Inagaki, K.; Higashimoto, H.; Kawamoto, S.; Shigeta, S.; Ono, K. Biochem. Biophys. Res. Commun. 255, 575-579, 1999
A;Title: Molecular cloning and functional characterization of rat delta-6 fatty acid des A;Reference number: JG0180; MUID:99160394; PMID:10049752
A;Accession: JG0180
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: DDBJ:AB021980; NID:g4514721; PIDN:BAA75496.1; PID:g4514722 C;Superfamily: cytochrome b5 core homology C;Keywords: heme; iron; metalloprotein; oxidoreductase; unsaturated fatty acid F;18-94/Domain: cytochrome b5 core homology <CB5> F;53,76/Binding site: heme iron (His) (axial ligands) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Delta6 fatty acid desaturase (EC 1.14.99.-) [imported] - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 21-Jul-2000
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A; Residues: 1-444 < AKI>
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                                              QPLE--YGKKKLKY-----LPYNHQHEYFFLIGPPLL-IPMY---FQYQIIMTMIRRRDW
                                                                                                                                                                                                                                                                                                                      AFH-----LDLDFVGKFLKPLLIGELAPEEPSLDRGKSSQITEDFRALKKTAEDMNLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGNDWFHQQTKGTLNITASAWWDWFHGGLHFQIEHHLFPRMPKCHFRKISPIVNKLCQKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RSQEILGYAAFLTWYSLLLSRLPNWPERVMYFTSCLAVAGFQHWQFSLNHFASNVYTGLP
                                                                                           NSLTSYYHNCKMTYDRAARFFVSFQHWTFY---PALLSVRLYLFILSFKVVFSNNKR---
                                                                                                                                                                               VMPNRKLNRLFQIIAGNVIAGVSVAWKLDHNTHHFACNSANLDPDIQHLPIIAISPKFF
                                                                                                                                                                                                                                KTNHLFFFLLLSHIIVMESIAWFILSYFGNGWIPTVITAFVLATSQAQAGWLQHDYGHLS
                                                                                                                                                                                                                                                                       KTPGKGVYCSIFFVSVLFALSVYGVLYCKSTW-AHLCSGLLMGMLWLQSGWVGHDSCHYQ
                                                                                                                                                                                                                                                                                                                                                                  AYHPGTAWQYLDRFFTGYYVQDYSV-----
                                                                                                                                                                                                                                                                                                                                                                                                               LOAPMPTFRWEEIQKHNLRTDRWLVIDRKVYNVTKWSORHPGGHRVIGHYSGEDATDAFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NLSYETATMWEA 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VSYYIRFFITYIPFYGILGALL----FLNFIRFLESHWFV-WVTQMNHIVMEI--DQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QPIEYGKKKLKY-----LPYNHQHEYFFLIGPPLLIPMYFQYQIIMTMIVHKNWVDLAWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RKPKWNHLVHKFVIGHLKGASANWWNHRHFQHHAKPNIFHKDPDVNMLHVFVLG----EW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PNRKLNRLFQIIAGNVIAGVSVAWWKLDHNTHHFACNSANLDPDIQHLPIIAISPKFFNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CSIFF-----VSVLFALSVYGVLYCKSTW-AHLCSGLLMGMLWLQSGWVGHDSCHYQVM
                                                                                                                                     VYKKSIWNHIVHKFVIGHLKGASANWWNHRHFQHHAKPNIFHKDPDIKSLHVFVLGE--W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GIEYQEKPLLRA 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AYRDWFSSQLTATCNVEQSFFNDWFSGHLNFQIEHHLFPTMPRHNLHKIAPLVKSLCAKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTSYYHNCKMTYDRAARFFVSFQHWTFY----PALLSVRLYLFILSFKVVFSN-NKRVYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---DLEFVGKFLKPLLIGELAPEEPSQDHGKNSKITEDFRALRKTAEDMNLFKTN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18.2%; Score 449; DB 2; 26.1%; Pred. No. 5.7e-30;
  ---VYKRSQEILGYAAFLTWYSLLLSRLPNWPERVMYFTSCLAVAGFQ 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                  ----SEMSKDYRRLVSEFSKMGLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 444;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      biosynthe
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Blochem. J. 330, 611-614, 1998
A;Title: Identification of a caenorhabditis elegans Delta6-fatty-acid-desaturase;
A;Reference number: Z21637; MUID:98149727; PMID:9480865
A;Accession: T37228
A;Accession: T37238
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-38,69-430,'V',432-473 <NAP>
A;Cross-references: EMBL:AF031477; NID:g3088519; PIDN:AAC15586.1; PID:g3088520
C;Genetics:
C;Genetics: CESP;W08D2.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linoleoyl-CoA desaturase (EC 1.14.19.3) W08D2.4 - C R;Alternate names: Delta6 fatty acid desaturase C;Species: Caenorhabditis elegans C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 C;Accession: T26280; T37238 R;Swinburne, J; Ainscough, R. R;Swinburne, J. Ainscough, R. Submitted to the EMBL Data Library, March 1996
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A;Mat position: 4
A;Introns: 13/3; 39/2; 234/3; 277/3; 378/1; 413/3
C;Superfamily: Caenorhabditis elegans Delta6 fatty acid desaturase
C;Keywords: alternative splicing; oxidoreductase; unsaturated fatt:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:Z70271; PIDN:CAA94233.1; GSPDB:GN00022; CESP:W08D2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: translated from GB/EMBL/DDBJ
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                  84
                                                                                                                                                                                                                                                                                                                                                                                                                                                         50
                                                                                                                                                                                                                                                                                                                                                                                                            65 LYFYRNSDATHIFHAFHEGSSQAYKQLDLLKKHGEHDEFLEKQLEKRLDKVDINVSAYDV 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 KQPGDLWISIKGK-VYDISKWTKEHPGG-----ELPLLS-----
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                                              MLPMLRFSWTGQSVQWVFKENQMEYKVYQRNAFWEQATIVGHWAWV-FYQLFL--LPTWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---FAGQDVTDAFIAYHPGTAWQY----
  ERVMYFTSCLAVAG--FQHWQFSLNHFASNVYTGLPSG----NDWFHQQTKGTLNITASA 361
                                                                                           ALLSVRLYLFILSFKVVFSNNKRVYKRSQE-----ILGYAAFLTWYSLLLSRLPNWP 307
                                                                                                                                                                                                                                  LGWYITSACLLALAWQQFGWLTHEFCHQQPTKNRPLNDTISLFFGNFLQGFSRDWWKDKH
                                                                                                                                                                                                                                                                     TWAHLCSGLIMGWLWLQSGWVGHDSCHYQVMPNRKINRLFQIIAGNVIAGVSVAWWKLDH 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HWQFSLNHFASNVYTGLPSGNDWFHQQTKGTLNITASAWWDWFHGGLHFQIEHHLFPRMP
                                                                                                                                         NTHHAATNVIDHDGDIDLAPLFÄFIP---GDLCKY----KASFEKAILKIVPYQHLYFTA 288
                                                                                                                                                                                 NTHHEACNSANLDEDIQHLEIIAISEKEENSLTSYYHNCKMTYDRAAREEVSEQHWTEYE
                                                                                                                                                                                                                                                                                                                    SVAQEKK----MVESFEKLROKLHDDGLMKANE----TYFLFKAISTLSIMAFAFYLOY 175
                                                                                                                                                                                                                                                                                                                                                                  SVSEMSKDYRRLVSEFSKM------GLFKTPGKGVYCSIFFVSVLFALSVYG-VLYCKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KCHFRKISPIVNKLCOKHNLSYETATMWEANKMVYSTLR 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KNASGLRMKVDGKWLYLSEELVKKHPGGAVIEQYSIPPLNKNIETRGIITTRGSSNALDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.2%; Score 449; DB 1; 28.2%; Pred. No. 6.1e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 187;
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R;Swinburne, J.
R;Swinburne, J.
submitted to the EMBL Data Library,
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A;Introns: 43/3; 80/3; 197/3; 295/3; 318/2; 349/1; 384/3
C;Superfamily: Caenorhabditis elegans Delta6 fatty acid desaturase
C;Keywords: oxidoreductase; unsaturated fatty acid biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: CESP:T13F2.1; des-5
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A;Molecule type: DNA
A;Residues: 1-197,'VSHIFNN',198-447 <WIL>
A;Cross-references: EMBL:Z81122; PIDN:CAB03352.1; GSPDB:GN00022; CESP:T13F2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A; Accession: T24875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Functional identification of a fatty acid delta5 desaturase A;Reference number: Z22422; MUID:99059458; PMID:9845325 A;Recforence number: Z22422; MUID:99059458; PMID:9845325 A;Reference number: Z22422; MUID:99059458; PMID:9845325 A;Reference number: Z22422; PMID:9845325 A;Residues: T447 <MIC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change C;Accession: T43319; T24875 R;Michaelson, L.V.; Napier, J.A.; Lewis, M.; Griffiths, G.; Laza FEBS Lett. 439, 215-218, 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Delta5 fatty acid desaturase (EC 1.14.99.-) T13F2.1 [validated] - Caenorhabditis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Species: Caenorhabditis elegans
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YEQVGLSLHWAWSLGQLYFLPDWSTRIMFFLVSHLVGGFLLSHVVTFNHYSVEKFALSSN
                                                                                                                                                                                                                                                                                                                               V-----SVLFALSVYGVLYCKSTWAHLCSGLLMGMLWLQSGWVGHDSCHYQVMPNRK 170
                                                                                                                                                                                                                                                                                                                                                                                                        VQDYSVSEMSKDYRRLVSEFSKMGLF-------KTPGKGVY--CSIFF 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WISIKGKVYDISKWT-KEHPGGELPLLSFAGQDVTDAFIAYHPGT--AWQYLDRFFTGYY
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                                                                                                                                                                                                                                                   LNRLFQIIAGNVIAGVSVAWWKLDHNTHHFACNSANLDPDIQHLPIIAISPKFFNSLTSY
                                                                                                                                                                                                                                                                                                                                                                     TQEPEIPDIKDDPIKGIDDVN-MGTFNISEKRSAQINKSFTDLRMRVRAEGLMDGSPLFY
                                                                                                                                                                                                                                                                                                                                                                                                                                            FIKIDGKWCQIDDAVLRSHPGGS-AITTYKNMDATTVFHTFHTGSKEAYQWLTELKKECP
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                                                                                               ---LGYAAFLTWYSLLLSRLPNWPERVMYFTSCLAVAG-----FQHWQFSLNHFASN
                                                                                                                                     LNN----YSQDSWVMTLFRWQHVHWTFMLPFLRLSWLLQSIIFVSQMPTHYYDYYRNTAI
                                                                                                                                                                         YHNCKMTYDRAARFFVSFQ----HWTFYPALLSVRLYLFILSFKVVFSNNKRVYKRSQEI
                                                                                                                                                                                                                                                                                         IRKILETIFTILFA-----FYLQYHTYYLPSAILMGVAWQQLGWLIHEFAHHQLFKNRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.6%; Score 385; DB 1; Length 447; 25.0%; Pred. No. 1.4e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T13F2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           October 1996
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C;Accession: H88791

R;anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology, A;Reference number: A75000; MUID:99069613; PMID:9881916

A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_elegans/ A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Accession: H88791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
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Best Local Similarity
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TVMPLVKEFAAANGLPYMVDDYFTGFWLEIEQFRNIANVAAKLTKKI 453
                                                                                                       LNHFASNVYTGLPSGNDWFHQQTKGTLNITASAWWDWFHGGLHFQIEHHLFPRMPKCHFR
                                                                                                                                                                                                                                                                            FNSLTSYYHNCKMTYDRAARFFVSFQ----HWTFYPALLSVRLYLFILSFKVVFSNNKRV 279
                                                                                                                                                                                                                                                                                                                                                             LNRLFQIIAGNVIA-----GVSVAWWKLDHNTHHFACNSANLDPDIQHLPIIAISPKF 223
                                                                                                                                                                                                                                                                                                                                                                                                                                            V-----SVLFALSVYGVLYCKSTWAHLCSGLLMGMLWLQSGWVGHDSCHYQVMPNRK 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VQDYSVSEMSKDYRRLVSEFSKMGLF-------KTPGKGVY--CSIFF 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FIKIDGKWCQIDDAVLRSHPGGS-AITTYKNMDATTVFHTFHTGSKEAYQWLTELKKECP
                                       KISPIVNKLCQKHNLSYETATMWEANKMVYSTLRAVAMEAKDVTKPV 435
                                                                            KFALSSNIM-----SNYACLQIMTTRNMRPGRFIDWLWGGLNYQIEHHLFPTMPRHNLN
                                                                                                                                                                                                                                        YATVAEHLNN----YSQDSWVMTLFRWQHVHWTFMLPFLRLSWLLQSIIFVSQMPTHYYD
                                                                                                                                                                                                                                                                                                                     YNDLASYFVGNFLOVSHIFNNGFSSGGWKEOHNVHHAATNVVGRDGDLDLVP-----F
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                                                                                                                                                           YYRNTAIYEQVGLSLHWAWSLGQLYFLPDWSTRIMFFLVSHLVGGFLLSHVVTFNHYSVE
                                                                                                                                                                                                 YKRSQEI---LGYAAFLTWYSLLLSRLPNWPERVMYFTSCLAVAG-----FQHWQFS
                                                                                                                                                                                                                                                                                                                                                                                                  IRKILETIFTILFA-----FYLQYHTYYLPSAILMGVAWQQLGWLIHEFAHHQLFKNRY 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EFAAANGLPYMVDDYFTGFWLEIEQFRNIANVAAKLTKKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.0%; Score 371.5; DB 2
24.6%; Pred. No. 1.9e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74; Mismatches 199;
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probable Delta6 fatty acid desaturase (EC 1.14.99.-) SCH35.42c [similarity] C;Species: Streptomyces coelicolor C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 20-Jun-2000 C;Accession: T36617 R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajan

S.D.; Parkhill, J.; Barrell, B.G.; Rajandream,

3 . .

Streptomyce

RESULT

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submitted to the EMBL Data Library, June 1999
A;Reference number: Z21610
A;Reference number: Z21610
A;Reference number: T36617
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-345 <OLI>
A;Cross-references: EMBL:AL078610; PIDN:CAB44385.1; GSPDB:GN00070; SCOEDB:SCH35.42c
A;Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-359 <RED>
A;Residues: 1-359 <RED>
A;Cross-references: GB:Ll1421; NID:g349562; PIDN:AAA27286.1; PID:g349563
A;Cross-references: GB:Ll1421; NID:g349563
A;Cross-references: GB:Ll1421; NID:g3495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Synechocystis sp.
C;Date: 19-Mar-1997 #sequence revision 19-Mar-1997 #text_change 20-Jun-2000
C;Date: 19-Mar-1997 #sequence revision 19-Mar-1997 #text_change 20-Jun-2000
C;Accession: S35157; MCC10, M.L.; Gross, L.M.; Thomas, T.L.
Plant Mol. Biol. 22, 293-300, 1993
A;Title: Isolation of a Delta(6)-desaturase gene from the cyanobacterium SynA;Reference number: S35157; MUID:93283633; PMID:8389613
A;Accession: S35157
A;Cross-references: EMBL:D90914; GB:AB001339; NID:g1653477; PIDN:BAA18502.1; PID:d101923
A;Experimental source: PCC 6803
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                        A; Accession: S76243
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-359 < KNAN>
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A;Gene: SCOEDB:SCH35:42c
C;Keywords: oxidoreductase; ur
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                                                                                                                                                                                                                                                                                                     A;Reference number: S74322;
                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocysti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Delta6 fatty acid desaturase (EC 1.14.99.-) [imported] - Synechocystis
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Best Local S
Matches 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRMPKCHFRKISPIVNKLCQKHNLSYETATMWEANKMVYSTLRAVAMEAKDVTKPVPKNM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGRAM--ANRRLKRRALDGALLLAHCA--VYLTALFWVLP--PGMAIAF---LAVHQCLF
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Pred. No. 6.1e-14;
52; Mismatches 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-368 <TAS>
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A; Accession: S54809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N;Alternate names: Delta6-desaturase
C;Species: Spirulina platensis
C;Date: 08-Jul-1995 #sequence_revisic
C;Accession: S54809
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 334 SNVY----TGLPSGNDWFHQQTKGTLNITA-SAWWDWFHGGLHFQIEHHLFPRMPKCHFR 388
                                                                                                                                                                                121 KFRHNVLHHTYTNILGHDVEIHGDELVRMSP-----
                                                                                                                                                                                                                192 KLDHNT-HHFACNSANLDPDIQHLPIIAISPKFFNSLTSYYHNCKMTYDRAARFFVSFQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   193 LDHN-THHFACNSANLDPDIQHLPIIAISPKFFNSLTSYYHNCKMTYDRAARFFVSFQHW
                                                                                                                                                                                                                                                     96 YSKYQWVNYLSGLT-----HDA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 VIFPVRLLGCMVLAIALAAFSFNVGHDANHNAYSSNPHINRVLGMTYDFV--GLSSFLWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90 KDYRRLVSE----FSKMGLFKTPGKGVYCSIFFVSVLFALSVYGVLYCKSTWAHLCSG-
                                                                                                                                                                                                                                                                                                                          Similarity 77; Conserv
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                                     ----FGVAVFLIIPIAVGYSPLEAVI---GASIVYMTHGLVACVV------FMLAHVI
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                                                                                                                                           W-----TFYPALLSVRLYLF------ILSFKVVFSNNKRVYKR
                                                                                                                                                                                                                                                                                        YCKSTWAHLCSGLLMGMLWLQSGWVGHDSCHYQVMPNRKLNRLFQIIAGNVIAGVSVAWW
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                                                                      SQEILGYAAFL----TWYSLLLSRLPNWPERVMYFT----SCLAVAGFQHWQFSLNHFA 333
                                                                                                          WFIWFVYPFIPYYWSIADVQTMLFKRQYHDHEIPSPTWVDIATLLAFKA------
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                                                                                                                                                                                                                                                                                                                                           7.4%; Score 183; DB 2; 22.1%; Pred. No. 1.1e-07;
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24.0%; Pred. No. 8.3e-11;
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omega-3 fatty acid desaturase (EC 1.14.99.-) - Synechocystis sp. (strain PCC6803)

N.Alternate names: delta 15 desaturase
C:Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C;Accession: $52650; $75843
R;Sakamoto, T;;Los, D.A.; Higashi, S.; Wada, H.; Nishida, I.; Ohmori, M.; Murata, N.
Plant Mol. Biol. 26, 249-263, 1994
A;Title: Cloning of omega-3 desaturase from cyanobacteria and its use in altering the de
A;Reference number: $52650
A;Accession: $52650
A;Accession: $52650
A;Accession: $52649; MUID:95035996; PMID:7524725
A;Cross-references: GB:D13780; NID:9600596; PIDN:BAA02924.1; PID:9600598
A;Cross-references: GB:D13780; NID:9600596; PIDN:BAA02924.1
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A, Accession: $75843
A, Status: nucleic acid sequence not shown; translation not shown A, Molecule type: DNA
A, Molecule type: DNA
A, Residues: 1-359 < KAN>
A, Cross-references: EMBL:D90913; GB:AB001339; NID:g1653348; PIDN
A, Note: the nucleotide sequence was submitted to the EMBL Data L
C, Genetics:
A, Start codon: GTG
C; Superfamily: omega-3 fatty acid desaturase
C; Keywords: oxidoreductase; unsaturated fatty acid biosynthesis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  389
341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                290 AAFLTWYSLLLSRLPNWP-----ERVMYFTSCLAVA-----GFQHWQFS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            230 YYHNCKMTYDRAARFFVSFQHWTFYPALLSVRLYLFILSFKVVFSNNKRVYKRSQEILGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   170 KLNRLFQIIAGNVIAGVSVAWWKLDHNTHHFACNSANLDPDIQHLPIIAISPKFFNSLTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 FFVSVLFALSVYGVLYCKSTWAHLCSGLLMGMLWLQSG---W----VGHDSCHYQVMPNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47 FFLDVGLIAGFYALA-----AYLDSWFFYPIFWLIQGTLFWSLFVVGHDCGHGSFSKSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TLNNWIGHLSHTPIL-VPYHGWRISHRTHH--ANTGNIDTDESWYP---VSEQKYNQMA-
QGSGVYYQSPSN 352
                                                                  EAKDVTKPVPKN 438
                                                                                                                                        GTHVAHHIFSNMPHYKLRRATEAIKPILGEYYR----
                                                                                                                                                                                                           HFQIEHHLFPRMPKCHFRK----ISPIVNKLCQKHNLSYETATMWEANKMVYSTLRAVAM 426
                                                                                                                                                                                                                                                                             PYLVFVVWLDLVTFLHHTEDNI----PWYRGDDWYF--LKGALSTIDRDYGFINPIHHDI
                                                                                                                                                                                                                                                                                                                                                                                                                             SHF-----MPGSPLFRPGEKAAVLTSTFALAAFVGFLGFLTWQFGWLFLLKFYVA
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22.6%;
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Pred. No. 7.5e
43; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129;
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A;Residues: 1-384 <LYE>
A;Cross-references: EMBL:Z49260; NID:g809081; PID:g809095; GSPDB:GN00013; MIPS:YMR272c
A;Experimental source: strain AB972
C;Genetics:
C;Genetics: SGD:SCS7; MIPS:YMR272c
A;Gene: SGD:SCS7; MIPS:YMR272c
A;Cross-references: SGD:SO004885
A;Map position: 13R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable fatty acid hydroxylase (EC 1.14.15.-) YMR2
N;Alternate names: protein YM8156.14c
C;Species: Saccharomyces cerevisiae
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
C;Accession: S54484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: yeast probable membrane protein YMR272c; C;Keywords: heme; iron; metalloprotein; oxidoreductase; F;9-89/Domain: cytochrome b5 core homology <CB5» F;200-216/Domain: transmembrane #status predicted <TM1» F;223-239/Domain: transmembrane #status predicted <TM2» F;223-303/Domain: transmembrane #status predicted <TM3» F;287-303/Domain: transmembrane #status predicted <TM3» F;45,72/Binding site: heme iron (His) (axial ligands) #s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library,
A;Reference number: S54014
A;Accession: S54484
A;Molecule type: DNA
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KLPPFMRKLKKYHLEHHYKNYQLGFGVTSWFWD
                                                                                                                                                                                                                                                         LFACFLFC-----
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                                   KISPIVNKL----CQKHNLSYE----TATMWE 412
                                                                                KYRLVMPPTLFVILCAPFYKLVFALLPLYWAYAGFAGGLFGYVCYDECHFF---
                                                                                                                           WFHQQTKGTLNITASA------WWDW--FHGGLHFQI---EHHLFPRMPKCHFR
                                                                                                                                                                                                              LGYAAFLTWYSLLLSRLPNW-PERVMYFTSCLAVAGFQHWQFSLNHFASNVYTGLPSGND 345
                                                                                                                                                                                                                                                                                                                                                                                                                                   PAEEKLSIATDYSNDYKKHKFLDLNRPLLMQILRSDFKKDFYVDQIHRPRHY----GKGS 182
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                                                                                                                                                                        ---DDWLPESNIAFATHFLLHGCHHY
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                                                                                                                                                                                                                                                           -VGVFVWT----LIEYGLHRFLFHF-----
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365
                                                                                                                                                                                                                                                                                                                                              ----PVAWLPVVVYHMGVALKNMNO
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Result
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Listing first 45 summaries
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2470
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       Length
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SCST_YEAST

FD61_SOYBN

CYBS_COYBN

CYBS_COYBN

CYBS_COYBN

CYBS_COYBN

CYBS_COYBN

CYBS_TOBAC

CYBS_TOBAC

CYBS_COYBN

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NIAL_FOAND

FD3C_SOYBN

NIAL_TOBAC

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FD3C_ARATH

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Q03529 saccharomyc
P49630 glycine max
P49100 oryza sativ
Q93672 arabidopsis
Q10352 schizosacch
Q42342 arabidopsis
Q10352 schizosacch
Q40312 saccharomyc
P49098 nicotiana t
Q48045 arabidopsis
P49097 cuscuta ref
P39866 phaseolus v
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P48621 glycine max
P11605 nicotiana t
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6 rattus norv
1 glycine max
4 phytophthor
3 glycine max
7 brassica na
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Query Match

6AA25A1DC1DC0F65 CRC64; DB 1;

18.0%; Score 444;

Length 444;

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LLCD_S
                                                                                                              Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamito S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S., Yamada M., Yasuda M., Tabata S., "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLCD_SYNY3
Q08871;
                                                                                                                                                                                                                                                                                                                                        Reddy A.S., Nuccio M.L., Gross L.M., Thomas T.L., "Isolation of a delta 6-desaturase gene from the carbon synechocystis sp. strain PCC 6803 by gain-of-funct Anabaena sp. strain PCC 7120.", Plant Mol. Biol. 22:293-300(1993).
    This
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28-FEB-2003
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                                                         Res. 3:109-136(1996).
CATALYTIC ACTIVITY: Linoleoyl-CoA
linolenoyl-CoA + A + 2 H(2)O.
                                           COFACTOR: IRON
    SWISS-PROT
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SCS7_
                                                           Bowman S., Churcher C.M., Badcock K., Brown D., Connor R., Dedman K., Devlin K., Gentles S., Har Jagels K., Lye G., Moule S., Odell C., Pearson I Rice P., Skelton J., Walsh S., Whitehead S., Ba
                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last amotation update)
Inositolphosphorylceramide-B C-26 hydroxylase
                                                                                                                                     PubMed=9169872;
                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=S288C / AB972;
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SCS7 OR FAH1 OR YMR272C OR YM8156.14C.
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                                                  ETATMWEANKMVYSTLRAVAMEAKDVTKPVPKNMVW-EAM
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                                                                                                        AICQIRTTANFATNNPFWNWFCGGLNHQVTHHLFPNICHIHYPQLENIIKDVCQEFGVEY
                                                                                                                                                                                                                   LPLALGESIPEVLIGASVTYMTYGIVVCTI----FMLAHVLESTEFLTPDGESGAIDDEW
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1425 MW; 33FB165AEB98C05F CRC64;
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- IASNYRWLEAM
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Best Local S
Matches 96
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                                                                                                                                                                                                                                                                                                                                       Pfam; PF04116; FA_hydroxylase; 1.
Pfam; PF00173; heme 1; 1.
PRINTS; PR00363; CYTOCHROMEB5.
ProDom; PD000612; CYT B5; 1.
PROSITE; PS00191; CYTOCHROME B5_1; 1.
PROSITE; PS50255; CYTOCHROME B5_2; 1.
Oxidoreductase; Fatty acid blosynthesis; Iron;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mitchell A.G., Martin C.E.;
Mitchell A.G., Martin C.E.;
"Fahlp, a Saccharomyces cerevisiae cytochrome b5 fusion protein, and
its Arabidopsis thaliana homolog that lacks the cytochrome b5 domair
its Arabidopsis thaliana homolog that lacks the cytochrome b5 domair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dunn T.M., Haak D., Monaghan E., Beeler T.J.;
"Synthesis of monohydroxylated inositolphosphorylceramide (IPC-C)
Saccharomyces cerevisiae requires Scs7p, a protein with both a
cytochrome b5-like domain and a hydroxylase/desaturase domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P04166; 1EUE.
SGD; S0004885; SCS7.
GO: GO:0005783; C:endoplasmic ret
GO; GO:0016491; F:oxidoreductase
InterPro; IPR001199; Cyt B5.
InterPro; IPR006087; Sterol desat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98220296; PubMed=9559540;
Dunn T.M., Haak D., Monaghan E.,
                                                                                                                                                                                                                                  METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; S54484; S54484.
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                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                   Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 y long chain fatty acids.";
Biol. Chem. 272:28281-28288 (1997).
FUNCTION: INVOLVED IN THE ALPHA-HYDROXYLATION OF SPHINGOLIPID-
ASSOCIATED VERY LONG CHAIN FATTY ACIDS. HYDROXYLATES THE C26-FATTY
ACID OF INGSITOLPHOSPHORYLCERAMIDE-B (IPC-B) TO FORM IPC-C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Contains 1 cytochrome b5 heme-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Integral membrane protein (Potential) DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SI AND/OR BE INVOLVED IN METAL ION BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COFACTOR: IRON (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                123
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                                                                                                                                                            96;
                                                                                                                                                                        Similarity
FA---LSV---YGVLYCKSTWAHLCSGLLMGML---WLQSGWVG--+DSCHYQVMPNRKL
                                           SDSAYEILEDEYLIGYLATDEEAA-----RLLTNKNHKVEVQLSADGTEFDSTTFVKEL
                                                                       PGTAWQYL-DRFFTGYYVQDYSVSEMSKDYRRLVSEFSKMGLFKTPGKGVYCSIFFVSVL
                                                                                                  SKKTVQEHNTANDCWVTYQNRKIYDVTRFLSEHPGGDESILDYAGKDITEIMKDSDVHEH
                                                                                                                             SQADLAKHKQPGDLWISIKG-KVYDISKWTKEHPGGELPLLSFAGQDVT----DAFIAYH
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                                                                                                                                                                                     DB 1;
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                                                                                                                                                                                                                                                                                                                                               Electron transport;
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                                                                                                                                                         Indels 149;
                                                                                                                                                                                    Length 384;
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P48630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heppard E.P., Kinney A.J., Stecca K.L., Miao G.H.;
"Developmental and growth temperature regulation of two different
microsomal omega-6 desaturase genes in soybeans:";
plant physiol. 110:311-319(1996).
-I- FUNCTION: ER (MICROSOMAL) OMEGA-6 FATTY ACID DESATURASE INTRODUCES
THE SECOND DOUBLEBOND IN THE BIGSYNTHESIS OF 18:3 FATTY ACIDS,
IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycine max (Soybean).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Omega-6 fatty acid (EC 1.14.19.-).
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                                                                                                     EMBL; L43920; AAB00859.1;
PIR; T07687; T07687.
InterPro; IPR005804; FA_de
                                                                                                                                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                             Pfam; PF00487;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=3847;
                                                                                                                                                                                                                                                                         s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Ew European Bioinformatics Institute. There are no restr by non-profit institutions as long as its content ified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PATHWAY: POLYUNSATURATED fatty acid biosynthesis.
SUBCELLULAR LOCATION: Endoplasmic reticulum.
TISSUE SPECIFICITY: STRONGLY EXPRESSED IN DEVELOPING DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACT AND/ OR BE INVOLVED IN METAL TON BYNDTHO
                                                                                                                                                                                                                                                                                                                                                                                                                                             AND/ OR BE INVOLVED IN METAL ION BINDING. SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
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        F0040; FACTY
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                                                                                                     87; T07687.
IPR005804; FA_desat_
FA_desaturase; 1.
81; FA_desat_fam; 2.
; Fatty_acid_biosynthesis; Endoplasmic_reticulum;
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Gukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                Smith M.A., Stobart A.K., Shewry P.R., N
"Tobacco cytochrome b5: CDNA isolation,
vitro protein targeting.",
Plant Mol. Biol. 25:527-537(1994).
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28-FEB-2003 (Rel. 41,
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                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EV
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                                                                                                                                                                  FUNCTION: Membrane bound hemoprotein which function as an electron carrier for several membrane bound oxygenases (By similarity). SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
                                                                                                                                                 SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
                                                 European Bioinformatics Institute.
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Pred. No. 8.4e-06;
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Gramene; P49100;
InterPro; IPR001199; Cyt_B5.
InterPro; IPR001199; Cyt_B5.
Pfam; PF00173; heme 1; 1.
ProDom; PD000612; Cyt_B5; 1.
PROSITE; PS00191; CYTOCHROME B5_2; 1.
PROSITE; PS00191; CYTOCHROME B5_2; 1.
PROSITE; PS00195; CYTOCHROME B5_2; 1.
PROSITE; PS00191; Transmembrane; Heme; Iron; Microsome.
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TCAND) (B'
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Q9HFV1;
28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21414663; PubMed=11523811;
Kunic B., Truan G., Breskvar K., Pompon D.;
"Functional cloning, based on azole resistance in Saccharomyces
cerevisiae, and characterization of Rhizopus nigricans redox can
that are differentially involved in the P450-dependent response
                                                                                                                                                              or send an email to license@isb-sib.ch).

    -I- FUNCTION: Membrane bound hemoprotein which funct
carrier for several membrane bound oxygenases (B
    -i- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   progesterone stress."
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Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;
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or send an email to license@isb-sib.ch).
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65
137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 41, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 157; DB 1;
Pred. No. 5.5e-06;
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Pfam; PF PRINTS;

PF00173;

heme 1; 1. 3; CYTOCHROMEB5

EMBL; AF290427; AAG23835.1; -.

1EUE

InterPro; IPR001199; Cyt_B5.

HSSP; P04166;

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Matches 46
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the Euro
use by
                                                              STRAIN-cv. Columbia;
Cooke R., Laudie M., Raynal M., Delseny M.;
Cooke R., Laudie M., Raynal M., Delseny M.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: Membrane bound hemoprotein which function as an electron carrier for several membrane bound oxygenases (By similarity).
-I- SUBCELLULIAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE
CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
-I- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q42342; Q9SB05;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cytochrome b5 isoform 1.
AT5G53560 OR MNC6.10.
Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosid, eurosids II, Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                         Sequence features of the regions physically assigned P1 and TAC cl DNA Res. 5:297-308(1998).
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CY51_ARATH
This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                      Plant
                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99097071; PubMed=9880378; Fukuchi-Mizutani M., Mizutani M., Tanaka Y., Kusumi T., Ohta D.; Fukuchi-Mizutani M., Mizutani M., Tanaka Y., Kusumi T., Ohta D.; Mizrosomal electron transfer in higher plants: cloning and heterologous expression of NADH-cytochrome beta5 reductase from
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
                                                                                                                                                                                                                                                                               Nakamura Y.,
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                     SEQUENCE OF
                                                                                                                                                                                                                                                                               MEDLINE=99087489; PubMed=9872454;
Nakamura Y., Sato S., Asamizu E.,
                                                                                                                                                                                                                                                      Structural analysis
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                                                                                                                                                                                                                                                                                                             Columbia;
                                                                                                                                                                                  1-113 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                        119:353-361(1999).
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                                                                                                                                                                                                                                      of Arabidopsis thaliana of the regions of 1,013,767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 153; DB 1;
; Pred. No. 1.1e-05;
19; Mismatches 51
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                                                                                                                                                                                                                            clones.";
                                                                                                                                                                                                                                                                               Kaneko T., Kotani H., Miyajima
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                                                                                                                                                                                                                                      chromosome 5. V
7 bp covered by
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               restrictions
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                              EMBL outstation
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SIMILARITY).
                                           a collaboration
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RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
James K., Jones L., Jones M., Leather S., McDean J.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Rutherford K., Rutter S., Squares R., Squares S., Stevens K.,
RA Rutherford K., Rutter S., Squares R., Squares S., Stevens K.,
RA Holroyd S., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Moodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Welljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Puchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Gorym K., Langer I., Beck A., Lebrach H., Reinhardt R., Pohl T.M.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 30
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R EMBL; F20001; CAA23377.1; -.

R EMBL; F20001; CAA23377.1; -.

R PIR; T52469; Cyt_B5.

R HSSP; P00171; 1EHB.
R InterPro; IP00193; heme 1; 1.

R PRINTS; PR00363; CYTOCHROMEB5.

R PROSITE; P800363; CYTOCHROMEB5.

R PROSITE; PS00191; CYTOCHROME B5_1; 1.

R PROSITE; PS00255; CYTOCHROME B5_2; 1.

R PROSITE; PS0255; CYTOCHROME B5_2; 1.

R PLECTRON TRANSPORT; TRANSMEMBTANE; Heme; Iron; Microsome;

W Electron transport; Transmembrane; Heme; Iron; Microsome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q10352;
01-OCT-1996
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METAL
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein SPACIF12.10C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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TRANSMEM 107
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                                                                                                                                                                                                                                                                                                                                                                                                           FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 34, Last sequence update)
(Rel. 41, Last annotation update)
l protein C1F12.10c in chromosome
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IRON (HEME AXIAL LIGAND) (
IRON (HEME AXIAL LIGAND) (
IRON (HEME AXIAL LIGAND) (
MSS -> ARA (IN REF. 3).

MS -> ARA (IN REF. 3).
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Pred. No. 1.2e-05;
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SIMILARITY).
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RESULT 9 CYB5_BOROF
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Best Local
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GeneDB_SPombe; SPACIF12.10c; -.
InterPro; IPR001199; Cyt B5.
Pfam; PF00173; heme 1; 1.
PRINTS; PR00363; CYTCCHROMEB5.
ProDom; PD000612; CYTCCHROME B5 1; 1.
PROSITE; PS00151; CYTCCHROME B5 2; 1.
PROSITE; PS50255; CYTCCHROME B5 2; 1.
     Sayanova O., Smith M.A., Lapinskas P.A., Stobart K., Dobson G., Christie W.W., Shewry P.R., Napier J.A.;
"Expression of a borage desaturase cDNA containing an N-terminal cytochrome b5 domain results in the accumulation of high levels of delta6-desaturated fatty acids in transgenic tobacco.";
Proc. Natl. Acad. Sci. U.S.A. 94:4211-4216(1997).
-1- FUNCTION: Membrane bound hemoprotein which function as an electron carrier for several membrane bound oxygenases (By similarity).
-1- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE CYTOCHROME B5 FAMILY.
-1- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001
16-OCT-2001
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                 Spermatophyta; Magnoliophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots: Asteridae; lamiids; Boraginaceae: Boraco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein; Heme.
METAL 106 106
METAL 129 129
SEQUENCE 147 AA; 16667 MV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z69944; CAA93814.1; -. PIR; S67453; S67453.
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                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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(Rel. 40,
(Rel. 41,
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Last sequence up
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IRON (HEME AXIAL LIGAND)
; E874859F52E1AF1D CRC64;
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Pred. No. 1.
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Sanchez M., del Rey F., Benito J.,
Armstrong J., Forsburg S.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
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SIMILARITY).
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CYB5 YEAST
CYB5 YEAST
P40312;
01-FEB-1995 (Rel. 31, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
CTPR-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                     MEDLINE=94237477; PubMed=8181746; Truan G., Epinat J.-C., Rougeulle C., Cullin C., Pompon D.; "Cloning and characterization of a yeast cytochrome b5-encoding which suppresses ketoconazole hypersensitivity in a NADPH-P-450 reductase-deficient strain.";
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METAL
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PRODOM; PD000612; Cyt B5; 1.

PROSITE; PS00191; CYTOCHROME B5 1; 1.

PROSITE; PS50255; CYTOCHROME B5 2; 1.

Electron transport; Transmembrane; Heme; Iron; Microsome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                between the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions
use by non-profit institutions as long as its content is in
modified and this statement is not removed. Usage by and for con
                                                                                                        Saccharomyces cerevisiae reveals an unusually high number of overlapping open reading frames."; Yeast 13:261-266(1997).
                                                                                                                                                           MEDLINE=97245296; PubMed=9090055; de Antoni A., D'Angelo M., Dal Pero F., Sartorello F., Pai Pallavicini A., Lanfranchi G., Valle G.; "The DNA sequence of cosmid 14-13b from chromosome XIV of
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Saccharomycetales; Saccharomycetales
                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
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                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                        Gene 142:123-127(1994).
                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=4932;
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Pfam; PF00173; heme 1; 1.
 carrier for several membrane bound oxygenases. It plays fatty-acid desaturation and is also involved in several the steroi biosynthesis patthway, particularly in the 4-demethylation of the 4,4'-dimethyl zymosterol.

SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMIL)
                                                                                              FUNCTION: Membrane bound hemoprotein which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF00173; heme
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132 AA;
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37
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IRON (HEME AXIAL LIGAND)

IRON (HEME AXIAL LIGAND)
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Pred. No. 1.5
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    (BY SIMILARITY).
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ХВ)
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HSSP; P04166; LEVEL

SGD; S0005055; CYB5.

GO; GO:0005792; C:microsome; IDA.

GO; GO:0005792; C:microsome; IDA.

GO; GO:0016126; P:sterol biosynthesis; IDA.

InterPro; IRR001199; Cyt B5.

Pfam; PF00173; heme 1; 1.

PRINTS; PR00363; CYTOCHROMEB5.

R PRODOm; PD000612; CYT DCHROME B5 2; 1.

R PROSITE; PS00191; CYTOCHROME B5 2; 1.

R PROSITE; PS00191; CYTOCHROME B5 2; 1.

KW Electron transport; Transmembrane; Heme; Irr

TRANSMEM 98 118 POTENTIAL.

FT TRANSMEM 98 118 IRON (HEME AX)

FT METAL 61 61 IRON (HEME AX)

FT METAL 61 61 IRON (HEME AX)

FT METAL 61 61 IRON (HEME AX)

FT METAL 70 17 17 E -> Q (IN RE

TONFLICT 17 17 17 E -> Q (IN RE
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CYB5_TO
        CCCCRATAXX
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Best Local S
Matches 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYB5_TOF
P49098;
                                                                                                                                                                                                                                                                                                                                                            Nicotiana tabacum (Common tobacco).
Eukaryota; Viridiplantae; Etreptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eu Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOBAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L22494; AAA67468.1; -.
EMBL; Z69382; CAA93396.1; -.
EMBL; Z71387; CAA95990.1; -.
PIR; S63052; S63052.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                     vitro protein targeting.",
Plant Mol. Biol. 25:527-537(1994).
-!- FUNCTION: CYTOCHROME B5 IS A M
                                                                                                                                                                MEDLINE=94325476; PubMed=8049375;
Smith M.A., Stobart A.K., Shewry P.R., I
"Tobacco cytochrome b5: cDNA isolation,
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytochrome b5
                                                                                                                                                                                                                                                           TISSUE=Leaf
                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4097;

    -!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.

FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND OXYGENASES. MAY PLAY A KEY ROLE IN THE MODIFICATION BY DESATURATION OF FATTY ACIDS IN THE ENDOPLASMIC RETICULUM, WHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOBAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 148.5; DB 1
Pred. No. 2.3e-05;
3; Mismatches 50
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IRON (HEME AXIAL LIGAND)
E -> Q (IN REF. 1).
; 598EF2A6730CAD19 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
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                                                                                                                                                                     expression analysis
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  RETICULUM, WHICH
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ХВ)
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SIMILARITY).
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Best Local
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EMBL; X68140; CAA48240.1; -.
HSSP; P04166; 1B5M.
InterPro; IPR001199; Cyt B5.
Pfam; PF00173; heme_1; 1.
Pr0Dom; PD000612; Cyt B5; 1.
PROSITE; P800191; CYTOCHROME B5_1; 1.
PROSITE; PS00255; CYTOCHROME_B5_2; 1.
Electron transport; Transmembrane; Heme; Ir
                                                                                                                                                                                                                                                                                                                                                    2_ARATH
CY52_ARATH
O48845;
16-OCT-2001
16-OCT-2001
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SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
MEDLINE=20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea
Fujii C.Y., Mason T.M., Bowman C.L.,
                                                                                                                                                                                                                            AT2G32720 OR F24L7.14.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta;
                                                                                                                                                                              Spermatophyta; Magnoliophyta; eudicotyledons; core e eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
Probable cytochrome b5 isoform 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
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                                                                                                                                                    NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
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64
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105
136 AA;
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40 I
64 I
11 L
11 M
105 MW;
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Pred. No. 2.9e-05;
1; Mismatches 42
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IRON (HEME AXIAL LIGAND) (BY SII
LA -> EF (IN REF. 1; CAM48240).
MISSING (IN REF. 1; CAM48240).
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     T.P., Beni
Barnstead
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                                                                                                                                                                                                        Embryophyta; Tracheophyta;
edons; core eudicots; Rosid
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     Benito M.-I., Town (
tead M.E., Feldblyum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 136;
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                                                                                                                                                                                                     eudicots; Rosidae;
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CRRRR RROCCO OCT THE
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Matches 28
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Pfam; PF00173; heme 1; 1.
PRINTS; PR00163; CYTCHROWEB5.
ProDom; PD000612; Cyt_B5; 1.
PROSITE; PS00151; CYTCCHROME B5 1; 1
PROSITE; PS00151; CYTCCHROME B5 2; 1
Electron transport; Transmembrane; H
                                                                                                                                                                                                                                                       CYB5 CUSRE
P49097;
          MEDLINE=95047507; PubMed=7959021;
Subramaniam K., Mahadevan S.;
"The cDNA sequence of cytochrome b5 assoc:
haustoria formation in Cuscuta reflexa.";
Gene 149:375-376(1994)
                                                                                                                                 Cuscuta reflexa (Southern Asian dodder).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tr
Spermatophyta; Magnoliophyta; eudicotyledons; core eudi
Asteridae; lamiids; Solanales; Convolvulaceae; Cuscuta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- FUNCTION: Membrane bound hemoprotein which function as an electroarrier for several membrane bound oxygenases (By similarity).
-!- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULIM (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo I Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Mallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creas Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fras
                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                              Cytochrome b5
                                                                                                                                                                                                                           01-FEB-1996
01-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Multigene family.
TRANSMEM 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AC003974; AAC04491.1; -.
                                                                                                                  NCBI_TaxID=4129;
                                                                                                                                                                                                             28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T00796; T00796.
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bound hemoprotein which
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bred. No. 3.8e-05;
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IRON (HEME AXIAL
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                                           cytokinin-induced
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Matches 30
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01-FEB-1995 (Rel. 31, Last seq
28-FEB-2003 (Rel. 41, Last anno
Nitrate reductase [NADH] 2 (EC
NIA2 OR NR2.
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SEQUENCE
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Jensen P.E., Hoff T., Stummann B.M., Henningsen K.W.;
Submitted (AUG-1993) to the EMBL/GenBank/DDBJ databases.
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Pfam; PP00173; heme 1; 1.

ProDom; PD000612; Cyt_B5; 1.

PROSITE; P800191; CYTOCHROME B5 1; 1.

PROSITE; PS00255; CYTOCHROME B5 2; 1.

Electron transport; Transmembrane; Heme;
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                                                                                                                                                    -!- FUNCTION: Nitrate reductase is a key enzyme involved in the fi
step of nitrate assimilation in plants, fungi and bacteria.
-!- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
-!- COFACTOR: REQUIRES FAD, A HEME GROUP (CALLED CYTOCHROME B-557)
                                                                                                                                                                                                                                                                                                              Phaseolus vulgaris (Kidney bean) (French bean).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eddicotyledons; core eudicots; Rosidae;

eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.
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                                                        N-TERMINAL DOMAIN.
SIMILARITY: Contains 1 cytochrome b5 heme-binding domain SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN .
                                                                                                       AND ONE MOLYBDENUM ATOM.
SUBUNIT: Homodimer (By similarity)
SIMILARITY: TO EUKARYOTIC MOLYBDOP
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                                              C-TERMINAL DOMAIN.
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135 AA;
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annotation update)
(EC 1.7.1.1) (NR-2).
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Pred. No. 8.2e-05;
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IRON (HEME AXIAL LIGAND)
IRON (HEME AXIAL LIGAND)
; CFF21C952981F5DA CRC64;
                                                                                                          MOLYBDOPTERIN
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R PRINTS; PRO0407; CYTOCHROMEBS.

R PRINTS; PRO0407; EUMOPTERIN.

R PRINTS; PRO0407; EUMOPTERIN.

R PRODOM; PD000612; CYt B5; 1.

R PRODOM; PD000612; CYTOCHROME B5 2; 1.

R PROSITE; PS00191; CYTOCHROME B5 2; 1.

R PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.

R PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.

R PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.

NCHORDERUM-PTERIN (POTENTIAL).

M Ultrate assimilation, Multigene family.

METAL 165 165 MOLYBDENUM-PTERIN (POTENTIAL).

T METAL 167 219 219 MOLYBDENUM-PTERIN (POTENTIAL).
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InterPro; IPR001814; Cyt B5 reductase.

InterPro; IPR001872; Euk Mb oxred.

InterPro; IPR001573; Euk Mb oxred.

InterPro; IPR001709; FPN cyt redctse.

InterPro; IPR001704; Mo-co dimer.

InterPro; IPR001433; Oxred FAD/NAD(P).

Pfam; PF00173; heme 1;

Pfam; PF00174; Mo-co dimer; 1.

Pfam; PF00175; NAD binding 1; 1.

Pfam; PF00174; Oxidored molyb; 1.
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p39869;

01-FEB-1995 (Rel. 3

01-FEB-1995 (Rel. 3

28-FEB-2003 (Rel. 4
SEQUENCE FROM N.A.

STRAIN=CV. Gifu / B-129;
Waterhouse R.N., Smyth A.J., Prosser I.M., Forde B.G., Clarkson D.T.;
Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.

1- FUNCTION: Nitrate reductase is a key enzyme involved in the first
step of nitrate assimilation in plants, fungi and bacteria.

1- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.

1- COFACTOR: REQUIRES FAD, A HEME GROUP (CALLED CYTOCHROME B-557)
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PIR; T11805; T11805.
HSSP; P17571; 2CND.
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                                                                                                                                                     Spermatophyta; Magnoliophyta; eurosids I; Fabales; Fabaceae;
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31, Last sequence update)
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[NADH] (EC 1.7.1.1) (NR).
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(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                   Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                             Query Match
Best Local S
Matches 37
                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PRO0970; PAD binding_6; 1.
Pfam; PR00173; heme_1; 1.
Pfam; PR03404; Mo-co dimex; 1.
Pfam; PR00175; NAD binding_1; 1.
Pfam; PR00174; oxidored_moTyb; 1
PRINTS; PR00405; CYTBSRDTASE.
PRINTS; PR00363; CYTOCHROMEB5.
                                                                                                                                                                                                            Nitrate assimilation.
METAL 172 172
METAL 226 226
DISULFID 411 411
METAL 556 556
METAL 579 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
PIR; S
HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                        PRINTS; PR00407; EUMOPTERIN.

PRINTS; PR00371; FPNCR.

PRODOM; PD000612; Cyt_B5; 1.

PROSITE; PS00191; CYTOCHROME_B5_1;

PROSITE; PS00255; CYTOCHROME_B5_2;

PROSITE; PS00559; MOLYBDOPTERIN_EUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001199; Cyt_B5.
InterPro; IPR001334; Cyt_B5_reductase.
InterPro; IPR000572; Euk_Mb_oxred.
InterPro; IPR001709; FPN_cyt_redctse.
InterPro; IPR005066; Mo-co_dimer.
InterPro; IPR001433; Oxred_FAD/NAD(P).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  +
                                                                                                                                                                                                                                                                                                            Oxidoreductase; Flavoprotein; FAD; NAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: Homodimer (By similarity).

SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE NOTERMINAL DOMAIN.

SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.

SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C-TERMINAL DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S47029; S47029.
; P17571; 2CND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AND ONE MOLYBDENUM
582
                                                               522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X80670; CAA56696.1; -.
                              99
                                                                                               σ
                                                                                                                             l Similarity
37; Conserv
                              TAWQYLDRFFTGY----YVQDYSVSEMS----KDYRRL--VSEFSKMGLFKTPGKGV 112
KAKKMLEDYRVGELITTGYTSDSSSPNNSLHGNSEFKHLAPIKEITTMSLPPLPRRKV
                                                               KMYSLSEVKKHNSPDSAWI I VHGHVYDCTRFLKDHPGGADS I LINAGTDCTEEFEAI HSD
                                                                                              KHISQADLAKHKQPGDLWISIKGKVYDISKWTKEHPGGELPLLSFAGQDVTDAFIAYHPG
                                                                                                                                                                                             900 AA;
                                                                                                                               Conservative
                                                                                                                                                                                               101420 MW;
                                                                                                                                              5.8%;
31.4%;
                                                                                                                               19; Mismatches
                                                                                                                                                                                            MOLYBDENUM-PTERIN (POTENTIAL).
MOLYBDENUM-PTERIN (POTENTIAL).
INTERCHAIN (POTENTIAL).
IRON (HEME AXIAL LIGAND) (BY S.
IRON (HEME AXIAL LIGAND) (BY S.)
IRON (HEME AXIAL LIGAND) (BY S.)
                                                                                                                                              Score 142.5; DB 1
Pred. No. 0.00069;
                                                                                                                                                                                                                                                                                                                               EUX;
                                                                                                                                                                                                                                                                                                          Heme; Molybdenum;
                                                                                                                                                             DB 1;
                                                                                                                               51;
                                                                                                                                                                                                                                                             (POTENTIAL).
                                                                                                                               Indels
                                                                                                                                                          Length
                                                                                                                                                               900;
                                                                                                                                                                                                              SIMILARITY).
SIMILARITY).
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L outstation -
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Perfect score:
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SPTREMBL 23:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_phage:*
11: sp_rodent:*
2: sp_virus:*
2: sp_virus:*
1: sp_unclassified:*
1: sp_mclassified:*
1: sp_rodent:*
2: sp_virus:*
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3: sp_varcheap:*
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Gapop 10.0 , Gapext 0.5
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2470
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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620	626	663.5	1293.5	1325	1372.5	1372.5	1391.5	1395.5	1405.5	1460.5	1461	1465.5	1509.5	1519.5	1543	Score
25.1	25.3	26.9	52.4	53.6	55.6	55.6	56.3	56.5	56.9	59.1	59.1	59.3	61.1	61.5	62.5	Query Match
523	520	483	469	446	449	449	458	449	448	448	446	448	448	448	446	Query Match Length DB
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Q9HDG8	09LEM9	Q9LEN0	Q9ZTU8	09FR82	Q9ZRP7	Q8LB96	Q43469	Q9ZRP8	Q8L717	004353	Q8LLD7	Q9SAU5	Q8VZZ1	Q8VZZ2	Q9ZTY9	ID
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                                                                                                                                    Query Match
Best Local S
Matches 255
                                                                                                                                                                                                                                                                                                                             InterPro; IPR001199; Cyt B5.
InterPro; IPR005804; FA desat fam.
Pfam; PF00487; FA desaturase; 1.
Pfam; PF00173; heme 1; 1.
ProDom; PD000612; Cyt B5; 1.
ProDom; PD001081; FA desat fam; 1.
PROSITE; PS50255; CYTOCHROME_B5_2; 1.
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01-MAR-2002
01-OCT-2002
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                                                                                                                                                                                                                                                                        Heme.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MAROTO F.G., Alonso D.L., Garrido J.-A.S., Ferron M.V., Ruiz Maroto F.G., Alonso D.L., Garrido J.-A.S., Ferron M.V., Ruiz Maroto F.G., Alonso D.L., Garrido of the D6-Desaturase Echium: Functional Expression in Yeast and Tobacco.";

Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
-!-SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.

EMBL, AY055117; AAL23580.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Asteridae; lamiids
NCBI_TaxID=173991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Delta-6-desaturase.
                                                                                                                                    Local Similarity
wes 255; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AYHPGTAWQYLDRFFTGYYVQDYSVSEMSKDYRRLVSEFSKMGLFKTPGKGVYCSIFFVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWMDWFHGGLQFQMEHHLFPRLPRVKLRKVSPFVRELCKKHNLPYDSASFWNANELTFKT
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(TrEMBLrel.
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                                                                                                                                    Conservative
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Last sequence update)
Last annotation update)
                                                                                                                                Score 1519.5; DB 10;
Pred. No. 4.8e-127;
90; Mismatches 98; ]
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-- SIMILARITY: BELONGS TO THE CYT

EMBL; AV055118; AAL23581.1; -.

InterPro; IPR001199; Cyt B5.

InterPro; IPR005804; FA desat fam.

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Best Local S
Matches 246
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Q9SAU5;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUN-1997) to the EMBL/GenBank/DDBJ-!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FEMBL; AF007561; AADD1410.1; -. InterPro; IPR001199; Cyt B5. InterPro; IPR005804; FA desat fam. Pfam; PF00487; FA_desaturase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00487; FA_desaturase; 1.
Pfam; PF00173; heme 1; 1.
Pr0Dom; PD000612; Cyt_B5; 1.
ProDom; PD001081; FA_desat_fam; 1.
PROSITE; PS50255; CYTOCHROME_B5_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Numberg A.N., Beremand P.D., Thomas T.L.; "Engineering of Plant Seed Oils to Produce Gamma Linolenic (GLA).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embry Spermatophyta; Magnoliophyta; eudicotyledons; Asteridae; lamiids; Boraginaceae; Borago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seg
01-OCT-2002 (TrEMBLrel. 22, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Delta 6-desaturase.
Borago officinalis (Bourrache) (Borage).
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MSVYGVLFCEGVLVHLFSGCLMGFLWIQSGWIGHDAGHYMVVSDSRLNKFMGIFAANCLS
                                                                                                                                                                                              KKYITSDELKNHDKPGDLWISIQGKAYDVSDWVKDHPGGSFPLKSLAGQEVTDAFVAFHP
                                                                                                                                                                                                                                                                                                                                                                                                    448 AA; 51626 MW; EAC3F0BF22E0DE00 CRC64;
                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                              59.3%; Score 1465.5; D
55.4%; Pred. No. 3.2e-1
Live 90; Mismatches 1
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Last annotation updat
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Best Local Similarity
Matches 251; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Longman A.J., Michaelson L.V., Napier J.A.;
"Isolation and characterization of a cDNA encoding a delta phingolipid deasturase from Aquilegia vulgaris.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
EMBL, AP406816; AAN03619.1; --
InterPro; IPR001199; CyU_B5.
InterPro; IPR001199; CyU_B5.
InterPro; IPR005804; FA desat fam.
Pfam; PF00487; FA_desaturase; 1.
Pfam; PF00173; heme 1; 1.
PRINTS; PR00363; CYTOCHROMEB5.
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01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Sphingolipid long chain base delta 8 desaturase.
Aquilegia vulgaris.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eypermatophyta; Magnoliophyta; eudicotyledons; Ranunculaceae;
Ranunculaceae; Aquilegia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom; PD000612; Cyt B5; 1.
ProDom; PD001081; FA desat fam; 1.
PROSITE; PS50255; CYTOCHROME_B5_2; 1.
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                                                                                                                                                     VLFALSVYGVLYCKSTWAHLCSGLLMGMLWLQSGWVGHDSCHYQVMPNRKLNRLFQIIAG
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  NCITGISIGWWKWNHNAHHIAVNSLDYDPDLQHIPFLAVSSDIFSSLTSKFYGRKMTFDP
                                                 NVIAGVSVAWWKLDHNTHHFACNSANLDPDIQHLPIIAISPKFFNSLTSYYHNCKMTYDR
                                                                                                      AFHPGSAWKYLDKFFIG-YLKDYTISEVSKDYRKLVAEFSKAGLYDKKGHHILFSLTFVT
                                                                                                                                                                                                                                                                                                                      MTEKRREITSEELKKHIKHGDIWISIQGKIYDVSEWIKDHPGGEAPLLNLAGQDVTDAFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51273 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                59.1%; Score 1461; 56.0%; Pred. No. 7.
                                                                                                                                                                                                                                                                                                                                                                                                                             82;
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                                                                                                                                                                                                                                                                                                                                                                                                                          ore 1461; DB 10;
ed. No. 7.9e-122;
Mismatches 113;
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Best Local Similarity
Matches 245; Conserv
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01-JUL-1997
01-OCT-2002
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EMBL; U79010; AAC49700.1; --

InterPro; IPR001199; Cyt_B5.

InterPro; IPR005804; FA_desat_fam.

Pfam; PF00487; FA_desaturase; 1.

Pfam; PF00173; heme_1; 1.

ProDom; PD00103; heme_1; 1.

ProDom; PD001081; FA_desat_fam; 1.

PROSITE; PS50255; CYTOCHROME_B5_2; 1.
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004353;
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Sayanova O., Smith.M.A., Lapinskas P., Stobart A.K., Dobson G.,
Christle W.W., Shewry P.R., Napier J.A.;
"Expression of a borage desaturase cDNA containing an N-terminal
"Expression of a borage desaturase cDNA containing of high levels
cytochrome b5 domain results in the accumulation of high levels
delta6-desaturated fatty acids in transgenic tobacco.";
Proc. Natl. Acad. Sci. U.S.A. 94:4211-4216(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnoliophyta; eudicotyledons;
Asteridae; lamiids; Boraginaceae; Borago.
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Borago officinalis (Bourrache) (Borage).
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                                               GVSVAWWKLDHNTHHFACNSANLDPDIQHLPIIAISPKFFNSLTSYYHNCKWTYDRAARF
                                                                             MSVYGVLFCEGVLVHLFSGCLMGFLWIQSGWIGHDAGHYMVVSDSRLNKFMGIFAANCLS
                                                                                                                               STWKNLDXFFTGYYLKDYSVSEVSKDYRKLVFEFSKMGLYDKKGHIMFATLCFIAMLFA
                                                                                                                                              GTAWQYLDRFFTGYYVQDYSVSEMSKDYRRLVSEFSKMGLFKTPGKGVYCSIFFVSVLFA
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                        GISIGWWKWNHNAHHIACNSLEYDPDLQYIPFLVVSSKFFGSLTSHFYEKRLTFDSLSRF
                                                                                                                                                                                    KKYITSDELKNHDKPGDLWISIQGKAYDVSDWVKDHPGGSFPLKSLAGQEVTDAFVAFHP
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                                                                                                                                                                                                                                                                                             448 AA;
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(TrEMBLrel. 04, Last sequence update)
(TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                             51635 MW;
                                                                                                                                                                                                                               59.1%; Score 1460.5; DB 10; Lengu
55.2%; Pred. No. 8.8e-122;
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ProDom; PD000612; CVr B5; 1.
ProDom; PD001081; FA desat fam; 1.
PROSITE; PS50255; CYTOCHROME_B5_2;
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InterPro; IPR001199; Cyt B5.
InterPro; IPR005804; FA desat_fam.
Pfam; PF00487; FA desaturase; 1.
Pfam; PF00173; heme_1; 1.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trachec
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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01-MAR-2003 (TrEMBLrel.
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tion and c
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Q9ZRP8;
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ProDom; PD001081; FA desat fam; 1.
PROSITE; PS50255; CYTOCHROME_B5_2;
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Interpro; IPR005804; FA desat
Pfam; PF00487; FA desatrase;
Pfam; PF00173; heme_1; 1.
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MEDLINE=99003197; PubMed=9786850;
Sperling P., Zaehringer U., Heinz E.;
"A Sphingolipid Desaturase from Higher Plants Identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids II; Brassicales; Brassicaceae; Brassica.
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Eukaryota; Viridiplantae;
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J. Biol. Chem. 273:28590-28596(1998)
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  NWQERIIFVFLSMAVTAIQHVQFCLNHFAADVYTGPPNGNDWFEKQTAGTLDISCRSYMD
                         NWPERVMYFTSCLAVAGFQHWQFSLNHFASNVYTGLPSGNDWFHQQTKGTLNITASAWWD
                                                                                                 FVSFQHWTFYPALLSVRLYLFILSFKVVFSNNKRVYKRSQEILGYAAFLTWYSLLLSRLP
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; campanulids; Asterales; Asteraceae; Asteroideae;
Heliantheae; Helianthus.
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ProDom; PD001081; FA desat fam;
PROSITE; PS50255; CYTOCHROME B5
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STRAIN=cv. inbred line HA89;
TISSUE=Cotyledons of developing sunflower
MEDLINE=96028121; PubMed=7588718;
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InterPro; IPR005804; FA_deeat_fam.
Pfam; PF00487; FA_deeaturase; 1.
Pfam; PF00173; heme_1; 1.
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HSSP; P00171; 1F03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sperling P., Blume A., Zaehringer U., Heinz E.; "Further characterization of delta 8-sphingolipid desaturases
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MEDLINE=21116801; PubMed=11171153;
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SIMILARITY: BELONGS TO THE CYTOCH
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                                                                            LSVYGVLYCKSTWAHLCSGLLMGMLWLQSGWVGHDSCHYQVMPNRKLNRLFQIIAGNVIA
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(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                               52231 MW;
                                                                                                                                                                                                                                                                                                                                           56.3%; Score 1391.5; DB 10
52.7%; Pred. No. 1.3e-115;
tive 90; Mismatches 119;
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c_B5; 1.
c_ast_fam;
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Matches 231
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SEQUENCE
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Haas B.J., Volfovsky N., Town C.D., Teldmann K.A., Flavell R.B., White O.
"Full-length messenger RNA sequences annotation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Delta-8 sphingolipid desaturase.

Arabidopsis thaliana (Mouse-ear cress).

Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid,

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid,

Spermatophyta; Magnoliophyta; eudicotyledons;

Spermatophyta; Magnoliophyta;

Spermatophyta; Magnoliophyta;

Spermatophyta; Magnoliophyta;

Spermatophyta; Magnoliophyta;

Spermatophyta; Magnoliophyta;

Spermatophyta;

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Q8LB96; O1-OCT-2002 (TrEMBLrel 22, Created)
O1-OCT-2002 (TrEMBLrel 22, Last sequence update)
O1-MAR-2003 (TrEMBLrel 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. Brover V., Troukha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom; PD000612; Cyt_B5; 1.
ProDom; PD001081; FA_desat_fam; 1.
PROSITE; PS50255; CYTOCHROME_B5_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Feldmann K.;
"Full-Length cDNA from Arabidopsis thaliana.";
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InterPro; IPR005804; FA_desat_fam.
Pfam; PF00487; FA_desaturase; 1.
Pfam; PF00173; heme_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                       55.6%; Score 1372.5; DB 10.1 clarity 51.7%; Pred. No. 6.2e-114; Conservative 95; Mismatches 120;
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O., Salzberg S.L.
es greatly improve
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Q9ZRP7;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Delta-8 sphingolipid desaturase (AT3G61580/F2A19_180)
SLD1 OR F2A19.180 OR AT3G61580.
Southwick A., Nguyen M., Tripp M., Palm C.J., Jones T., Wu T., Carninci P., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hayashizaki Y., Hsuan V.W., Lee J.M., Ishida J., Kamiya Kawai J., Kim C.J., Narusaka M., Quach H.L., Sakurai T., Satou M., Seki M., Shinn P., Tang C.C., Toroumi M., Wallender E.K., Wong C., Wu H.C., Yamada K., Yu G., Yuan S., Shinozaki K., Ecker J.,
                                                                                                                                                                                                                                                                              Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=cv. Columbia; TISSUE=Flower, MAINLY MEDLINE=99003197; PubMed=9786850; Sperling P., Zaehringre, Heinz E; "A sphingolipid desaturase from higher plar cytochrome b5 fusion protein."; J. Biol. Chem. 273:28590-28596(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabio
                                                                                                                                                                                                          "Arabidopsis cDNA clones.";
Submitted (OCT-2001) to the
                                                                                                                                                                                                                                                                         Yamamura Y., Yu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EU Arabidopsis sequencing Submitted (JAN-2000) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   De Haan M., Maarse A.C., Grivell L.A., Mayer K.F.X., Quetier F., Salanoubat M Submitted (NOV-1999) to the EMBL/GenBa
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the EMBL/Ge
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edons; core eudicots; Rosidae;
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RESULT
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AC Q9
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AC Q9
AC DT 01
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Best Local S
Matches 231
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Submitted (SEP-2002) to the EMBL/GenB
-! SIMILARITY BELONGS TO THE CYTOCH
EMBL; AJ224161; CAA11858.1; -.
EMBL; AJ224161; CAA11858.1; -.
EMBL; BT000442; AAL16189.1; -.
EMBL; BT000442; AAL17419.1; -.
HSSP, P00171; 115U
InterPro; IPR001199; Cyt B5.
InterPro; IPR005804; FA desat fam.
Pfam; PF00487; FA desaturase; 1.
ProDom; PD000612; Cyt B5; 1.
ProDom; PD001081; FA desat fam; 1.
PROSITE; PS50255; CYTOCHROME_B5_2; 1.
Heme.
                                                                                  O9FR82 PRELIMINARY; PRT; 446 AA.

O9FR82;
O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
O1-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Delta 8-sphingolipid desaturase.
SLD1.
                                             Borago officinalis (Bourrache) (Borage).
Eukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnoliophyta; eudicotyledons;
Asteridae; lamiids; Boraginaceae; Borago.
SEQUENCE FROM N.A.
MEDLINE=21092516; PubMed=11162428;
Libisch B., Michaelson L.V., Lewis
                                    NCBI_TaxID=13363;
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                                                                                                                                                                                          KTAAYQARDVANPVVKNLVWEALNTHG
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Pred. No. 6.2e
  Lewis
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                                                        Embryophyta; Tracheophyta; edons; core eudicots;
  Shewry
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 P.R.,
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Best Local S
Matches 227
                                                               Q9ZTU8;
Q9ZTU8;
01-MAY-1999
01-MAY-1999
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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-!- SIMILARITY: BELONGS TO 7
EMBL; AF133728; AAG43277.1;
HSSP; P00171; 1I5U.
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                                                               (TrEMBLrel.) (TrEMBLrel.)
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                                                                                                     PRELIMINARY;
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InterPro; IPRO01199; Cyt B5.
InterPro; IPRO05804; FA_desat_fam.
Pfam; PF00487; FA_desaturase; 1.
Pfam; PF00173; heme_1; 1.
ProDom; PD000612; Cyt B5; 1.
ProDom; PD001081; FA_desat_fam; 1.
PROSITE; PS50255; CYTOCHROME_B5_2; 1
Triticum aestivum (Wheat).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideau
Triticeae; Triticum.
NCBI_TaxID=4565;
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Sperling P., Libisch B., Zaehringer U., Napier J.A.,
"Functional identification of a delta 8-sphingolipid
Borago officinal1s.";
Arch. Biochem. Biophys. 388:293-298(2001).
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ijochem. Biophys. Res. Commun. 279:779-785(2000).
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TO THE CYTOCHROME
                                                                                                                              Created)
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Last ann
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Pred. No. 1.1e-109;
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RESULT
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Best Local S
Matches 230
Q9LENO; PRELIMINARY; PRT; 483 AA.
Q9LENO;
Q01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
01-OCT-2002 (TremBlrel. 22, Last annotation update)
01-OCT-2002 (TremBlrel. 22, Last annotation update)
Delta 6-fatty acetylenase.
Ceratodon purpureus (Moss).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Dicranidae; Dicranales; Ditrichaceae; Ceratodon.
NCBI_TaxID=3225;
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SEQUENCE FROM N.
STRAIN=cv. ET3;
Delhaize E., Heb
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SEQUENCE
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ProDom; PD0001081; Cyt B5; 1.
PRODOM; PD001081; FA desat fam; 1.
PROSITE; PS50255; CYTOCHROME B5_2;
PROSITE; PS00038; HLH_1; 1.
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-!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
EMBL; AF031194; AAD10250.1; -.
HSSP; P00171; 115U.
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InterPro; IPR005804; FA desat fam.
InterPro; IPR001092; HLH_basic.
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52.0%; Pred. No. 7.3;
tive 75; Mismatches
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O9LEM9;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-7002 (TrEMBLE). 22, Last annotation update
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Eur. J. Biochem. 267:3801-3811(2000).
-!- SIMILARITY: BELONGS TO THE CYTOCHROME
EMBL; AJ250734; CAB94992-1; -.
HSSP; P04166; 1B5M.
InterPro; IPR001199; Cyt. B5.
InterPro; IPR005804; AGEBat_fam.
InterPro; IPR005804; AGEBat_fam.
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Pfam; PF00173; heme 1; 1.
ProDom; PD000612; Cyt_B5; 1.
ProDom; PD001081; FA_desat_fam; 2.
PROSITE; PS50255; CYTOCHROME_B5_2;
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MEDLINE=20307617; PubMed=1084899;
Sperling P. Lee M., Girke T., Zachringer U., Stymne S., Heinz
"A bifunctional delta 6-fatty acyl acetylenase/desaturase from
"A bifunctional delta 6-fatty acyl acetylenase/desaturase from
"B Ceratodon purpureus. A new member of the cytochrome b5
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35.7%;
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Pred. No. 1.1e-
71; Mismatches
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Ceratodon purpureus (Moss). Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta; Bryopsida; Dicranidae; Dicranales; Ditrichaceae; Ceratodon.

Delta 6-fatty acid desaturase.

SEQUENCE FROM N.A.
STRAIN=wt3; TISSUE=Protonemata;

NCBI_TaxID=3225;

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Search completed: January 1, 2004, 06:33:52 Job time : 43.4085 secs
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InterPro; IPRO05804; FA_desat_fam.
Pfam; PF00487; FA_desaturase; 1.
Pfam; PF00173; heme_1; 1.
ProDom; PD000612; Cyt_B5; 1.
ProDom; PD001081; FA_desat_fam; 2.
PROSITE; PS50255; CYTOCHROME_B5_2; 1.
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Eur. J. Biochem. 267:3801-3811(2000).
-!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
EMBL; AJ250735; CAB94993.1; -.
HSSP; P00171; 1EHB.
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Sperling P., Lee M., Girke T., Zaehringer U., Stymne S., Heinz E.;
"A bifunctional delta 6-fatty acyl acetylenase/desaturase from the
moss Ceratodon purpureus. A new member of the cytochrome b5
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                                                                     LVYEDVSMASGTYRVLKTLKDVÁ
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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## TELECOMMUNICATION INFORMATION: : TELEPHONE: (516) 742-4343 : TELEFAX: (516) 742-4366 : TELEFAX: (516) 742-4366 : TELEFAX: 230 901 SANS UR : INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: : EENGTH: 448 amino acids : TYPE: amino acid : TYPE: amino acid : TYPE: amino acid : TYPE: DNA (genomic) US-08-366-779-5 US-08-366-779-5 ; Sequence 5, Application ; Patent No. 5614393 ; GENERAL INFORMATION: ZIP: 11530 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS: ATTORNEY/AGENT INFORMATION: APPLICANT: Thomas, Terry L. APPLICANT: Reddy, Avutu S. APPLICANT: Nuccio, Michael APPLICANT: Freyssinet, Georges L. APPLICANT: Numberg, Andrew N. TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY TITLE OF INVENTION: DELTA 6-DESATURASE NAME: Presser, Leopold REGISTRATION NUMBER: 19, REFERENCE/DOCKET NUMBER: APPLICATION NUMBER: FILING DATE: 30-DEC-CLASSIFICATION: 800 ADDRESSEE: SSEE: Scully, Scott, Murphy & Presser T: 400 Garden City Plaza Garden City Application US/08366779 New York United States 30-DEC-1994 US/08/366,779 19,827 8383ZYXW

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Query Match Best Local Similarity Matches 245; Conserv

Conservative

59.1%; Score 1459.5; DB 1; 55.2%; Pred. No. 3.6e-150; ative 90; Mismatches 108;

Indels Length 448;

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APPLICANT:
APPLICANT:
                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/366,779
FILING DATE: 30-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Freyssinet, Georges L.
APPLICANT: Numberg, Andrew N.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY
TITLE OF INVENTION: DELTA 6-DESATURASE
NUMBER OF SEQUENCES: 25
                                                                      NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 83
TELECOMMUNICATION INFORMATION:
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                 TELEPHONE: (516) 742-4366
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400 Garden City Plaza
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Reddy, Avutu S.
Nuccio, Michael
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Best Local Similarity
Matches 245; Conserv
                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,254
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 19,
                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
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LENGTH: 448 amino acid
                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                  STREET: 400 Garden
CITY: Garden City
STATE: New York
                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                  COUNTRY:
REFERENCE/DOCKET NUMBER:
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Pred. No. 3.6e-150;
0; Mismatches 108;
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TELECOMMUNICATION INFORMATION:

TELEPHONE: (516)

(516) 742-4343

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Sequence 5, Application US/VULLE.

Sequence 5, Application:
Patent No. 597264

Patent No. 597264

Patent No. 5972664

Patent No. 5972664

Papplicant: KNUTZON, DEBORAH

APPLICANT: MURKERJI, PRADIP

APPLICANT: HUANG, YUNG-SHENG

APPLICANT: THURMOND, JENNIFER

APPLICANT: CHAUDHARY, SUNITA

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS

TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:
ADDRESSE: RAE-VENTER LAW GROUP, P.C.

ADDRESSE: RAE-VENTER LAW GROUP, P.C.
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US-08-833-610-5
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TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
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RESULT 5
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                                                                                                                                   Sequence 15, Application Patent No. 6075183
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
TYPB: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 58.8%; Score 1451.5; DB 2; Best Local Similarity 55.2%; Pred. No. 2.6e-149; Matches 244; Conservative 90; Mismatches 107;
APPLICANT: KNUTZON, DEBORAH
APPLICANT: MUKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
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REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA: US/08/833,610 APPLICATION NUMBER: US/08/833,610
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CLASSIFICATION: 435
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                                                                                                                                                           5, Application US/08834033A 6075183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FVSYQHWTFYPIMCAARLNMYVQSL-IMLLTKRNVSYRAQELLGCLVFSIWYPLLVSCLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GVSVAWWKLDHNTHHFACNSANLDPDIQHLPIIAISPKFFNSLTSYYHNCKMTYDRAARF 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KKYITSDELKNHDKPGDLWISIQGKAYDVSDWVKDHPGGSFPLKSLAGQEVTDAFVAFHP
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ADDRESSEE: LIMBACH AND LIMBACH, L.L.P. STREET: 2001 FERRY BUILDING CITY: SAN FRANCISCO

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US-08-934-254-27
; Sequence 27, Application US/08934254
; Patent No. 6355861
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Best Local Similarity 55.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834
FILING DATE: 11-APR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CAB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEPHONE: (415) 433-8716
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INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: not
TOPOLOGY: linear
MOLECULE TYPE: pepti
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 MSVYGVLFCEGVLVHLFSGCLMGFLWIQSGWIGHDAGHYMVVSDSRLNKFMGIFAANCLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 GTAWQYLDREFTGYYVQDYSVSEMSKDYRRLVSEFSKMGLFKTPGKGVYCSIFFVSVLFA 124
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                                                                                                                                AMEAKDVTKPVPKNMVWEAMNT 446
                                                                                                                                                                                                         WFHGGLHFQISHHLFPRMPKCHFRKISFIVNKLCQKHNLSYETATMWEANKMVYSTLRAV
                                                                                                                                                                                                                                                                                                                                    FVSYOHWTFYPIMCAARLNMYVQSL-IMLLTKRNVSYRAQELLGCLVFSIWYPLLVSCLP
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                                                                                                                                                                                                                                                             NWGERIMFVIASLSVTGMQQVQFSLNHFSSSVYVGKPKGNNWFEKQTDGTLDISCPPWMD
                                                                                                                                                                                                                                                                                    NWPERVMYETSCLAVAGFQHWQFSLNHFASNVYTGLPSGNDWFHQQTKGTLNITASAWWD
                                                                                                                                                                                                                                                                                                                                                                                                               GISIGWWKWNHNAHHIACNSLEYDPDLQYIPFLVVSSKFFGSLTSHFYEKRLTFDSLSRF
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                                                                                                               ALQARDITKPLPKNLVWEALHT 446
                                                                                                                                                                                      WFHGGLQFQIEHHLFPKMPRCNLRKISPYVIELCKKHNLPYNYASFSKANEMTLRTLRNT
                                                                                                                                                                                                                                                                                                                                                             FVSFQHWTFYPALLSVRLYLFILSFKVVFSNNKRVYKRSQEILGYAAFLTWYSLLLSRLP
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Pred. No. 2.6e-149;
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NAME: PRESET, LEODOLD
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 8383
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEPAX: (516) 742-4346
TELEPAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acids
TYPE: amino acids
TOPOLOGY: linear
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Best Local S
Matches 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Thomas, TITITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Scully, Scott, Murphy & Presser STREET: 400 Garden City Plaza CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: United States
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 421
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                                                                                                                                                                                                                                                                               182 VIAGVSVAWWKLDHNTHHFACNSANLDPDIQHLFIIAISPKFFNSLTSYYHNCKMTYDRA 241
                                                                                                                                                                                                                                                                                                                                124 MMAAIVYGVLASESVGVHMLCGALLGLLWIQAAYVGHDSGHYQVMPTRGYNRITQLIAGN
                                                                                                                                                                                                                                                                                                                                                   233;
                                                                                                                                                                                                                                                                                                                                                                                                     64 HPGTAWRHLDPLFTGYYYLKDFEVSEISKDYRRLLNEMSRSGIFEKKGHHIMWTFVGVAV 123
                                                                                                                                                                                                                                                                                                                                                                                                                              63 HPGTAWQYLDRFFTG-YYVQDYSVSEMSKDYRRLVSEFSKMGLFKTPGKGVYCSIFFVSV
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                                                                                                                                                RLPNWPERVMYFTSCLAVAGFQHWQFSLNHFASNVYTGLPSGNDWFHQQTKGTLNITASA 361
                                                                                                                                                                                                        ARFFVSFQHWTFYPALLSVRLYLFILSFKVVFSNNKRVYKRSQEILGYAAFLTWYSLLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EAKKYITAEDLRRHNKSGDLWISIQGKVYDCSRWAAEHPGGEVPLLSLAGQDVTDAFIAY 63
 LRAVAMEAKDV-TKPVPKNMVW-EAMNTFG
                                                          WWDWFHGGLHFQIEHHLFPRMFKCHFRKISPIVNKLCQKHNLSYETATMW-EANKMVYST
                                                                                                            CLPNWPERFGFVLISFAVTAIQHVQFTLNHFSGDTYVGPPKGDNWFEKQTKGTIDITCPP
                                                                                                                                                                                   ARFLVSYQHWTYYPVMIFGRVNLFIQTFLLLLT-RRDVPDRALNLMGIAVFWTWFPLFVS
                                                                                                                                                                                                                                                         ILTGISIAWWKWTHNAHHLACNSLDYDPDLQHIPVFAVSTRLFNSITSVFYGRVLKFDEV
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PRODUCTION OF GAMMA LINOLENIC ACID
DELTA 6-DESATURASE
: 27
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Best Local Similarity 49.4
Matches 124; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: N/A
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,655
FILING DATE: 11-APR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CG1
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: KNUTZON, DEBORAH
APPLICANT: MURKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: (650) 328-4400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH:
  242
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                                                                                                                                                                                                                                                                 SVAWWKLDHNTHHFACNSANLDPDIQHLPIIAISPKFFNSLTSYYHNCKWTYDRAARFFV 246
                                                                                                                                                      SYQHFTYYPVNCFGRINLFIQTFLLLFS-KREVPDRALNFAGILVFWTWFPLLVSCLPNW
                                                                                                                                                                                              SFOHWTFYPALLSVRLYLFILSFKVVFSNNKRVYKRSQEILGYAAFLTWYSLLLSRLPNW 306
                                                                                                                                                                                                                                       SIAWWKWTHNAHHLACNSLDYDPDLOHIPVFAVSTKFFSSLTSRFYDRKLTFGPVARFLV
                                                                                                                                                                                                                                                                                                                     LYGVLACTSVFAHQIAAALLGLLWIQSAYIGHDSGHYVIMSNKSYNRFAQLLSGNCLTGI
FGGLOFOLEHH 252
                                       HGGLHFQIEHH 377
                                                                             PERFFFVFTSFTVTALQHIQFTLNHFAADVYVGPPTGSDWFEKQAAGTIDISCRSYMDWF
                                                                                                                PERVMYFTSCLAVAGFOHWOFSLNHFASNVYTGLPSGNDWFHQQTKGTLNITASAWWDWF 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                       29.7%;
                                                                                                                                                                                                                                                                                                                                                                                                    52; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                  74; Indels
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415) 433-871
TELEX: N/A
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY AGENT INFORMATION:

NAME: WARD, MICHAEL R.

REGISTRATION NUMBER: 3,651
REFERENCE/DOCKET NUMBER: CGAE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,033
FILING DATE: 11-APR-1997
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acids
STRANDEDNESS: not
TOPOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH, L.L.P
STREET: 2001 FERRY BUILDING
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nes 124; Conserva
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367 HGGLHFQIEHH 377
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                                                                                                                                                                                                                63 SIAWWKWTHNAHHLACNSLDYDPDLQHIPVFAVSTKFFSSLTSRFYDRKLTFGPVARFLV
                                                                                                                                                                                                                                                                                              3 LYGVLACTSVFAHQIAAALLGLLWIQSAYIGHDSGHYVIMSNKSYNRFAQLLSGNCLTGI
                                                                                                                                                                                                                                     SVAWWKLDHNTHHFACNSANLDPDIQHLPIIAISPKFFNSLTSYYHNCKWTYDRAARFFV 246
                                                    PERFFFVFTSFTVTALQHIQFTLNHFAADVYVGPPTGSDWFEKQAAGTIDISCRSYMDWF
                                                                                                                                SYQHFTYYPVNCFGRINLFIQTFLLLFS-KREVPDRALNFAGILVFWTWFPLLVSCLPNW 181
                                                                                                                                                                      SFQHWTFYPALLSVRLYLFILSFKVVFSNNKRVYKRSQEILGYAAFLTWYSLLLSRLPNW 306
                                                                                        PERVMYFTSCLAVAGFOHWOFSLNHFASNVYTGLPSGNDWFHQQTKGTLNITASAWWDWF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THURMOND, JENNIFER CHAUDHARY, SUNITA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       not relevant
                                                                                                                                                                                                                                                                                                                                                                            29.7%; Score 733.5; DB 3;
49.4%; Pred. No. 1.7e-71;
ative 52; Mismatches 74;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Length 252;
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RESULT 9 US-09-363-574-7 ; Sequence 7, Application US/09363574

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US-09-363-526-7

Sequence 7, Application US/09363526

; Patent No. 6410288

; GENERAL INFORMATION:
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                                                                   RESULT 10
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 124;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: N/A
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: KNUTZON, DEBORAH
APPLICANT: MURKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
LENGTH: 252 amino acid
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TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCE: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
STREET: 2001 FERRY BUILDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEPAX: (415) 433-8716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 2001 FERRY I
CITY: SAN FRANCISCO
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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                                                                                                                                                                                        PERFFFVFTSFTVTALQHIQFTLNHFAADVYVGPPTGSDWFEKQAAGTIDISCRSYMDWF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               29.7%; Score 733.5; DB 3; nilarity 49.4%; Pred. No. 1.7e-71; Conservative 52; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        252 amino acids
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                                                                                                       RESULT 11
                               Sequence 2, Application US/08834655
Patent No. 5968809
GENERAL INFORMATION:
APPLICANT:
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; TOPOLOGY: linear ; MOLECULE TYPE: peptide US-09-363-526-7
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 29.7%; Score 733.5; DB 4; Best Local Similarity 49.4%; Pred. No. 1.7e-71;
                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION UNMER: 38,651
REFERENCE/DOCKET NUMBER: CGAB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY AC
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 2001 FERRY CITY: SAN FRANCISCO STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: LIMBACH AND LIMBACH L.L.P. STREET: 2001 FERRY BUILDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                     367
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242 FGGLQFQLEHH 252
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                                   нестнестенн 377
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                                                                                                                                                                          SFQHWTFYPALLSVRLYLFILSFKVVFSNNKRVYKBSQEILGYAAFLTWYSLLLSRLPNW 306
                                                                                                               PERVMYFTSCLAVAGEQHWQFSLNHFASNVYTGLPSGNDWFHQQTKGTLNITASAWWDWF
                                                                                                                                                      SYOHFTYYPVNCFGRINLFIQTFLLLFS-KREVPDRALNFAGILVFWTWFPLLVSCLPNW
                                                                           PERFFFVFTSFTVTALQHIQFTLNHFAADVYVGPPTGSDWFEKQAAGTIDISCRSYMDWF
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HUANG, YUNG-SHENG
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KNUTZON, I

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434 EGTAEVFSRLNEVSKAASKMGK 455

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,655
FILING DATE: 11-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.124.00US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 328-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 147;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
TYPE: amino acid
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CORRESPONDENCE ADDRESS:
ADDRESSEB: RAE-VENTER LAW GROUP, P.C.
ADDRESSEB: 260 SHERIDAN AVENUE, P.O. BOX 60039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY AC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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TOPOLOGY: li
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                         412
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                                                                 374 ITGRDVHPGLFANWFTGGLNYQIEHHLFPSMPRHNFSKIQPAVETLCKKYNVRYHTTGMI 433
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EANKMYYSTLRAVAMEAKDVTK 433
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                                                                                                                                                                                                                                                                                                                                                                                                                            TLANVLSAALLGLFWQQCGWLAHDFLHHQVFQDRFWGDLFGAFLGGVCQGFSSSWWKDKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YSVSEMSKDYRRLVSEFSKMGLFKTPGKGVYCSIFFVSVLFALSVYG---VLYCK----S
                                                                                                    KGTLNITASAWWDWFHGGLHFQIBHHLFPRMPKCHFRKISPIVNKLCQKHNLSYETATMW 411
                                                                                                                                                         FLFIKDPVNMLVYFLVSQAVCGNLLAIVFSLNH-----NGMPVISKEEAVDMDFFTKQI
                                                                                                                                                                                                                                             NQTWFYFPILSFARLSWCLQSILFVLPNGQAHKPSGARVPISLVEQLSLAMHWTWYLATM
                                                                                                                                                                                                                                                                                         FOHWTFYPALLSVRLYLFILSFKVVFSNNK-----RVYKRSQEILGYAAFLTWYSLLL 300
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                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 147; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: N/A
INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/834,0334
FILING DATE: 11-APR-1997
CLASSIFICATION: 800
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NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: peptide
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LENGTH: 457 amino acids
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APPLICANT: MUKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: not
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ZIP: 94111
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TELEFAX: (415) 433-8716
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                                                                                                                                                                                                                                                                           YSVSEMSKDYRRLVSEFSKMGLFKTPGKGVYCSIFFVSVLFALSVYG---VLYCK----S
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NQTWFYFPILSFARLSWCLQSILFVLPNGQAHKPSGARVPISLVEQLSLAMHWTWYLATM
                                       FQHWTFYPALLSVRLYLFILSFKVVFSNNK------RVYKRSQEILGYAAFLTWYSLLL 300
                                                                                                                 NTHHEACNSANLDPDIQHLPIIAISPKFFNSLTSYYHNCKMTYD-----RAARFFYS 247
                                                                                                                                                                                               TWAHLCSGLLMGMLWLQSGWVGHDSCHYQVMPNRKLNRLFQIIAGNVIAGVSVAWWKLDH
                                                                              NTHHAAPNVHGEDPDIDTHPL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    not relevant
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US-09-363-574-2
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Best Local Similarity
Matches 147; Conserv
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ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
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                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: N/A
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                      TYPE: amino acids
STRANDEDNESS: not
TOPOLOGY
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APPLICANT:
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TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
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ZIP: 941
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TWAHLCSGLLMGMLWLQSGWVGHDSCHYQVMFNRKLNRLFQIIAGNVIAGVSVAWWKLDH 195
                                                            IKNDDFAAEVRKLRTLFQSLGYYDS-SKAYYA----FKVSFNLCIWGLSTVIVAKWGQTS
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                                                                                                 YSVSEMSKDYRRLVSEFSKMGLFKTPGKGVYCSIFFVSVLFALSVYG----VLYCK----S
                                                                                                                                           IDNKVYDVREFVPDHPGGSV-ILTHVGKDGTDVFDTFHPEAAWETLANFYVGDIDESDRD
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MURKERJI, PRADIP
                                                                                                                                                                                                                     22.2%; Score 549; DB 3; Length 457; ilarity 33.3%; Pred. No. 5.1e-51; Conservative 58; Mismatches 181; Indels
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                  Query Match
Best Local (
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                                                                                                                                                INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
TYPE: amino acid
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APPLICANT:
                                                                                            STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
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NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
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APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY AV
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CORRESPONDENCE ADDRESS:
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                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
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MURKERJI, PRADIP
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  Conservative
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linear
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22.2%; Score 549; DB 4; 33.3%; Pred. No. 5.1e-51; ative 58; Mismatches 181
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                                      DB 4; Length 457;
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RESULT 15
US-09-330-235-18
US-09-330-235-18
Sequence 18, Application US/09330235
Patent No. 6459018
GENERAL INFORMATION:
APPLICANT: KNULZON, Debbie
TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN FILE REFERENCE: MOCO.156.00US
CURRENT APPLICATION NUMBER: US/09/330,235
CURRENT FILING DATE: 1999-06-10
PRIOR APPLICATION NUMBER: 60/089,043
PRIOR APPLICATION NUMBER: 60/089,043
PRIOR APPLICATION NUMBER: 60/089,043
PRIOR FILING DATE: 1998-06-12
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.0
SEQ ID NO 18
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; TYPE: PRT
; ORGANISM: Mortierella alpina
US-09-330-235-18
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    260 NQTWFYFPILSFARLSWCLQSILFVLPNGQAHKPSGARVPISLVEQLSLAMHWTWYLATM
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                                          196 NTHHFACNSANLDPDIQHLPIIAISPKFFNSLTSYYHNCKMTYD------RAARFFVS 247
                                                                                                                                                                                                                                                                                                                                                147;
                                                                                                                                                                     95 IKNDDFAAEVRKLRTLFQSLGYYDS-SKAYYA----FKVSFNLCIWGLSTVIVAKWGQTS
                                                                                                                                                                                                                                                                                      26 IKGKVYDISKWTKEHPGGELPLLSFAGQDVTDAFIAYHPGTAWQYLDRFFTGYYVQ---D
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                                                                                                                            TWAHLCSGLLMGMLWLQSGWVGHDSCHYQVMPNRKLNRLFQIIAGNVIAGVSVAWWKLDH 195
                                                                                                                                                                                                             YSVSEMSKDYRRLVSEFSKMGLFKTPGKGVYCSIFFVSVLFALSVYG---VLYCK----S
                                                                                                                                                                                                                                                       IONKVYDVREFVPDHPGGSV-ILTHVGKDGTDVFDTFHPEAAWETLANFYVGDIDESDRD 94
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                                                                                  TLANVLSAALLGLFWQQCGWLAHDFLHHQVFQDRFWGDLFGAFLGGVCQGFSSSWWKDKH 209
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  NTHHAAPNVHGEDPDIDTHPL----
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                                                                                                KGTLNITASAWWDWFHGGLHFQIEHHLFPRMPKCHFRKISPIVNKLCQKHNLSYETATMW 411
                                                                                                                                                                                 SRLPNWP-ERVMYFTSCLAVAG-FQHWQFSLNHFASNVYTGLP-----SGNDWFHQQT 351
EGTAEVFSRLNEVSKAASKMGK
                                   EANKMVYSTLRAVAMEAKDVTK 433
                                                                         ITGRDVHPGLFANWFTGGLNYQIEHHLFPSMPRHNFSKIQPAVETLCKKYNVRYHTTGMI
                                                                                                                                                    FLFIKDPVNMLVYFLVSQAVCGNLLAIVFSLNH-----NGMPVISKEEAVDMDFFTKQI 373
                                                                                                                                                                                                                               NQTWFYFPILSFARLSWCLQSILFVLPNGQAHKPSGARVPISLVEQLSLAMHWTWYLATM 319
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Search completed: January 1, 2004, 06:38:12 Job time: 16.7646 secs

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Perfect score:
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Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

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5: /cgn2_6/ptodata/1/pubpaa/US07 NEW PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US08 NEW PUB.pep:*

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9: /cgn2_6/ptodata/1/pubpaa/US08 PUBCOMB.pep:*

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16: /cgn2_6/ptodata/1/pubpaa/US108 PUBCOMB.pep:*

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18: /cgn2_6/ptodata/1/pubpaa/US108 PUB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

15	14	13	12	11	10	9	8	7	6	ហ	4.	u	N	1	Result No.
449	451.5	461	477	519	519	519	549	549	549	560.5	1314.5	1391.5	1459.5	1460.5	Score
18.2	18.3	18.7	19.3	21.0	21.0	21.0	22.2	22.2	22.2	22.7	53.2	56.3	59.1	59.1	Query Match
473	444	443	366	453	453	453	458	458	457	459	452	458	448	448	Length
12	15	12	12	12	12	12	15	15	12	10	14	12	14	12	DB
US-10-369-493-6108	US-10-262-617-3	US-10-340-779A-20	US-10-369-493-4137	US-10-431-952-14	US-10-054-534B-14	US-09-769-863-14	US-10-191-513A-41	US-10-191-513A-11	US-10-278-391-4	US-09-967-477B-8	US-10-029-756-27	US-10-340-779A-11	US-10-029-756-5	US-10-340-779A-13	ID
	Sequence 3, Appl	Sequence 20, App	Sequence 4137, A	Sequence 14, App		•	•	Ξ,	Sequence 4, Appl	8 A	27,	11	5,	Sequence 13, App	Description

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. 9 444 15 US-10-191 . 8 445 15 US-10-191 . 4 432 15 US-10-191 . 4 465 15 US-10-191 . 0 323 15 US-10-340 . 0 454 12 US-10-340 . 0 447 12 US-10-054 . 8 470 12 US-10-120 . 6 433 12 US-10-120 . 6 433 12 US-10-120 . 6 433 12 US-10-120 . 6 436 12 US-10-120 . 6 437 12 US-10-120 . 6 438 12 US-10-120 . 6 439 12 US-10-120 . 7 446 12 US-10-340 . 1 456 10 US-09-967 . 0 446 12 US-10-10-10 . 1 456 10 US-09-967 . 0 446 12 US-10-10-10 . 0 446 12 US-10-190 . 0 447 15 US-10-190 . 0 446 12 US-10-190 . 0 447 15 US-10-190 . 0 448 19 10 US-09-967 . 0 449 10 US-09-967 . 0 439 12 US-10-191 . 0 439 12 US-10-191 . 0 439 12 US-10-191	308	308	311	316	316	316	319.5	320	320	320	320	320	320.5	324	333	333	336	336	342	342	342	350	371.5	374.5	419	429	429	$\mathbf{L}$	440	442.5
15 US-10-191 15 US-10-262 15 US-10-261 15 US-10-262 15 US-10-191 15 US-10-191 15 US-10-054 12 US-10-054 12 US-10-054 12 US-10-054 12 US-10-054 12 US-10-10-10 12 US-10-10-10 12 US-10-10-10 12 US-10-10-10 12 US-10-10-10 12 US-10-10-10 12 US-10-10-10-10 13 US-10-10-10-10-10-10-10-10-10-10-10-10-10-	12.5															13.5	13.6	13.6	13.8	13.8	13.8	14.2	15.0	15.2	17.0					17.9
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	-10-191-513A-	-10-191-513A-	-10-054-534B-	-10-431-952-2	-10-054-534B-	-09-769-863-2	-09-967	-10-191-513A-	-10-408	-10-156-911-3	-10-278	-09-903	-09-967	-10-156-761-913	-10-	-10-	-10-120	-10-120	-10 - 431		US-09+769-863-20	US-10-054-534B-35	-10-369	-10-340-779A-	-10-191-513A-1	-10-191-513A-3	-10-191-513A-	-10-262-617-	-10-1	1-01-
	•	14, App	-	•	29, App		4, Appl:	10, Appl	27, App.		2, Appli		6, Appli	9130, A	_	3, Appli					20, Appl	•		4, Appl:	17, Appl		9, Appl:		-	

## ALIGNMENTS

124	Qy 65 GTAWQYLDRFFTGYYVQDYSVSEMSKDYRRLVSEFSKMGLFKTPGKGVYCSIFFVSVLFA 124 ;  :   :	
65	6 KKYITSDELKNHDKPGDLWISIQGKAYDVSDWVKDHPGGSFPLKSLAGQEVTDAFVAFHP	
64	Qy 5 KKHISQADLAKHKQPGDLWISIKGKVYDISKWTKEHPGGELPLLSFAGQDVTDAFIAYHP	
<u> </u>	Õ	
	Query Match 59.1%; Score 1460.5; DB 12; Length 448;	
	, ORGANISM: Borago officinalia US-10-340-779A-13	
	TYPE: PRT	
	; SEQ 1D NO 13	
	; SOFTWARE: FASESEQ for Windows Version 4.0	
	; NUMBER OF SEQ ID NOS: 23	
	; PRIOR FILING DATE: 1997-12-23	
	; PRIOR ETLING DATE: 1998-12-23	
	; PRIOR APPLICATION NUMBER: US 09/582,034	
	; CURRENT FILING DATE: 2003-03-24	
	CURRENT APPLICATION NUMBER: US/10/340,779A	
	: FILE REFERENCE: 005407.00004	-
	. HTMLE OF THURSHOLD, Destinate	
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	; GENERAL INFORMATION:	
	; Publication No. US20030152983A1	
	; Sequence 13, Application US/10340779A	
	RESULT 1 US-10-340-779A-13	

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US-10-029-756-5
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                                      US-10-029-756-5
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Publication No. US20020108147A1
GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
   Query Match
                                                                                                                                                TELEX: 230 901 SANS UR INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/934,254
FILING DATE: <UNknown>
ATTORNEY/AGENT INFORMATION:
                                                       SEQUENCE DESCRIPTION:
                                                                         TOPOLOGY: linear MOLECULE TYPE: Protein
                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Thomas, Terry L.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              365 WFHGGLHFQIEHHLFPRMPKCHFRKISPIVNKLCQKHNLSYETATMWEANKMVYSTLRAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246 FVSYQHWTFYPIMCAARLNMYVQSL-IMLLTKRNVSYRAHELLGCLVFSIWYPLLVSCLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 GISIGWWKWNHNAHHIACNSLEYDPDLQYIPFLVVSSKFFGSLTSHFYEKRLTFDSLSRF
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                                                                                                                                                                                                                                                        NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 8383ZYXWVU
                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/10/029,756 FILING DATE: 21-Dec-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Scully, Scott, Mur. STREET: 400 Garden City Plaza CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALQARDITKPLPKNLVWEALHTHG 448
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                                                                                                             TYPE: amino acid
                                                                                                                                                                                                      TELEPHONE: (516) 742-43
TELEFAX: (516) 742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: New York
                                                                                                                               LENGTH: 448 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: United States
   59.1%;
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                                                       SEQ ID
 Score 1459.5;
                                                         NO:
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Length 448;
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                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Napier,
                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                            LENGTH: 458
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 65 GTAWQYLDRFFTGYYVQDYSVSEMSKDYRRLVSEFSKMGLFKTPGKGVYCSIFFVSVLFA 124
                                      16 KKYITSKELKKHNNPNDLWISILGKVYNVTEWAKEHPGGDAPLINLAGQDVTDAFIAFHP
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Sequence 11, Application US/10340779A Publication No. US20030152983A1 GENERAL INFORMATION:
                                                     Query Match
Best Local Similarity
Matches 234; Conserv
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PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: PCT/GB98/03895
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: UK 9814034.6
PRIOR FILING DATE: 1998-06-29
PRIOR APPLICATION NUMBER: UK 9727256.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 005407.00004
CURRENT APPLICATION NUMBER: US/10/340,779A
CURRENT FILING DATE: 2003-03-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Stobart, Keith TITLE OF INVENTION: Desaturase
                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 1997-12-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Michaelson,
                                                                                                                                                                                      ORGANISM: Helianthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             305 NWPERVMYFTSCLAVAGFOHWOFSLNHFASNVYTGLPSGNDWFHQQTKGTLNITASAWWD
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5 KKHISQADLAKHKQPGDLWISIKGKVYDISKWTKEHPGGELPLLSFAGQDVTDAFIAYHP
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                                                          Conservative
                                                                                                                                                                                                                                                                                         for Windows Version
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                                                                                                                                                                                      annus
                                                        56.3%; Score 1391.5; DB 12
52.7%; Pred. No. 2.2e-128;
tive 90; Mismatches 119;
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tive 90; Mismatches 108;
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                                                                                                             DB 12;
                                                          Indels
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RESULT 4
US-10-029-756-27
US-10-029-756-27
; Sequence 27, Application US/10029756
; Publication No. US20020108147A1
; GENERAL INFORMATION: Terry L.
APPLICANT: Thomas, Terry L.
APPLICANT: TNUENTION: PRODUCTION OF GAMMA LINOLENIC ACID
; TOPOLOGY: linear;; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: US-10-029-756-27
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                                                                                            TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-436
TELEFEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/10/029,756
FILING DATE: 21-Dec-2001
CLASSIFICATION: 4Unknown>
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: 08/934,254
FILING DATE: 4Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: SCUlly, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 8383ZYXWVU TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FVSYQHYLYYPIMCVARVNLYLQTILLLISKRK-IPDRGLNILGTLIFWTWFPLLVSRLP
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                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALQARDLTNPAPQNLAWEAFNTHG 458
                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: New York
                                                                LENGTH: 452 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: United States
                      27:
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Best Local S
Matches 149
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; TYPE: PRT ; ORGANISM: Thraustochytrium sp US-09-967-477B-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/09967477B Patent No. US20020156254A1
                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/967,477B CURRENT FILING DATE: 2002-04-16 PRIOR APPLICATION NUMBER: 60/236,303 PRIOR FILING DATE: 2000-09-28 PRIOR APPLICATION NUMBER: 60/297,562 PRIOR FILING DATE: 2001-06-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Haiping Hong
TITLE OF INVENTION: FAD4, FAD5, FAD5-2, AND FAD6, NOVEL
TITLE OF INVENTION: FATTY ACID DESATURASE FAMILY MEMBERS AND USES THEREOF
FILE REFERENCE: BNZ-001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 MMAAIVYGVLASESVGVHMLCGALLGLLWIQAAYVGHDSGHYQVMPTRGYNRITQLIAGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 HPGTAWRHLDPLFTGYYYLKDFEVSEISKDYRRLLNEMSRSGIFEKKGHHIMWTEVGVAV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 KKHIŞQADLAKHKQPGDLWİSİKGKVYDİSKWTKEHPGGELPLLSFAGQDVTDAFIAYHP
                                                                                                                                                                                            Similarity 31.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HPGTAWQYLDRFFTG-YYVQDYSVSEMSKDYRRLVSEFSKMGLFKTPGKGVYCSIFFVSV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LRAVAMEAKDV-TKPVPKNMVW-EAMNTFG 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARFLVSYQHWTYYPVMIFGRVNLFIQTFLLLLT-RRDVPDRALNLMGIAVFWTWFPLFVS
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SSALKLLEQFYVG-----DVDETSKAEIEGEPASDEERARRERINEFIASYRRLRVKVK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WMDWFFGGLQFQLEHHLFPRLPRGQLRKIAPLARDLCKKHGMPYRSFGFWDDANVRTIRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARFFVSFOHWTFYPALLSVRLYLFILSFKVVFSNNKRVYKRSQEILGYAAFLTWYSLLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LRDAAVQARDLNSAPCPKKLGYGEAYNTHG
                                                                                                   KRLVSWKEIREHATPATAWIVIHHKVYDISKW-DSHPGGSV-MLTQAGEDATDAFAVFHP
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                                                                                                                                                                                              22.7%; Score 560.5; DB 10; 31.0%; Pred. No. 1.8e-46; tive 70; Mismatches 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  452
                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                               Length 459;
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RESULT 6
US-10-278-391-4
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                                                                                                                                             TELEFAX: (415) 397-83
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
STRANDENNESS: NO. US20030159164A1 Relevant TOPOLOGY: No. US20030159164A1 Relevant MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                  NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OHU-03348
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/087,578
FILING DATE: 29-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       271 VVFSNNK-----RVYKRSQEILGYAAFLTWYSLLLSRLPNWP--ERVMYF----TSC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158 HDSCHYQVMPNRKLNRLFQIIAGNVIAGVSVAWWKLDHNTHHFACNSANL------DPD 210
                                                                                              LENGTH: 457 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/10/278,391
FILING DATE: 23-Oct-2002
CLASSIFICATION: 800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAVAGFQHWQFSLNHFASNYYTGLPSGNDWFHQQTKGTLNITASAWWDWFHGGLHFQIEH 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YVFTEFSFGIFDKVEFDGPEKAGLIVHYIW-QLAIPYFCNMSLFEGVAYFLMGQASCGLL 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IQHLPIIAISPKFFNSLTSYYHNCKMTYDRAARFFVSFQHWTFYPALLSVRLYLFILSFK 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KMGLEKTPGKGVYCSIFFVSVLFALSVYGVLYC---KSTWAHLCSGLLMGMLWLQSGWVG 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: CALIFORNIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GMGLY--DASALYYAWKLVST-FGIAVLSMAICFFFNSFAMYMVAGVIMGLFYQQSGWLA 177
                                                                                                                                                                                                             TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INVENTION: COMPOSITIONS AND METHODS FOR THE SYNTHESIS OF FATTY ACIDS, THEIR DERIVATIVES AND DOWNSTREAM
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HUANG, YUNG-SHENG
KIRCHNER, STEPHEN J.
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KELDER, BRUCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11, Application US/10191513A Publication No. US20030104596A1 GENERAL INFORMATION:
  Query Match
Best Local Similarity
                                                                                  LENGTH: 458

TYPE: PRT

ORGANISM: Homo sapiens
FEATURE:

NAME/KEY: VARIANT
LOCATION: (458)...(458)

OTHER INFORMATION: Xaa =
                                                                                                                                                                                                                                                        SEQ ID NO 11
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                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 1997-04-11
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSEQ for Windows
                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/191,513A
CURRENT FILING DATE: 2002-09-25
PRIOR APPLICATION NUMBER: US 09/227,613
PRIOR FILING DATE: 1999-01-08
PRIOR APPLICATION NUMBER: PCT/US98/07422
PRIOR FILING DATE: 1998-04-10
PRIOR APPLICATION NUMBER: US 08/833,610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF FILE REFERENCE: 6295.US.D3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Abbott Laboratories APPLICANT: Mukerji, Pardip
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196 NTHHEACNSANLDEDIQHLFITAISEKEFNSLTSYYHNCKMTYD-----RAARFFVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136 TWAHLCSGLLMGMLWLQSGWVGHDSCHYQVMPNRKLNRLFQIIAGNVIAGVSVAWWKLDH 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83 YSVSEMSKDYRRLVSEFSKMGLFKTPGKGVYCSIFFVSVLFALSVYG---VLYCK----S
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Leonard, Amanda E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Huang,
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  22.2%;
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                                                                                       = Unknown or other at position 458
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                                                                                                                                                                                                                                                                             Version 4.0
Score 549; DB 15;
Pred. No. 2.4e-45;
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Pred. No. 2.4e-45;
8; Mismatches 181;
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                     Length 458
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                                                                                                                                               US-10-191-513A-41
                                                                 Best Local Similarity Matches 147; Conserv
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 41
LENGTH: 458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 41, Application US/10191513A Publication No. US20030104596A1
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                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 09/227,613
PRIOR FILING DATE: 1999-01-08
PRIOR APPLICATION NUMBER: PCT/US98/07422
PRIOR FILING DATE: 1998-04-10
PRIOR APPLICATION NUMBER: US 08/833,610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Huang, Yung-Sheng
APPLICANT: Tapas, Das
TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
FILE REFERENCE: 6295.US.D3
CURRENT APPLICATION NUMBER: US/10/191,513A
CURRENT FILING DATE: 2002-09-25
                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PCT/US98/07422
PRIOR FILING DATE: 1998-04-10
PRIOR APPLICATION NUMBER: US 08/833,610
PRIOR FILING DATE: 1997-04-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Abbott Laboratories APPLICANT: Mukerji, Pardip
                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: VARIANT
LOCATION: (458)...(458)
OTHER INFORMATION: Xaa = Unknown or
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26 IKGKVYDISKWTKEHPGGELPLLSFAGQDVTDAFIAYHPGTAWQYLDRFFTGYYVQ---D
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Leonard, Amanda E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NQTWFYFPILSFARLSWCLQSILFVLPNGQAHKPSGARVPISLVEQLSLAMHWTWYLATM
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                                                                 Conservative
                                                             22.2%; Score 549; DB 15; 33.3%; Pred. No. 2.4e-45; tive 58; Mismatches 181;
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                                                                                                                                                                other at
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                                                                                                    Length 458;
                                                               Indels
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US-09-769-863-14
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APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
FILE REFERENCE: 6763.US.01
CURRENT APPLICATION NUMBER: US/09/769,863
CURRENT FILING DATE: 2001-01-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/09769863 Publication No. US20030157144A1 GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 453
                                                                                                                                                                                                                                                                                                                   Match 21.0%; Score 519; DB 12; Local Similarity 30.2%; Pred. No. 2.1e-42; Les 132; Conservative 78; Mismatches 165;
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                                                                                                                         114 --CSIFFVSVLFALSVYGVLYCKSTWAHLCSGLLMGMLWLQSGWVGHDSCHYQVMPNRKL
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                                                                                                                                                                                                                                                                              8 ISQADLAKHKQPGDLWISIKGKVYDISKWTKEHPGGELPLLSFAGQDVTDAFIAYHPGTA 67
    GDLVGVMVGNLWQGFSVQWWKNKHNTHHAIPNLHATPEIAFHGDPDIDTMPILAWSLKWA
                                           NRLFQIIAGNVIAGVSVAWWKLDHNTHHFACN-----SANLDPDIQHLPIIAISPKFF
                                                                              YKCASTLSIALVSAAI--CLHFDSTAMYMVAAVILGLFYQQCGWLAHDFLHHQVFENHLF 184
                                                                                                                                                                LKLLEQYYVGDVDQSTAAVDTSISDEVKKSQSDFIASYRKLRLEVKRLGLYDS-SKLYYL
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Das, Tapas
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Huang, Yung-Sheng
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FILE REFERENCE: 6763.US.P1
CURRENT APPLICATION NUMBER: US/10/054,534B
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: US 09/769,863
PRIOR FILING DATE: 2001-01-25
NUMBER OF EQ ID NOS: 55
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 453
TYPE: PRT
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US-10-054-534B-14
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Matches
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APPLICANT: Mukerji, Pradip
APPLICANT: Huang, Yung-Sheng
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APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: DESATURASE GENES AND USES
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APPLICANT: Das, Tapas
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les 132; Conserv
329 LNHFASNVYTGLPSGNDWFHQQTKGTLNITASAWWDWFHGGLHFQIEHHLFPRMPKCHFR
                                                          296 VQYPLLERAGLLLYY------GWNLGLVYAANMSLLQAAAFLFVSQASCGLFLAMVFS
                                                                                                                                                                           225 NSLTSYYHNCKMTYDRAARFFVSFQHWTFYPALLSVRLYLFILSFKVVFSN---NKRVYK
                                                                                                                                                                                                               185 GDLVGVMVGNLWQGFSVQWWKNKHNTHHAIPNLHATPEIAFHGDPDIDTMPILAWSLKMA
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                                                                                                RSQEILGYAAFLTWYSLLLSRLPNWPERVMY----
                                                                                                                                      QHAVD-----SPVGLFFMRYQAYLYFPILLFARISWVIQSAMYAFYNVGPGGTFDK
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APPLICANT: Thurmond, Jennifer
APPLICANT: Pereira, Suzette L.
ITITLE OF INVENTION: DESATURASE GENES AND USES THI
FILE REFERENCE: 6763.US.O1
CURRENT APPLICATION NUMBER: US/10/431,952
CURRENT FILING DATE: 2003-05-08
PRIOR APPLICATION NUMBER: US/09/769,863
PRIOR APPLICATION NUMBER: US/09/769,863
PRIOR APPLICATION NUMBER: US/09/769,863
PRIOR FILING DATE: 2001-01-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
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US-10-431-952-14
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Best Local
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APPLICANT: Huang, Yung-Sheng
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 453
TYPE: PRT
ORGANISM: Saprolegnia diclina
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                                    389
                                                                          348
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                                                                                                                                                                                                                                                                                                                                            172 NRLFQIIAGNVIAGVSVAWWKLDHNTHHFACN-----SANLDPDIQHLPIIAISPKFF
                                                                                                                                                                                                                                                                                                                                                                                                                               114 -- CSIFFVSVLFALSVYGVLYCKSTWAHLCSGLLMGMLWLQSGWVGHDSCHYQVMPNRKL 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 348 VGHNGMEVF-DKDSKPDFWKLQVLSTRNVTSSLWIDWFMGGLNYQIDHHLFPMVPRHNLP 406
407
                                                                                                                                                                                                                                                                                                                                                                                        127 YKCASTLSIALVSAAI--CLHFDSTAMYMVAAVILGLFYQQCGWLAHDFLHHQVFENHLF 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 LKLLEQYYVGDVDQSTAAVDTSISDEVKKSQSDFIASYRKLRLEVKRLGLYDS-SKLYYL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 WQYLDRFFTGYYVQ-----DYSVSEMSK------DYRRLVSEFSKMGLFKTPGKGVY- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 ISQADLAKHKQPGDLWISIKGKVYDISKWTKEHPGGELPLLSFAGQDVTDAFIAYHPGTA
                                    KISPIVNKLCQKHNLSY 405
                                                                                                                                                                                                                                  QHAVD---
                                                                                                                                                                                                                                                                     NSLTSYYHNCKMTYDRAARFFVSFQHWTFYPALLSVRLYLFILSFKVVFSN---NKRVYK 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Huang, Lapas
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                                                                                                               LNHFASNVYTGLPSGNDWFHQQTKGTLNITASAWWDWFHGGLHFQIEHHLFPRMPKCHFR 388
                                                                                                                                                                                                                                                                                                             GDLVGVMVGNLWQGFSVQWWKNKHNTHHAIPNLHATPEIAFHGDPDIDTMPILAWSLKMA
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                                                                                                                                                     VQYPLLERAGLLLYY------GWNLGLVYAANMSLLQAAAFLFVSQASCGLFLAMVFS
                                                                                                                                                                                            RSQEILGYAAFLTWYSLLLSRLFNWPERVMY------FTSCLAVAGFQHWQFS 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALNVLVKSLCKQYDIPY
                                                                          VGHNGMEVF-DKDSKPDFWKLQVLSTRNVTSSLWIDWFMGGLNYQIDHHLFPMVPRHNLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.0%; Score 519; DB 12;
30.2%; Pred. No. 2.1e-42;
rative 78; Mismatches 165
                                                                                                                                                                                                                                  ----SPVGLFFMRYQAYLYFFILLFARISWVIQSAMYAFYNVGPGGTFDK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 453;
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                                                                                                                                                                                                                                                                                                             244
                                                                            406
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US-10-369-493-4137 ; Sequence 4137, Application US/10369493 ; Publication No. US20030233675A1

RESULT 12

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APPLICANT: Michaelson, Louise
APPLICANT: Stobart, Keith
TITLE OF INVENTION: Desaturase
FILE REFERENCE: 005407.0004
CURRENT APPLICATION NUMBER: US/10/340,779A
CURRENT FILING DATE: 2003-03-24
PRIOR APPLICATION NUMBER: US 09/582,034
PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: PCT/GB98/03995
PRIOR FILING DATE: 1998-12-23
PRIOR PILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: UK 9814034.6
PRIOR FILING DATE: 1998-06-29
PRIOR FILING DATE: 1998-06-29
PRIOR FILING DATE: 1997-12-23
NUMBER OF SEQ ID NOS: 23
NUMBER OF SEQ ID NOS: 23
NUMBER OF SEQ ID NOS: 23
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US-10-340-779A-20
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SEQ ID NO 4137
LENGTH: 366
TYPE: PRT
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 443
                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Napier, Johnathan A.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20, Application US/10340779A Publication No. US20030152983A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianteng
TITLE OF INVENTOR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  376 HHLFPRMPKCHFRKISPIVNKLCQKHNLSYETATMWEANKMVYSTLRAVAMEAKDVTK 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 316 CLAVAGFQHWQFSLNHFASNVYTGLPSGNDWFHQQTKGTLNITASAWWDWFHGGLHFQIE 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SANLDPDIQHLPIIAISPKFENSLTSYYHNCKMTYDRAARFFVSFQHWTFYPALLSVRLY 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SHAVTSPLHVOITLSHFAMST-SDLGPHESFPORMLRTTMDVDCPEWLDFFHGGLOFOAI 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LYRLSWEYLLKGQAPKHGPAWWHRHLELVGQVFFWCWFGYGIMYKAIDGNW-NRFVFFMI 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LFILSFKVVF----SNNKRVYKRSQEILGYAAFLTW--YSLLLSRLP-NWPERVMYFTS 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPEHDPDIEHLPFFAISHRFFTNLRSTYYDRVMEYDIFAKFFVSLQHYLYYIIMMFARLN 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FCLGSFWHQLVFTAHDAGHMGITHHFHVDTVIGIIIADFIGGLSLGWWKRNHNVHHIITN 114
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Slater, Steven (
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ilarity 31.6%;
Conservative 6:
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Pred. No. 2.2e-38;
3; Mismatches 156; Indels 2
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APPLICANT: Shah, Purvi
APPLICANT: Shah, Purvi
TITLE OF INVENTION: DELTA-6 DESATURASE HOMOLOGS
FILE REFERENCE: PF-0494-1 DIV
CURRENT APPLICATION NUMBER: US/10/262,617
CURRENT FILING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: 09/048,888
PRIOR APPLICATION NUMBER: 09/048,888
PRIOR FILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PERL Program
SEQ ID NO 3
                                                                                      ; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030077747A1 2056310CD1
US-10-262-617-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/10262617 Publication No. US20030077747A1 GENERAL INFORMATION:
  Query Match
Best Local Similarity
Matches 121; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 136;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
                                                                                                                                                                                                 LENGTH: 44
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      V Match 18.7%; Score 461; DB 12; Local Similarity 29.5%; Pred. No. 1.1e-36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 LKKHGEHDEFLEKQLEKRLDKVDINVSAYDVSVAQEKK----MVESFEKLRQKLHDDGLM 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VKYVKEWCKENNLPYLVDDYFDGYAMNLQQLKNMAEHIQAK 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPIVNKLCOKHNLSYETATMWEANKMVYSTLRAVA--MEAK 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DKY---PANSRILNNFAALQILTTRNMTPSPFIDWLWGGLNYQIEHHLFPTMPRCNLNAC 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NVYTGLPSG----NDWFHQQTKGTLNITASAWWDWFHGGLHFQIEHHLFPRMPKCHFRKI 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNAFWEQATIVGHWAWV-FYQLFL--LPTWPLRVAYFIISQMGGGLLIAH-VVTFNHNSV 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E-----ILGYAAFLTWYSLLLSRLPNWPERVMYFTSCLAVAG--FQHWQFSLNHFAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GDLCKY----KASFEKAILKIVPYOHLYFTAMLPMLRFSWTGQSVQWVFKENQMEYKVYQ 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NSLTSYYHNCKMTYDRAARFFVSFQHWTFYPALLSVRLYLFILSFKVVFSNNKRVYKRSQ 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFKNRPLNDTISLFFGNFLQGFSRDWKDKHNTHHAATNVIDHDGDIDLAPLFAFIP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KOPGDLWISIKGK-VYDISKWTKEHPGGELPLLSFAGODVTDAFIAYHPGTAWQY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KTPGKGVYCSIFFVSVLFALSVYG-VLYCKSTWAHLCSGLLMGMLWLQSGWVGHDSCHYQ 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KNASGLRMKVDGKWLYLSEELVKKHPGGAV-IEQYKNSDATHIFHAFHEGSSQAYKQLDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KANE----TYPLFKAISTLSIMAFAFYLQYLGWYITSACLLALAWQOFGWLTHEFCHQQ 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
    Conservative
18.3%; Score 451.5; DB 15; 27.0%; Pred. No. 9.4e-36; tive 69; Mismatches 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -LDRFFTGYYVQDYSVSEMSKDYRRLVSEFSKM-----GLF 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65; Mismatches 188;
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  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 72;
                                           Length
                                               444
    65;
  Gaps
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KHISQADLAKHKQPGDLWISIKGKVYDISKWTKEHPGGELPLLSFAGQDVTDAFIAYH--

OY 136 TWAHLCSGILMGMLWLQSGWVGHDSCHYQVMPNRKLNRLPQIIAGNVIAGVSVAWWKLDH 195	Qy 84 SVSEMSKDYRRLVSEFSKMGLFKTPGKGVYCSIFFVSVLFALSVYG-VLYCKS 135   ;   ;   ;   ;   ;   ;   ;   ;   ;	Qy 50FAGQDVTDAFTAYHPGTAWQYLDRFFTGYVVQDY 83	Qy 17 KQPGDLWISIKGK-VYDISKWTKEHPGGELPLLS	Query Match 18.2%; Score 449; DB 12; Length 473; Best Local Similarity 28.2%; Pred. No. 1.8e-35; Matches 138; Conservative 65; Mismatches 187; Indels 100; Gaps 18;	CURRENT APPLICATION NUMBER: US/10/369,493 CURRENT FILING DATE: 2003-02-28 PRIOR APPLICATION NUMBER: US 60/360,039 PRIOR APPLICATION NUMBER: US 60/360,039 PRIOR FILING DATE: 2002-02-21 NUMBER OF SEQ ID NOS: 47374 SEQ ID NO 6108 LENGTH: 473 TYPE: PRT ORGANISM: Caenorhabditis elegans US-10-369-493-6108	 RESULT 15 US-10-369-493-6108 ; Sequence 6108, Application US/10369493 ; Publication US2030233675A1 ; GENERAL INFORMATION	Qy 395 NKLCQKINLSYETATMWEANKMVYSTLR 422	Qy 335 NVYTGLESGNDWFHQQTKGTLNITASAWWDWFHGGLHFQIEHHLFPRMPKCHFRKISPIV 394 ::	Qy 278RVYKRSQEILGYAAFLTWYSLLLSRLDNWPERVMYFTSCLAVAGFQHWQFSLNHFAS 334   :	Qy 231 YHNCKMTYDRAARFFVSFQHWTFYPALLSVRLYLFILSFKVVFSNNK 277	Qy 171 LNRLFQIIAGNVIAGVSVAWWKLDHNTHHPACNSANLDPDIQHLPIIAISPKFFNSLTSY 230	Qy 118 FVSVLFALSVYGVLYCKSTWAHLCSGLLMGMLWLQSGWVGHDSCHYQVMPNRK 170	Qy 64 PGTAWQYLDRFFTGYYVQDYSVSEMSKDYRRLVSEFSKWGLFKTPGKGVYCSIF 117   : : :     : : :     : : :     : : :     : : :     : : :       : : : :       : : : :       : : : :       : : : :       : : : :       : : : :       : : : :       : : : :       : : : :       : : : :       : : : :       : : : :       : : : :       : : : :       : : : :       : : : :       : : : :       : : : :       : : : :       : : : :       : : : :       : : : :       : : : :       : : : :       : : : :     : : : :     : : : :     : : : :   : : :   : : :   : : :   : : :   : : : :   : : : :   : : : :   : : : :   : : : : :   : : : : :   : : : : :   : : : : :   : : : :   : : : : :   : : : : :   : : : : :   : : : : :   : : : : : :   : : : : : :   : : : : : : : : :   : : : : : : : : : : : : : : : : : : : :	Db 18 RYFTWDEVAQRSGCEERWLVIDRKVYNISEFTRRHPGGSRVISHYAGQDATDPFVAFHIN 77
								Search completed: January 1, 2004, 06:58:34 Job time : 86.3457 secs	Qy 422 RAVAMEAK 429 : :  ::   Db 462 KNMAEHIQAK 471	Qy 362 WWDWFHGGLHFQIEHHLFPRMPKCHFRKISPIVNKLCQKHNLSYETATMWEANKMVYSTL 421	Qy 308 ERVMYFTSCLAVAGFQHWQFSLNHFASNVYTGLPSGNDWFHQQTKGTLNITASA 361	Qy 256 ALLSVRLYLFILSFKVVFSNNKRVYKRSQEILGYAAFLTWYSLLLSRLPNWP 307	Qy 196 NTHHPACNSANLDPDIOHLPIIAISPKFFNSLTSYYHNCKMTYDRAARFFVSFQHWTFYP 255	Db 176 LGWYITSACLLALAWQQFGWLTHEFCHQQFTKNRPLNDTISLFFGNFLQGFSRDWWKDKH 235

5.1.6

Run

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Minimum DB
Maximum DB
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Maximum Match 10
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Pred. No. 18 the number of results predicted by chance to have

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

## Regult No. 1074.8 1000.6 536.2 535.6 384.2 370.2 367.2 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 365.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 366.4 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AUTHORS TITLE	REFERENCE	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AF031194	RESULT 1
Delhaize, E., Hebb, D.M., Gardner, R.C. and Richards, K.D. Aluminum tolerance in yeast conferred by over-expression of wheat	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum. 1 (bases 1 to 1788)	Triticum aestivum  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Triticum aestivum (bread wheat)	•	AF031194.1 GI:4104055	AF031194	Triticum aestivum S276 (S276) mRNA, complete cds.	AF031194 1788 bp mRNA linear PLN 29-JAN-1999		

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2 (bases 1 to 1788)
2 Pelhaize, E., Hebb, D.M., Gardner, R.C. and Richar
Direct Submission
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ASFVITGIQHVQFCLNHFSSAVYVGPPKGNDWFERQTAGTLDIKCSPWMDWFHGGLQF
QVEHHLFPRLFRCHYRMVAPIVRDLCKKHGLSYGAATFWEANVMTWKTLRAAALQARE
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1208 CCTIGGATGGATTGGTTCCACGGTGGCCTGCAGTTCCAGATTGAGCACCATCTGTTTCCC	B &	GCCGCGGGCGCCGACGTGCGCATGATCTCCTCCAAGGAGCTCCGCGCTCACGCTTCC	ર્શ્વ
1148 CCCAAGGCAATGACTGGTTTGAGAAGCAGACGGCAGGCACGCTCGACATCCTGTGCTCT	02 24	68 CATCCGAGCCACGGCGCGATGCCGCCCTCTGTCGATGCCAATGCCGGCCCCCGGCGAC 127	g S
2 8	P &	8 CTCCCTCTCTCTCCCCAATCCTCCCCGCCTACCAAATCAGCACCAACCCAAGGCG 67	유 성
6 8	) B &	Query Match 56.7%; Score 1000.6; DB 2; Length 96312; Best Local Similarity 77.2%; Pred. No. 1.7e-134; Matches 1307; Conservative 0; Mismatches 349; Indels 37; Gaps 6;	_
968 CAGCGGTTGCTTGAGATCGCGGGGGTCGCCACATTCTGGGCTTGGTACCCGTTGCTGGTG 	P 68	/chromosome="9" /clone="0J118_A10" BASE COUNT 26463 a 21050 c 21390 g 27309 t 100 others ORIGIN	BA OR
908 GCCAGGATAAATCTTCTCGCGCAGTCCGCCCTGTTCGTTC	QQ	/db/ /mc/ /db/	
848 GCCGCCTCGAJATTCTTCATCAGCTACCAGCACTGGACCTTCTACCCGGTAJTGTGCATC	Qy.	* by the finished sequence as soon as it is available and  * the accession number will be preserved. FEATURES Location/Qualifiers source 196312	ri Fi
788 TCCCCCAAGCTGTTCGGCAACATATGGTCCTACTTCTACCAACGGACCCTGGCGTTCGAT	Qy Db	ience will be replaced by the finished sequence as liable and the accession number will be preserved. This is a 'working draft' sequence.	
728 ATCGCCTGCAACAGCCTGGACCATGACCCGGACCTCCAGCACATGCCGCTCTTTGCCGTC	da VQ	NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This	
668 GGGAACTGCCTCACCGGCCTCAGCATCGCCTGGTGGAAGTGTAACCACAACACGCACCAC 	Оу	(E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7469) The nucleotide sequence of the BAC clone was generated by combining Monsanto and RGP-Japan sequencing data	8
608 TCGGGCCACCGCATCACCGGCCATCCGGTCCTCGACCGCGTCGTGCAGGTGCTCTCC	ОУ		
548 CTCCTCGCGGGGGGTCTCATTGGCTTCGTCTGGATCCGGTGGATGGGCCACGAC	Q dq	2002) tori,M., Sakaki,Y.	R E
488 GCCGTCCTCTTCTACGCCGCCTGTACCTCGTCCTCGCATGCGCCAGCGCCTGGGCGCAC	B 8	Ehrhartoideae; Oryzeae; Oryza.  AUTHORS Sasaki,T., Matsumoto,T., Hattori,M., Sakaki,Y. and Katayose,Y.  TITLE Oryza sativa nipponbare(GA3) genomic DNA, Chromosome 9, BAC	RE
428 TCCTCCGCGGGCCTCTTCGAACGCGTCGGCCCCACCCCA	Qy db	MS	so
368 CTCTCTGACTACGCCGTCTCCCCCGCGTCCGCCGACTACCGCCGCCTCCTCGCGCAGCTA	ОУ	OJ1118_A10, *** ŠEQUENCING IN PRŐGRESS ***. AP005554 AP005554.1 GI:21952922 HTG; HTGS PHASE2.	a sa
308 TTCGCCGCCTACCACCCGCCCTCGGCGCCCCCCCCCCCGCCGCTTCTTCGTCGCCGC	β <i>δ</i>	RESULT 2  APO05554  APO05554  DEFINITION Orvea sativa (japonica cultivar-group) chromosome 9 clone	8 6 4 8
248 CACCACCGGGGGGGGGACGTCCCGGCTTCTCACCCTGGCGGGGGAGGACGCCACCGACGCC	ρ Q		문 5
188 GCCGACGACCTCTGGATCTCCATCTCCGGCGACGTCTACGACGTCACGCCCTGGCTCCCC	B 8		S B :
88171 AGCCGCGCCGGCGCGCGCGTCCGCATGATCTCCTCGGAGGAGCTCCGCGCGCACGCGTCG 88230	da		δ.

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Sayanova, O.V., Beaudoin, F.,
Napier, J.A.
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1 (bases 1 to 1681)
Sayanova,O.V., Beaudoin,F., Michaelson,L.V., Shewry,P.R. and
                                                                                                                                             Submitted (10-FEB-2003) Crop Performance & Improvement, Research Station, Long Ashton, Bristol BS41 9AF, UK
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Location/Qualifiers
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/product="sphingolipid delta-8
/protein_id="AAP23033.1"
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/db_xref="taxon:133892"
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                                                          note="cytochrome b5 fusion desaturase"
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HPGGTAPLMALAGHDVTDAFLAYHPPSTARLLPPLSANLLLEHYSVSPTSSDYRKLLH
NFHKLDLFQTKSHTTCFTFVAMVVLFFLSLLGVPCSDSTWVHLASGGVMGVAWIQSGW
LGHDSGHYQLMSSRKKINRFAQVLSGNCLAGIS AWWKWNHNAHHLACNSLDYDPDLQH
MPFFVVSSKFFNSLTSRFYDRKLNFDGVSRFILVSYQHMSFYPVMCLARINLFAQSFML
LFSSRKVPSRFORVQEIFGIGVFWWYPLLVSCLDNWGERIMFVVASFSVTGIQHVQFCLR
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KVSPFVRDLCKKHNLFYNVTSFTMANVLTLKTLRNAAIQARDLSNPTPKNLVWEAVNT
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992 GTCGCCACATTCTGGGCTTGGTACCCGTTGCTGGTGGCTTCCCTGCCGAATTGGTGGGAG 155 ATCTCCTCCAAGGAGCTCCGCGCTCACGCTTCCGCCGACGACCTCTGGATCTCCATCTCC Similarity TTCGTCTGGATCCAGTCCGGCTGGATGGGCCACGACTCGGGCCACCGCATCACCGGC CTCGGGGTCTTTTGCAGCGACAGCACGTGGGTGCATTTGGCTAGCGGCGGGGTCATGGGG CTCACCCTGGCGGGGCAGGACGCCACCGACGCCTTCGCCGCCTACCACCCGCCCTCGGCG GGCGACGTGTACGACGTCACGCCTGGCTCCCCCACCACCCGGGCGGCGACCTCCCGCTT TACCAGCACTGGACCTTCTACCCGGTAATGTGCATCGCCAGGATAAATCTTCTCGCGCAG ACTTCTCGTTTCTACGATAGGAAGCTGAACTTCGACGGCGTGTCGAGGTTCTTGGTTAGC TGGTCCTACTTCTACCAACGGACCCTGGCGTTCGATGCCGCCTCGAAATTCTTCATCAGC GACCCGGACCTCCAGCACATGCCGCTCTTTGCCGTCTCCCCCAAGCTGTTCGGCAACATA ATCGCCTGGTGGAAGTGTAACCACAACACGCACCACATCGCCTGCAACAGCCTGGACCAT CATCCGGTCCTCGACCGTCGTGCAGGTGCTCTCCGGGAAACTGCCTCACCGGCCTCAGC TACCTCGTCCTCGCATGCGCCAGCGCCTCGGGGGCGCCTCCTCGCGGGGGGGTCTCATTGGC AAATCCCACACCACCTGCTTCACGTTCGTCGCCATGGTAGTCTTGTTCCTCAGCCTG GTCGGCCCACCCCAAGGTCCAGCTCCTGATGGCCGTCCTCTTCTACGCCGCGCTG ACCTCCTCCGACTACCGCAAACTCCTCCACAACTTCCATAAACTCGACCTTTTCCCAGACC GCGTCCGCCGACTACCGCCCCCCCCCCCCGCGCAGCTATCCTCCGCGGGCCTCTTCGAACGC GCCCGTCTCCTCCCTCTCCCCCCAACCTCCTTCTAGAACACTACTCCGTCTCCCCC ceccecrecrececrecricineerrececrecrere---acracecererecec TCCGCCCTGTTCGTTCTCACGGAGAAGAGGGTGCCGCAGCGGTTGCTTGAGATCGCGGGG TACCAGCATTGGTCGTTTTATCCGGTTATGTGCTTGGCTAGGATCAATCTGTTTGCTCAG GATCCCGACCTCCAGCATATGCCCTTCTTCGTCGTCTCCTCCAAGTTCTTCAATTCCCTT AGCAGGAAAACTAACAGGTTCGCGCAGGTCCTGAGCGGAAACTGCCTCGCTGGGATTAGT GTTGCTTGGATCCAGAGCGGTTGGCTAGGACACGATTCCGGCCATTACCAGATTATGTCT ATGGCCCTCGCAGGACACGACGTGACCGACGCTTTCCTTGCTTACCATCCCCCTTCCACC GGCCAAGTCTACGACGTCTCCTCGTGGGCCGCCCTTCATCCGGGGGGCACCGCCCCCCTC ATAACCAGCTCAGACCTGAAAGCCCACAACAAGGCAGGTGACCTATGGATATCAATCCAT TCGTTTATGTTGCTTTTCTCGAGTAGGAAGGTGCCTGATAGGGTTCAAGAGATTTTCGGA ATCGCGTGGTGGAAGTGGAACCACAACGCCCACCACCTCGCCTGCAACAGCTTGGATTAC Conservative 445 30.4%; a 0; Score 536.2; DB 8 Pred. No. 1.4e-67; 404 g Mismatches 478; 479 8 Indels Length 6 751 928 991 868 931 808 871 748 811 889 628 691 568 631 508 571 448 511 388 451 328 391 268 334 208 274 148

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Primula vialii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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Primula vialii sphingolipid delta-8 desaturase mRNA,
AY234126
                                                                                                                               Submitted (10-FEB-2003) Crop Performance & Improvement, Research Station, Long Ashton, Bristol BS41 9AF, UK Location/Qualifiers
                                                                                                                                                                   2 (bases 1 to 1385)
Sayanova,O.V., Beaudoin,F.,
Napier,J.A.
Direct Submission
                                                                                                                                                                                                                                      Identification of Primula fatty acid Delta(6)-desaturases with substrate preferences(1) FEBS Lett. 542 (1-3), 100-104 (2003)
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                                                            note="cytochrome b5 fusion desaturase"
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HPGGSAPLMALAGHDVTDAFLAYHPPSTARLLPPLSTNLLLQNHSVSPTSSDYRKLLH
NFKKIGLFQTKSHTTCVTFVANVALFFLSLYCVFCSDSAWYHLASGGVMGVANIQSGW
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Query Match Best Local Similarity 155 ATCTCCTCCAAGGAGCTCCGCGCTCACGCTTCCGCCGACGACCTCTGGATCTCCATCTCC GACCCGGACCTCCAGCACATGCCGCTCTTTGCCGTCTCCCCCCAAGCTGTTCGGCAACATA GTCGGCCCACCCCAAGGTCCAGCTCCTCGTCCTGATGGCCGTCCTTCTTACGCCGCGCTG ACCTCCTCACTACCGCAAACTCCTCCACAACTTCCATAAGATTGGCCTTTTCCAGACC TGGTCCTACTTCTACCAACGGACCCTGGCGTTCGATGCCGCCTCGAAATTCTTCATCAGC AGCAGGAAAACCAATCGGTTCGCGCAGGTCCTGAGCGGAAACTGCCTCGCTGGGATCAGC GTGGCCTGGATCCAGAGTGGTTGGCTAGGACACGACTCCGGCCATTACCAGATTATGTCT TACGGGGTCTTTTGCAGCGACAGCGCGTGGGTGCATTTGGCTAGCGGCGGGGTCATGGGG **AAATCCCACACTACATGCGTCACCTTCGTCGCCATGGTAGCCTTGTTCTTCCTCAGCCTG** GCCCGCCTCCCTCCCCTCTCCACCAACCTCCTCCTTCAAAACCACTCCGTCTCCCCC CTCACCCTGGCGGGGGACGCCACCGACGCCTTCGCCGCCTACCACCCGCCCTCGGCG ATAACCAGCTCAGACCTGAAAGGGCACAACAAGGCAGGAAACCTATGGATATCAATCCAC TCCGCCCTGTTCGTTCTCACGGAGAAGAGAGGGGTGCCGCAGCGGTTGCTTGAGATCGCGGGG TACCAGCATTGGTCGTTTTATCCGGTTATGTGCTTGGCTAGGATCAATCTGTTTGCTCAG TACCAGCACTGGACCTTCTACCCGGTAATGTGCATCGCCAGGATAAATCTTCTCGCGCAG ACTTCTCGTTTCTATGACAGGAAGCTCAGGTTTGATTCGGTGTCGAGGTTCTTGGTTAGC GATCCTGACCTCCAGCACATGCCCTTCTTTGTCGTCTCCTCCAAGTTCTTCGGTTCCCTT ATTGCGTGGTGGAAGTGGAACCACAACGCACCACCTCGCGTGCAACAGCCTTGATTAC ATCGCCTGGTGGAAGTGTAACCACAACACGCCACCACATCGCCTGCAACAGCCTGGACCAT CATCCGGTCCTCGACCGCGTCGTGCAGGTGCTCTCCGGGAACTGCCTCACCGGCCTCAGC TTCGTCTGGATCCAGTCCGGCTGGATGGGCCACGACTCACCGGC GCGTCCGCCGACTACCGCCGCCTCCTCGCGCACCTATCCTCCGCGGGCCTCTTCGAACGC cecceerrecececricines reserves contrated and contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated contrated c ATGGCCCTCGCAGGACACGACGTAACCGACGCTTTTCTAGCGTATCATCCTCCTTCTACC eeceacereraceacercaceccreecrecccaccaccaceeeceeceaccreccecrr TCCTTTATGTTGCTTTTCTCGAGTAGGAAGGTGCCCGATAGGTTTCAAGAGATATTCGGA 902 Conservative 392 30.4%; a <u>.</u> Score 535.6; DB 8; Pred. No. 1.8e-67; 341 g Mismatches 474; 358 t Indels Length 6, 842 931 811 751 991 782 871 722 662 602 691 542 631 482 571 422 511 362 451 302 391 242 334 182 274 122

35 CGCCCGCTCCTCCGCCGCTTCTTCGTTGGCCGCCTCTCTGACTACGCCGTCTCC 38	QY 275 CTCACCCTGGCGGGGCAGGACGCCACCGACGCCTTCGCCGCCTACCACCGCCCTCGGCG 334	Qy 215 GGCGACGTGTACGACGCCCTGGCTCCCCCACCACCGGCGGGCG	OY 155 ATCTCCTCCAAGGAGCTCCGCGCTCACGCTTCCGCCGACGACCTCTGGATCTCCATCTCC 214	Query Match 27.8%; Score 491.2; DB 6; Length 1702; Best Local Similarity 62.0%; Pred. No. 4.1e-61; Matches 832; Conservative 0; Mismatches 498; Indels 12; Gaps 3;	rce NT 358	AUTHORS Thomas, T. L. AUTHORS Thomas, T. L. TITLE Production of gamma linolenic acid by a .DELTA.6-desaturase JOURNAL Patent: US 6355861-A 26 12-MAR-2002; FEATURES FEATURES	URCE Unknown. ORGANISM Unknown. Unclassified.	ITION Sequence 26 from patent US 6355861. SION AR200409 ON AR200409.1 GI:20250483	1702 b	Qy 1472 GGATAA 1477 	2 AGGACCG	QY 1352 ACATTCTGGGGTGCAAATGTGCTTACATGGAAGACACTCAGGGCTGCTGCATTGCAGGCC 1411	Qy 1292 AAGGTTGCACCGGCCGTCCGCGACCTTTGCAAGAAGCATGGGCTCACTTATTCTGCAGCC 1351	Db 1143 GGTTTGCAGATCAGATCAGACCACCATCTGTTCCCGCGTTTGCCTAAGGTTCAAGGT1202	1172 AAGCAGACGGCAGGCAGGCTCGACATCCTGTGCTCTCCTTGGATGGA	QY 1112 CTGAACCACTTCTCGTCCGACGTGTATGTCGGGCCACCCAAGGGCAATGACTGGTTTGAG 1171	QY 1052 AGGGTCGCGTTTGTGCTTTTCAGCTTCACCATCTGCGGGATTCAGCACGTCCAATTCTGC 1111	Db 903 ATAGGCGTGTTCTGGGTTTGGTATCCGCTCCTGGTTTCTTGCCTTCCTAACTGGGGAGAG 962
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                                                                                   CGCCCGCTCCTCCGCCGCTTCTTCGTTGGCCGCCTCTCT---GACTACGCCGTCTCCCCC
                                                   ATGGCCCTTGCAGGACACGACGTGACCGATGCTTTCCTCGCGTACCATCCCCCTTCCACT
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for n-3 fatty acid substrates"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (09-MAR-2000) The Institute for Genomic Research, Medical Center Dr., Rockville, MD 20850, USA 3 (bases 1 to 110149)
Town,C.D. and Kaul,S.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (27-FEB-2002) The Institute for Genomic Research, 9 Medical Center Dr, Rockville, MD 20850, USA, cdtown@tigr.org On Apr 18, 2002 this sequence version replaced gi:6598465.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 110149)
Rounsley, S.D., Lin, X.,
Shen, M., Ronning, C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC005397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (1. .7273)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chromosome="2"
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                                                                                                                                                                                                                        family="(GAA)n"
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Fraser,C.M., Somerville,C.R. and Venter,J.C.
                                                                                                                                                                                                                                                     .4921)
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QTIvsggedaairiwdaetgkllkQsdeevghkeaitslckaaddshfltgshdktak
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ement(110738)
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Best Local Similarity
Matches 784; Conserv
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                                                                           45965
                                                                                                                                                                                               784;
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                                                                                                                                                                                                      Conservative
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complement(20549. .20570)
/rpt_family="(GA)n"
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                                                                                                                                                                                                                                                                                                                      /translation="MRGSNNTDLFDPKTEMDSNFSRHGSSSEGDFGFAFNDSNFSDRL
LRIEILGGPSDSRSDAEGCTSIADWARHRKRRREDNKKDNGVAISDIVACAEEQILTD
NNQPDMDDAPGGDNLDDEGEAMVEEALSGDDDASSEPNWGIDCSTVVRVKELHISSPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (join (25105. .25936, 26015. .26686. .26804, 26942. .27076, 27202. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (24966. .27557)
/gene="At2g46260"
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/gene="At2g46270"
/note="synonym: T3F17.8; identical to PIR:S20885;
/note="synonym: T3F17.8; identical to PIR:S20885;
supported by cDNA: gi 600862 gb U17891 1 ATU17891"
complement(join(<20403. .20846, 20932. .21057, 21169. .212.
21338. .21513,21600. .21648,21737. .21943,22028. .22069,
22157. .22240,22334. .22429,22512. .22556;22644. .22754,
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/gene="At2g46280"
join(18175. .18358,18507. .18722,18818. .18951.19049. 1
                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="At2g46260"

/codon_start=1

/product="expressed protein"

/protein_id="AAC62880.2"

/db_xref="GI:20197378"
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/db_xref="GI:3702321"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="synonym: T3F17.9; supported by full length
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                                                                                                   CTCGGCTTCCTCGTTGTCATCTCCGGACAGTATCGCCGGTGGTTAAGGAGCTTTGTAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAm: Nguyen, M., Tripp, M., Southwick, A., Palm, C.J., Jones, T., Wu, T., Chen, H., Cheuk, R., Chan, M., Chang, C.H., Dale, J.M., Deng, J.M., Hsuan, V.W., Lee, J.M., Kim, C.J., Quach, H.L., Onodera, C.S., Shinn, P., Tang, C.C., Toroumi, M., Wong, C., Wu, H.C., Yamada, K., Yu, G., Yuan, S., Ecker, J., Theologis, A. and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Saturai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nguyen,M., (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W. (SSP/Stanford) contributed equally to this work as PIs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (29-JAN-2003) DNA Sequencing and Technology Stanford University, 855 California Avenue, Palo Alto,
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/product="delta-8 sphingolipid
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                                                                          /gene="At3g61580"
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GDTVI LNLVGQDVTDAF I AFHFGTAWHLDHLFTGYHI RDFQVSEUSRDYRRMAAEFR
KLGLFENKGHVTLYTLAFVAAWFLGVLA'GVLAGTSVFAHQI AAALLGLLWI QSAY I GH
DSGHYYLMSNKSYNRFAQLLSGNCLTGI SI AWWKWTINAHHLACNGLDYDDDLOH I FW
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PVVQELCKKHNLFYRSWSWFEANVLTINTLKTAAYQARDVANDVVKNLVWEALNTHG"
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Sequence 3 from Patent
AX007241
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ZAEHRINGER ULRICH (DE); HEINZ ERNST (DE);
SPERLING PETRA (DE); GVS GES FUER ERWERB 1
LOCATION/Qualifiers
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Sphingolipid-desaturase
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408 c 339 g 515 t
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/protein_id="CAC07390.1"
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Cheuk,R., Chen,H., Kim,C.J., Koesema,E., Meyers,M.C., Banh,J.,

Bowser,L., Carninci,P., Dale,J.M., Goldsmith,A.D., Hayashizaki,Y.,

Bowser,L., Carninci,P., Dale,J.M., Goldsmith,A.D., Hayashizaki,Y.,

Ishida,J., Jiang,P.X., Jones,T., Kamiya,A., Karlin-Neumann,G.,

Kawai,J., Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M.,

Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J., Pham,P.K.,

Quach,H.L., Sakurai,T., Satou,M., Seki,M., Southwick,A., Tang,C.C.,

Toriumi,M., Yamada,K., Yamamura,Y., Yu,G., Yu,S., Shinozaki,K.,

Davis,R.W., Theologis,A. and Ecker,J.R.

Direct Submission
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Cheuk,R., Chen,H., Kim,C.J., Koesema,E., Meyers,M.C., Banh,J., Bowser,L., Carninci,P., Dale,J.M., Goldsmith,A.D., Hayashizaki,Y., Ishida,J., Jiang,P.X., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Lian,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Kawai,J., Lam,B., Lee,J.M., Condera,C.S., Palm,C.J., Pham,P.K., Quach,H.L., Sakurai,T., Satou,M., Seki,M., Southwick,A., Tang,C.C., Toriumi,M., Yamadaj,K., Yamamura,Y., Yu,G., Yu,S., Shinozaki,K., Davis,R.W., Theologis,A. and Ecker,J.R.
  The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL CDNAs: Cheuk, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Shinn, P., Bahh, J. Bowser, L., Dale, J.M., Goldsmith, A.D., Jiang, P.X., Jones, T., Karlin-Neumann, G.
                                                                                                                                  RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL CDNAs (RAFL CDNA: 'RIKEN Arabidopsis Full-Length CDNA): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
                                                                                                                                                                                                                                                Submitted (05-OCT-2001) Salk Institute Genomic Analysis Laboratory (SIGnAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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Arabidopsis thaliana AT3g61580/F2A19_180 mRNA,
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Hayashizaki,Y. and Shinozaki,K.
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/chromosome="3"
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Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Onodera, C.S., Palm, C.J., Pham, F.K., Quach, H.L., Tang, C.C., Toriumi, M., Yamada, K., Yamamza, Y., Davis, R.W., Theologis, A., and Ecker, J.R.
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                                                                                                                                                                                                                                                                                                                 Score 445; DB 8;
Pred. No. 1.7e-54;
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Ecker, J.R. (SSP/Salk)
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ADVYVGPPTGSDWFEKQAAGTIDISCRSYMDWFFGGLQFQLEHHLFPRLPRCHLRKVS
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DSGHYVIMSNKSYNRFAQLLSGNCLTGISIAWKKWTHNAHHLACNSLDYDPDLQHIPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Southwick, A., (SSP/Stanford) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Davis, R.W. (SSP/Stanford) contributed equally to this work as PIs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequencing and annotation of the RAFL cDNAs: Southwick, A., Tripp, M., Nguyen, M., Palm, C.J., Jones, T., Wu, T., Chen, H., Cheuk, R. Chan, M.M., Chang, C.H., Dale, J.M., Deng, J.M., Hsuan, V.W., Lee, J.M., Kim, C.J., Quach, H.L., Shinn, P., Tang, C.C., Toroumi, M., Kim, C.J., Quach, H.L., Shinn, P., Tang, C.C., Toroumi, M., Wallender, B.K., Wong, C., Wu, H.C., Yamada, K., Yu, G., Yuan, S., Wallender, B.K., Wong, C., Wu, H.C., Yamada, K., Yu, G., Yuan, S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BT000442 1743 bp mRNA linear PLN 24-SEP-2
Arabidopsis thaliana delta-8 sphingolipid desaturase (At3g61580)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spermatophyta; Magnoliophyta; eudicotyledons; corosids; eurosids II; Brassicales; Brassicaceae;
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/note="This clone is i
ecotype: Columbia"
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/mol_type="mRNA"
/db_xref="taxon:3702"
/chromosome="3"
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                                                                                                                                                                                                                                                                                                                                                                                    http://www.genoscope.cns.fr
Information on performance of analysis and a more detailed
annotation of this entry and other sequences of chromosomes 3, 4
and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (31-JAN-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mai lemcke@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project Coordinator: Marcel Salanoubat and Francis Quetier, Groupement d'Interet Public, Centre National de Sequencage - GENOSCOPE; 2 Gaston, Cremieux, BP191, 91006 Evry Cedex, France;
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16123. .16396,16503. .16538)
/gene="F2A19.10"
                                        Arabidopsis thaliana,
                                                                                                                                                                                            analysis and annotation"
                                                            note="similarity to protein kinase
                                                                                                                                             gene="F2A19.10"
                                                                                                                                                                                                                /note="overlap to BAC T20K12,
                                                                                                                                                                                                                                                           /db_xref="taxon:3702"
/chromosome="3"
                                                                                                                                                                                                                                                                                                 /mol_type="genomic
/variety="Columbia"
codon_start=1/product="putative protein"
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                               TGGCTTCCCTGCCGAATTGGTGGGAGAGGGTCGCGTTTGTGCTTTTCAGCTTCACCATCT 1085
                                                                                CGCAGCGGTTGCTTGAGATCGCGGGGGTCGCCACATTCTGGGCTTGGTACCCGTTGCTGG
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Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA
Malibu, CA 90265, USA
This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A
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Haas, B.J., Volfovsky, N., Town, C.D., Troukhan, M., Alexandrov, N., Feldmann, K.A., Flavell, R.B., White, O. and Salzberg, S.L. Full-length messenger RNA sequences greatly improve genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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/product="delta-8 sphingolipid desaturase"
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KLGLFENKGHVTLYTLAFVAAMFLRVLYGVLACTSVFAHQIAAAUSLDXDDDLQHIPV
BSGHYVIMSNKSYNRFAQLLSGWCLTGISIAWWKWTHNAHHLACNSLDXDDDLQHIPV
FAVSTKFFSSLTSRFYDRKLTFDPVARFLVSYQHFTYYPVMCFGRINLFIQTFLLLFS
KREVPDRALNFAGILVFWTWFPLLVSCLPNWPERFFVFFGFTVTALQHIQFTLHNFA
ADVYUGPFTGSDWFEKQAAGTIDISCRSYMDWFFGGLQFQLEHHLFPRLPRCHLRKVS
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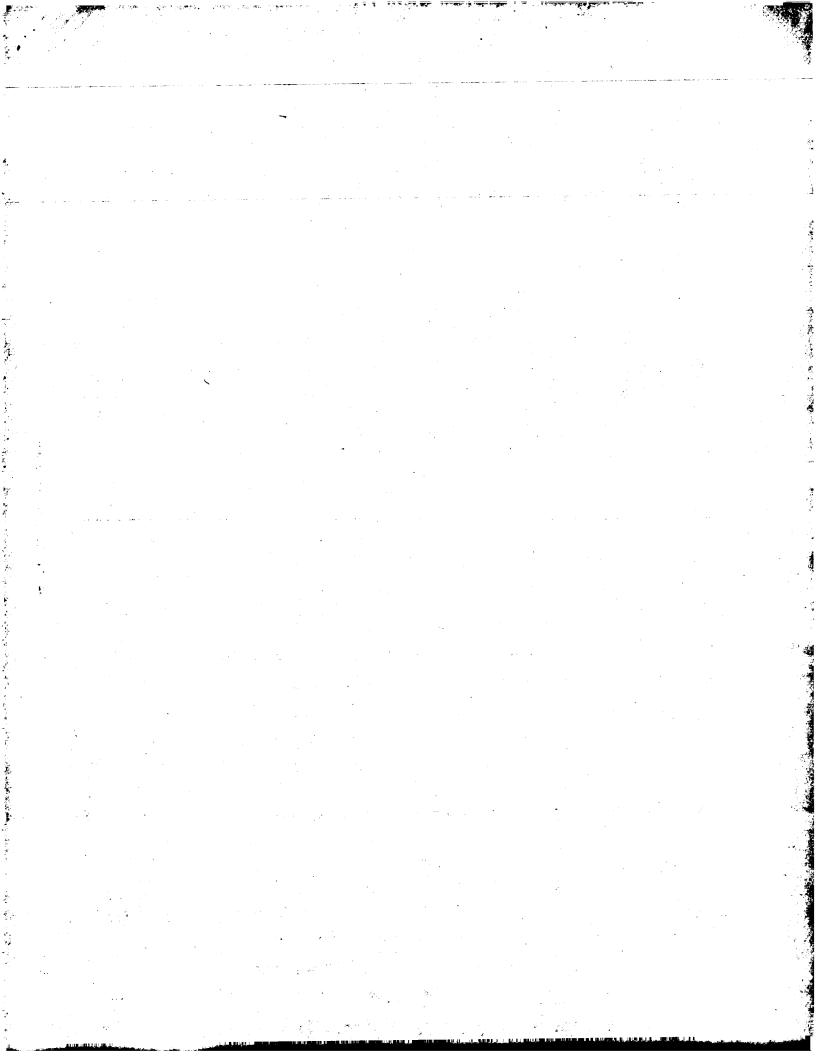
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                                                      Harper,J.F., Kreps,J., Wang,X. and Zhu,T.
Stress-regulated genes of plants, transgenic
same, and methods of use
                                                                                                               Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                     Arabidopsis thaliana (thale
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1319 TGGTTTGGGAAGCTTTGAATACTCATGGCTAA 1350	Db
1446 TGGTATGGGAGGCTGTGAACACCCATGGATAA 1477	Q
1262 CTTTGAAGACAGCTAGTCAAGCTAGAGACGTGGCTAATCCGGTGGTTAAGAACT 1318	Db
1386 CACTCAGGGCTGCTGCATTGCAGGCCAGGACCGCTACAAGTGGTGGTGGTGCTCCGAAGAATT 1445	Q
1202 AGCATAATCTTCCGTATAGGAGTATGTCGTGGTTTGAAGCAAATGTGTTGACCATTAACA	DЬ
1326 AGCATGGGCTCACTTATTCTGCAGCCACATTCTGGGGTGCAAATGTGCTTACATGGAAGA	γŞ
1142 CTCGCTTACCTCGTTGCCATCTCCCGGAAAGTTTCTCCGGTGGTTCAAGAGCTTTGCAAGA	Db
1266 CCCGCCTACCTCGGTGCCACCTTCGCAAGGTTGCACCGTCCGCGGCCGTCCTTTGCAAGA	Ş
1082 GATCATACATGGATTGGTTCTTTGGTGGATTACAGTTTCAGCATCATTTGTTCC	Db
1206 CTCCTTGGATGGATTGGTTCCACGGTGGCCTGCAGTTCCAGATTGAGCACCATCTGTTTC	γ
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Search completed: December 31, 2003, 21:04:25 Job time: 4432.43 secs



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                                                                                                                                                                                                                                                                                                                                                                                                                Score
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14225.873 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
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Corn sphingolipid wheat sphingolipid DNA encoding Eveni Evening primrose d Soybean sphingolip Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Corner thaliana shallong thaliana shallong by the sphingolipid by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by the shallong by th
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S. chrysomallus ac	AAF25795	22	3849	4.6	81.8	45
Aspergillus oryzae	ABZ53094	25	462	4.6	81.8	44
Phaeodactylum tric	ABV74258	24	1434	4.7	83	43
P. tricornutum D6	ABQ76780	24	1434	4.7	83	42
œ	0	22	1815	4.7	'n	41
Human gene express	AAZ17263	20	1337	4.8	4	40
Leishmania major P	AAF74867	22	1313	4.8	84.6	39
i um	AAD49077	25	1320	4.9	J	38
ERD48 insert DNA i	AAD17193	22	2700	5.0	87.8	37
legnia	AAD49064	25	1362	5.0	œ	36
Human colon cancer	AAA02484	21	1000	5.1	9	35
Streptomyces nours	AAD17184	22	65140	5.4	٠.	34
Streptomyces nours	AAD17186	22	125401	5.7	99.8	ω ω
a	AAD17185	22	27541	5.7	99.8	32
	ABK98592	24	12739	5.7	100.4	31
Vector pspsf14 con	ABK98631	24	12733	5.7	100.4	30
Pythium irregulare	AAD35090	24	1380	6.3	112	29
Human GDP-mannose	ABX27196	25	263	6.5	114	28
Arabidopsis thalia	ABX61024	25	480	6.5	115.2	27
Arabidopsis thalia	ABL93274	24	476	7.3	129	26
Human GDP-mannose	ABX21201	25	287	8.6	152.4	25
Arabidopsis thalia	ABQ65917	24	657		203.8	24
n ear-der:	ABX84796	25	266	•	215.8	23
C. purpureus delta	AAF25733	22	535		219.4	22
Corn ear-derived p	ABX83506	25	291	٠	275.6	21
Soybean sphingolip	AAD01351	21	880		302	20
Wheat sphingolipid	AAD01354	21	823	17.8	314.8	19
Bud	AAD01349	21	1471		352	18
-de	ABX15366	25	1685	•	365.4	17
m	ABK49502	24	1685	•	•	16
Borage delta-6-des	AAT30395	17	1685	٠	365.4	15
delta-6	491	20	1684	•	365.4	14
	AAV34398	19	1684	•	•	13
hingolipid d	AAZ44851	21	1606	•	•	12
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Arabidopsis thalia	AAC33846	21	1650	5	441.8	9

## ALIGNMENTS

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Cahoon EB, Cahoon RE, Hitz WD, Kinney AJ;
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CGCTTCCGCCGACGACCTCTGGATCTCCATCTCCGGCGACGTGTACGACGTCACGCCCTG
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                                                                                       GGCGCACCTCCTCGCGGGGGGTCTCATTGGCTTCGTCTGGATCCAGTCCGGCTGGATGGG
                                                                                                   GGCGCACCTCCTCGCGGGGGGTCTCATTGGCTTTCGTCTTGGATCCAGTCCGGCTGGATGGG
                                                                                                                                  CCTGATGGCCGTCCTCCTACGCCGCGCTGTACCTCGTCCTCGCATGCGCCAGCGCCTG
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                            AAGATTAAAAAAAAAAAAAAAAAAA
                                                                 CTCCCTATCACGGTAACTATATGATGATGATCCTTGCTTTAATTCATGAACACTTGTTTC
                                                                                                 GAAGACACTCAGGGCTGCTGCATTGCAGGCCAGGACCGCTACAAGTGGTGGTGCTCCGAA
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RESULT 2
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P-PSDB; AAY71555.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 48-49; 57pp; English.
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                                                                                                                                                                                                                                                                                          08-JAN-1992;
14-SEP-1994;
28-JAN-1997;
                                       Novel nucleic acid encoding evening primrose delta6-desaturase which converts linoleic acid to gamma linolenic acid useful for producing gamma linolenic acid in transgenic plant or bacteria .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                delta6-desaturase; sunflower; soybean; maize; peanut; carrot; oil seed rape; gamma linolenic chilling tolerance; gene; ds; evening primrose
    Claim 2;
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P-PSDB; AAU79851.
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10-OCT-1991;
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92US-0817919.
94US-0307382.
97US-0789936.
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Matches 832; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention describes an isolated nucleic acid encoding an evening primrose Delta6-desaturase. The nucleic acid and a vector expressing the nucleic acid are useful for producing a plant such as sunflower, soybean, maize, tobacco, peanut, carrot or oil seed rape plant, with increased gamma linolenic acid (GLA) content, and also for inducing or increasing production of GLA in a bacteria or plant deficient, lacking in or producing low levels of GLA. The nucleic acid is also useful for inducing chilling tolerance in plants. This sequence encodes the evening primrose delta6 desaturase involved in the production of gamma linoleic acid.
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                         CAGACCTTTTTATTGCTCCTCACCAGGCGCGACGTCCCTGACCGCGCTCTAAACTTAATG
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62.0%;
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628

491 568 431 805 371

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791 868 731 808 671 748 611 889 551 448

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                                                          13-OCT-1992;
19-SEP-1997;
10-OCT-1991;
08-JAN-1992;
14-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Delta-6-desaturase; gene; ss; delta-12-desaturase; sunflower; soybean; maize; tobacco; peanut; carrot; oil seed rape; gamma-linolenic acid; Goctadecatetraenoic acid; alpha-linolenic acid; delta-15-desaturase;
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Best Local Similarity
Matches 832; Conserv
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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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                            AAZ44833 standard; DNA; 1678 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                       CTCCTTGGATGGATTGGTTCCACGGTGGCCTGCAGTTTCCAGATTGAGCACCATCTGTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCGGGATTCAGCACGTCCAATTCTGCCTGAACCACTTCTCGTCCGACGTGTATGTCGGGC
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                                                                                                  TTGTTTGGGTTAAATTTGATG
                                                                                                                           crrcregrerrcaccrreere 1526
                                                                                                                                                                                  TGGTATGGGAGGCTGTGAACACCCATGGATAAATGGGATGAAGATACGGGCTAATGGCAA 1505
                                                                                                                                                                                                                                           CACTCAGGGCTGCTGCATTGCAGGCCAGGACCGCTACAAGTGGTGGTGCTCCGAAGAATT
                                                                                                                                                                                                                                                                                                  AGCATGGGCTCACTTATTCTGCAGCCACATTCTGGGGTGCAAATGTGCTTACATGGAAGA
                                                                                                                                                                                                                                                                                                                               CTCGCTTACCTCGTTGCCATCTCCGGAAAGTTTCTCCGGTGGTTCAAGAGCTTTGCAAGA
                                                                                                                                                                                                                                                                                                                                                CCCGCCTACCTCGGTGCCACCTTCGCAAGGTTGCAACGCCGTCCGCGGACCTTTGCAAGA
                                                                                                                                                                                                                                                                                                                                                                                        GATCATACATGGATTGGTTCTTTGGTGGATTACAGTTTCAGCTTGAGCATCATTTGTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CACCCACCGGTAGCGACTGGTTCGAGAAGCAAGCGGCGGGAACAATCGATATCTCTTGTA 1287
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                                                                                                                                                                                                                CTTTGAAGACAGCAGCTTATCAAGCTAGAGACGTGGCTAATCCGGTGGTT---AAGAACT
                                                                                                                                                                                                                                                                        {	t AGCATAATCTTCCGTATAGGAGTATGTCGTGGTTTGAAGCAAATGTGTTGACCATTAACA}
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ACCACCCGGGCGGCGGCCTCCCGCCTCTCACCCTGGCGGGGCAGGACGCCACCGACGGCCT

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248

CTCATCCCGGAGGCGACACGGTGATTCTCAATCTCGTTGGTCAAGACGTCACCGATGCTT

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CCGACGACCTCTGGATCTCCATCTCCGGCGACGTGTACGACGTCACGCCCTGGCTCCCCCC

CTGGAGATCTATGGATCGCGATTCAAGGCAAGGTCTACAACGTCTCCGATTGGATTAAAA 292

유정

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This invention describes a novel sphingolipid desaturase that selectively controduces a double bond into the sphingobase of the ceramide residue of sphingolipids and capnoids. A DNA sequence encoding the sphingolipid code desaturase, or a vector containing the DNA sequence, can be used to compensate for a delta-8-unsaturated long-chain base content or an altered codelta-8-unsaturated long-chain base cis/trans ratio, especially to compensate for a delta-8-unsaturated long-chain base cis/trans ratio, especially to compensate for a delta-8-unsaturated long-chain base, to increase tolerance corresistance to soil salinity, ion stress or toxicity, drought, wet conditions, cold or frost and/or phytopathogenic microorganisms, or to calter size growth and flowering time. Cells, transgenic organisms or complants containing the DNA sequence can be used to produce sphingolipids can be used in cosmetics, pharmaceuticals and foods and as chemical raw materials. This sequence encodes the Arabidopsis thaliana sphingolipid codesaturase sldl protein described in the method of the invention.
Query Match
Best Local Similarity
Matches 795; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sphingolipid desaturase; sld1; sphingobase; ceramide; capnold; transgenic plant; crop plant; delta-8-unsaturase; tong-chain base; tolerance; resistance; soil salinity; ion stress; toxicity; drought; cold; frost; phytopathogenic microorganism; flowering time; cosmetic; pharmaceutical; food; chemical raw material; ds.
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                                                                  Sequence 1678 BP; 416 A; 408 C; 339 G; 515 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Fig 3; 62pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heinz E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New sphingolipid desaturase that selectively introduces double bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GVSE-) GVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   sphingolipids
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   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "sphingolipid desaturase'
                                                                                                                                                                                                                                                                                                                                                                                                                                                   and capnoids
              25.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schmidt H,
0;
                Score 445; DB 21;
Pred. No. 1.5e-80;
   Mismatches 540;
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                                Length 1678;
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AGCATGGGCTCACTTATTCTGCAGCCACATTCTGGGGTGCAAATGTGCTTACATGGAAGA
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               CTTTGAAGACAGCATTATCAAGCTAGAGACGTGGCTAATCCGGTGGTT---AAGAACT
                                      CACTCAGGGCTGCTGCATTGCAGGCCAGGACCGCTACAAGTGGTGGTGCTCCGAAGAATT
                                                                                                                        CTCGCTTACCTCGTTGCCATCTCCGGAAAGTTTCTCCGGTGGTTCAAGAGCTTTGCAAGA
                                                                                                                                                                               GATCATACATGGATTGGTTCTTTGGTGGATTACAGTTTCAGCTTGAGCATCATTTGTTCC
                                                                                                                                                                                                                                   CACCCACCGGTAGCGACTGGTTCGAGAAGCAAGCGGCGGGAACAATCGATATCTCTTGTA
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                                                                    AGCATAATCTTCCGTATAGGAGTATGTCGTGGTTTGAAGCAAATGTGTTGACCATTAACA
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28-MAY-1999;
01-JUN-1999;
04-JUN-1999;
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07-JUN-1999;
10-JUN-1999;
10-JUN-1999;
                                                                                                                                                 25-FBB 1999
05-MAR 1999
09-MAR 1999
23-MAR 1999
25-MAR 1999
25-MAR 1999
26-APR 1999
06-APR 1999
08-APR 1999
11-APR 1999
23-APR 1999
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23-APR 1999
23-APR 1999
24-MAY 1999
14-MAY 1999
11-MAY 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-SEP-2000
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99US-0126785.
99US-0126785.
99US-0128714.
99US-0129845.
99US-0130047.
99US-0130449.
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Query Match Best Local Similarity

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                                                          (b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention.

Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                          cell has been exposed, comprising:
(a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant
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26-JAN-2001; 2001US-264647P.
22-JUN-2001; 2001US-300111P.
   Sequence 1350 BP; 325 A; 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to identifying a stress condition to which a plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stress
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GATCATACATGGATTGGTTCTTTGGTGGATTACAGTTTCAGCTTGAGCATCATTTGTTCC
                                                                    CACCCACCGGTAGCGACTGGTTCGAGAAGCAAGCGGCGGGAACAATCGATATCTCTTGTA
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                              CTCCTTGGATGGATTGGTTCCACGGTGGCCTGCAGTTCCAGATTGAGCACCATCTGTTTC
                                                                                                       TTGGAAGAATCAATCTCTTCATTCAAACGTTTCTCTTGCTCTTCTCCAAACGTGAAGTAC
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This invention describes a novel sphingolipid desaturase that selectively introduces a double bond into the sphingolapide and capnoids. A DNA sequence encoding the sphingolipid desaturase, or a vector containing the DNA sequence, can be used to produce transgenic plants, especially crop plants, with an increased or decreased delta-8-unsaturated long-chain base content or an altered delta-8-unsaturated long-chain base content or containing the compensate for a delta-8-unsaturated long-chain base deficiency, to exclude production of delta-8-unsaturated long-chain bases, to increase tolerance or resistance to soil salinity, ion stress or toxicity, drought, wet conditions, cold or frost and/or phycopathogenic microorganisms, or to alter size growth and flowering time. Cells, transgenic organisms or

Claim 11;

Fig 1; 62pp; German

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                                                                                                                                                                                                                                                                                                                                                                                                 New sphingolipid desaturase that selectively introduces double into sphingolipids and capnoids -
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Matches 772
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                                        TATCCTTCCTACCAAACTGGCAAGAGAGGATCATCTTTGTCTTTTTAAGCATGGCCGTCA
                                                                 TGGCTTCCCTGCCGAATTGGTGGGAGAGGGTCGCGTTTGTGCTTTTTCAGCTTCACCATCT
                                                                                                                             CTGATCGAGCCTTGAACATAGCTGGGATTCTTGTTTTCTGGACGTGGTTTCCTCTTTTAG
                                                                                                                                                                                                                TGGGGAGAATCAATCTCTTTATCCAAACGTTACTTTTGCTATTCTCGAGACGTTACGTTC
                                                                                                                                                                                                                                                  ATCCACTAGCTCGATTCTTGATCAGCTACCAACACTGGTCGTTTTATCCAATCATGTGTG
                                                                                                                                                                                                                                                                                                                                       ATGCCGCCTCGAAATTCTTCATCAGCTACCAGCACTGGACCTTCTACCCGGTAATGTGCA
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Pred. No. 6.1e-79;
0; Mismatches 515;
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1145

This invention describes introduces a double bond

a novel sphingolipid into the sphingobase

desaturase that of the ceramide

selectively residue of

Disclosure;

Fig 15;

62pp;

German

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RESULT 12
AAZ44851
ID AAZ444851
AC AAZ44
XX AAZ44
XX Sphin
XX Sphin
XX Sphin
XX Sphin
XX Sphin
XX Cold;
XW Cold;
XW Cold;
XW Cold;
XW Dharm
XX Dhide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sphingolipid desaturase; sld1; sphingobase; ceramide; capnoid; transgenic plant; crop plant; delta-8-unsaturated long-chain base; tolerance; resistance; soil salinity; ion stress; toxicity; drought; cold; frost; phytopathogenic microorganism; flowering time; cosmetic; phytopathogenic microorganism; flowering time; cosmetic;
                                                                                                                                                                                                                                                                                                                                                                                           27-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                              27-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sphingolipid desaturase DNA.
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                                                                                                                              sphingolipid desaturase that sphingolipids and capnoids -
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 97US-0831570
                          98WO-US07178
                                                                                                                             /*tag=
                                                                                                                                        /product= "delta-6 desaturase"
complement (616..632)
                                                                                                                  1165..1181
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Query Match
Best Local S
Matches 740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New sunflower albumin 5' altered lipid metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1684 BP; 430 A; 277 C; 358 G; 619 T; 0 other;
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ACCTCTCATTTCTATGAGAAAAAGGTTGACTTTTGACTCTTTATCAAGATTCTTTGTAAGT
                              TGGTCCTACTTCTACCAACGGACCCTGGCGTTCGATGCCGCCTCGAAATTCTTCATCAGC
                                                                                           GACCCGGACCTCCAGCACATGCCGCTCTTTGCCGTCTCCCCCAAGCTGTTCGGCAACATA
                                                                                                                                                           ATCGCCTGGTGGAAGTGTAACCACAACACGCGCACCACATCGCCTGCAACAGCCTGGACCAT
                                                                                                                                                                                             GATTCAAGGCTTAATAAGTTTATGGGTATTTTTGCTGCAAATTGTCTTTCAGGAATAAGT
                                                                                                                                                                                                                     CATCCGGTCCTCGACCGCGTCGTGCAGGGTGCTCTCCGGGAACTGCCTCACCGGCCTCAGC
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Pred. No. 1.8e-64;
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                                  09-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid containing oleosin 5'-regulatory region - useful for modulating fatty acid synthesis and lipid metabolism in plants, particularly to increase content of gamma-linolenic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1684 BP; 430 A; 277 C; 358 G; 619 T; 0 other;
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                                       ATCGCCTGGTGGAAGTGTAACCACAACACGCACGCACGTGGCCTGGAACAGCCTGGACCAT
                                                                                               GATTCAAGGCTTAATAAGTTTATGGGTATTTTTGCTGCAAATTGTCTTTCAGGAATAAGT
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                                                                                                                                      Delta-6-desaturase; gamma-linolenic acid; transgenic plant; polyunsaturated fatty acid; octadecatetraeonic acid; chilling resistance; ollseed; ss; ds.
                                                                                            Borago
                                                                                                                                                                                                                                     Borage
                                                                                                                                                                                                                                                                                                                                  AAT30395
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                                                                                               officinalis.
                                                                                                                                                                                                                                   delta-6-desaturase
                                                                                                                                                                                                                                                                                                                                                                              standard; DNA; 1685 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGACCGCTACAAGTGGTGGTGCTCCGAAGAATTTGGTATGGGAGGCTGTGAACACCCCAT 1471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTTTCTCCAAGGCCAATGAAATGACACTCAGAACATTGAGGAACACAGCATTGCAGGCT
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Location/Qualifiers
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1266

1206

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Query Match
Best Local Similarity
Matches 740; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A DNA clone (AAT30395) codes for borage delta-6-desaturase (AAR98455), which catalyses the conversion of linoleic acid to gamma-linolenic acid (GLA). It was isolated from a borage membrane-bound polysomal library using probes based on abundantly expressed sed storage protein cDNAs and with an isolated partial cDNA clone. The gene can be incorporated into a vector, pref. incorporating a tissue-specific promoter, for the expression of delta-6-desaturase in transgenic plants, esp. sunflower, soybean, maize, tobacco, peanut, carrot or oilseed rape, resulting in increased GLA prodn. Alteration of plant lipids may also lead to improved chilling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transgenic plants comprising the borage delta-6-desaturase gene show increased production of gamma linolenic acid and having increased resistance to chilling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1685 BP; 431 A; 277 C; 357 G; 620 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Page 51-52; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1996-333997/33
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                                                    TTTCTTTGGATTCAGAGTGGTTGGATTGGACATGATGCTGGGCATTATATGGTAGTGTCT
                                                                                                        TTCGTCTGGATCCAGTCCGGCTGGATGGGCCACGACTCGGGCCACCACCGCATCACCGGC
                                                                                                                                                          TATGGGGTTTTGTTGTGAGGGTGTTTTGGTACATTTGTTTTCTGGGTGTTTGATGGGG
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B 8	B &	8 8	dg VQ	gg Qy	B 8	B 8	g Qy	g &	B 8	B 8	gg Qy	용왕	B 8	DЬ
Oy 1472 GGATAAA 1478             Db 1385 GGTTAAA 1391	1412 1328	1352 1268	Qy 1292 AAGGTTGCACCGGCCGTCCGCGACCTTTGCAAGAAGCATGGGCTCACTTATTCTGCAGCC	Qy 1232 GGCCTGCAGTTCCAGATTGAGCACCATCTGTTTCCCCGCCTACCTTCGGTGCCACCTTCGC	Qy 1172 AAGCAGACGGCAGGCACGCTCGACATCCTGTGCTTCCTTGGATGGA	Qy 1112 CTGAACCACTTCTCGTCCGACGTGTATGTCGGGCCACCCAAGGGCAATGACTGGTTTGAG	Qy 1052 AGGGTCGCGTTTGTGCTTTTCAGCTTCACCATCTGCGGGATTCAGCACGTCCAATTCTGC	Qy 992 GTCGCCACATTCTGGGCTTGGTACCCGTTGCTGGTGGCTTCCCTGCCGAATTGGTGGGAG	Qy 932 TCCGCCCTGTTCGTTCTCACGGAGAAGAGGGTGCCGCAGCGGTTGCTTGAGATCGCGGGG	Qy 872 TACCAGCACTGGACCTTCTACCCGGTAATGTGCATCGCCAGGATAAATCTTCTCGGCGAG	Qy 812 TGGTCCTACTTCTACCAACGGACCCTGGCGTTCGATGCCGCCTCGAAATTCTTCATCAGC	Qy 752 GACCCGGACCTCCAGCACATGCCGCTCTTTGCCGTCTCCCCCAAGCTGTTCGGCAACATA	Oy 692 ATCGCCTGGTGGAAGTGTAACCACAACACGCCACCACTCGCACCACCACCACGCTGGAACAGCCTTGAACAC	
	CCAT 1471      CAT 1384		AGCC 1351    NGCA 1267	rCGC 1291 	CGGT 1231     RGGT 1147	rgag 1171       rgag 1087	TGC 1111 	3GAG 1051     GAA 967	3GGG 991     3GGA 907	GCAG 931    ACAA 847	CAGC 871    AAGT 787	CATA 811   ACTC 727	CCAT 751    ATAT 667	 NAGT 607

Search completed: December 31, 2003, 16:16:37 Job time : 339.729 secs

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Result
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Copyright (c) 1993 - 2003 Compugen Ltd.
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46468	J4646	19.7	47	43
BH229657 100615	2 28 BH22965	9.9 4		42
4635	1 10 BE44635	0.1 5	53.	41
4571	6 10 BE44571	0.6 5	36	40
5851	0 10 BG15851	0.9 4	69.	39
5303	8 14 CD45303	1.0 7	70.	38
BH229798 1006154	9 28 BH22979	1.0 4		37
4427	6 29 CC34427	1.1 5	72.	36
8590	3 6 AL81065	1.2 5	74.	35
B460EFB 9966 B430996	8 12 BJ3099	1.3 6	76.	34
2970	9 28 BH22970	1.4 4	78.	3
8304	5 9 AL818304	1.6 5	မှ	32
5852	7 10 BG15852	1.6 4	81.	μ
0154	4 14 CA50154	1.6 5		30
3076	0 12 BJ23076	1.7 6	82.	29
0684	3 13 BQ60684	1.9 5	38	28
2106	9 12 BJ32106	2.7 6	99.	27
0936	5 12 BJ30936	2.9 6	03.	26
3043	8 14 CD23043	2.9 5		25
4698	3 12 BJ44698	3.0 6	05.	24
9894	3 14 CA49894	3.2 5	41	23
2965	5 28 BH22965	3.3 4		22
7810	2 14 CB2781	3.5	_	21
3008	5 28 BH23008	3.6 4	-	20
2999	5 28 BH2299	3.6 4	41	19
BI075599 IP1 22	8 12 BI07559	4.3 5	429.2	18
2387	8 12 BM3238	4.5	43	17
CA50252	5 14 CA50252	4.6		16
1910	5 9 AI691910	5.0	4	5
BQ788546 WHE4151	9 13 BQ78854	5.8	55.	14
D23034	2 14 CD23034	5.9 5	56.	13
J46538	1 12 BJ46538	6.2 6		12
BH785221 fzmb013	9 28 BH7852	6.2 4	62.	11
D48448	7 14 CD48448	7.6 4	4	10
D48448	9 14 CD48448	7.9 4	92.	9
BZ730988 OGEDJ37	7 29 BZ730	8.1 4	495.4	œ
B38126	5 14 CB38126	8.9 5	09.	7
028135	4 13 BQ28135	9.7 7	23	o
M32247	9 12 BM32247	1.0 6	46.	S

COMMENT	TITLE JOURNAL	JOURNAL	TITLE	AUTHORS		SOURCE ORGANISM	ACCESSION VERSION KEYWORDS	RESULT 1 AY103762 LOCUS
Missouri, Columbia, MO 65211, USA  If you are interested in getting corresponding physical clones  these are publicly available from ZmDB and may be found by By searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the sourcy	Direct Submission Submitted (25-APR-2002) Maize Mapping Project, University of	Overgo Probes Unpublished (2002) 2 (bases 1 to 1764)	Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V. Maize Mapping Project/DuPont Consensus Sequences for Design of	<pre>l (bases 1 to 1764) Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S.,</pre>	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.	Zea mays Zea mays	AY103762.1 GI:21206840 HTC.	AY103762 1764 bp mRNA linear HTC 16-OCT-2002

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Schnable, Iowa State, then clones may be requested from ZmDB:
www.zmdb.lastate.edu.
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GCACCACATCGCCTGCAACAGCCTGGACCATGACCCGGACCTCCAGCACATGCCGCTCTT
                              GCTCTCCGGGAACTGCCTCACCGGCCTCAGCATCGCCTGGTGGAAGTGTAACCACAACAC
                                              GCTCTCCGGGAACTGCCTCACCGGCCTCAGCATCGCCTGGTGGAAGTGTAACCACACAC
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Mapping Project 456 g 396 t
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/mol_type="mRNA"
/mol_type="mRNA"
/db_xref="maizeDB:634923"
/db_xref="taxon:4577"
/clone_lib="Maize Mapping Project/DuPont Cornsensus
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GSS.
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Fax: 301-838-0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Other_GSSs: OGEDJ37TC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mmpratt@uga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science; plant material and RNA prepared at Texas A & M University;
sequencing done in the Laboratory for Genomics and Bioinformatics,
University of Georgia. Sequence ends have been trimmed to exclude
vector and regions below Phred quality 16. Three-prime sequences
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Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
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744 bp mRNA linear EST 04-JUN-2003
ETH1_42_C07.g1_A002 Ethylene-treated seedlings Sorghum bicolor cDNA
clone ETH1_42_C07_A002 5', mRNA sequence.
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Seq primer: Sug5 (CTTCTGCTCTAA
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An EST database from Sorghum: 1-aminocyclopropane-1-carboxylic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sorghum bicolor (sorghum)
Sorghum bicolor
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Fax: 706 583 0210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 744)
/db_xref="taxon:4558"
/clone="ETH1 42 C07_A002"
/lab host="DH108-T1 phage-resistant E. coli"
/lab host="DH108-T1 phage-resistant E. coli"
/lab host="DH108-T1 phage-resistant E. coli"
/clone lib="Ethylene-treated seedlings"
/clone lib="Ethylene-treated seedlings"
/note="Vector: pME18S-FL3; Site 1: XhoI; Site 2: XhoI; The
/intery was prepared from polyA+ RNA from seedlings grown
in hydroponic culture. At 8 days of age, medium was supplemented with 0.5 mM 1-aminocyclopropane-1-carboxylic
acid (ACC) to induce endogenous ethylene (ETH) production.
Roots and shoots were harvested after 27 and 72 hr and
                                                                                                                                                                                                                                                                                                                                                                                                   r: Sug5 (CTTCTGCTCTAAAAGCTGCG).
Location/Qualifiers
                                                                                                                                                                                                                                                                                        mol_type="mRNA"
cultivar="BTx623"
                                                                                                                                                                                                                                                                                                                                               organism="Sorghum bicolor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement and
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KEYWORDS
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Best Local Similarity
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                                                             mRNA sequen
BI075898
BI075898.1
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Sorghum bicolor (sorghum)
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                             BI075898
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                                                                                                             _22_F11.b1_A002 Immature
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                                                                                             sequence.
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91.6%;
tive
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Pred. No. 9.4e-93;
0; Mismatches 52;
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                                                                                                           pannicle 1 (IP1)
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ACCTCCTCGCGGGGGGTCTCATTGGCTTCGTCTGGATCCAGTCCGGCTGGATGGGCCACG

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JOURNAL
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plant Sciences Bu:
Tel: 706 542 1860
Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for high quality sequence : Delow Phred sprime sequences, which are obtained with PolyTMNx or Tesquencing primer, are presented as the reverse complement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 634)
Klein,R.R., Cordonnier-Pratt,M.-M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spermatophyta; Magnoliophyta; Liliopsida; Poales; clade; Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequencing primer, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mmpratt@uga.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   An EST database from Sorghum:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACGCCGCGGGGCGCGACGTGCGCATGATCTCCTCCAAGGAGCTCCGCGCTCACGCTT 185
                                                                                                                                                                       TATCCTCCGCGGGCCTCTTCGAACGCGTCGGCCCCAACCCCCAAGGTCCAGCTCGTCCTGA
                                                                                                                                                                                                                          CCCACCACCCGGCGGCGACCTCCCGCTCATCACCCTCGCGGGCAGGACGCCACCGACG
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                       TGGCCGTCCTCTTCTACGCCGCGCTGTACCTCGTCCTCGCATGCGCCAGCGCCTGGGCGC
                                                                          TCTCCTCCGCGGGCCTCTTCGAGCGCGTCGGCCCCAACCCCCAAGGTCCAGCTCGCCCTCA
                                                                                                                                                   GCCTCTCCGACTACACCGTCTCCCCCGCGTCCGCCGACTACCGCCGCCTCCTCGCGCAGC
 TGGCCGTCCTCTTCTACGCCGCGCTCTACCTCGTCCTCGCCTGCGCCACCGCCTCCGCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Immature pannicle 1 (IP1)"
/note="Organ: Developing preanthels I; Site_1: XhoI;
pBluescript II SK(-) from Lambda Zap II; Site_1: XhoI;
Site_2: EcoRI; The library was made from poly-A RNA in cloning vector lambda ZaP II. Clones to be sequenced w prepared by mass excision."

297 c 171 g 95 t
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/cultivar="BTx623"
/db_xref="taxon:4558"
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Pred. No. 1.3e-87;
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIC1 5_C04.b1_A002 Pathogen-infected compatible 1 (PIC1) Sorghum bicolor cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector, and regions
below Phred quality 16. The threshold for highest quality sequence
below Phred prime sequences, which are obtained with PolyTMix or
10. Three-prime sequences, which are obtained with PolyTMix or
T7 sequencing primer, are presented as the reverse complement.
Seq primer: JEN REV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   An EST database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cordonnier-Pratt, M.-M., Gingle, A., Fang, G.C., Sudman, M. and Pratt, L.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 609)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 706 542 1860
Fax: 706 583 0210
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        108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           quality sequence stop:
Collectrictum graminicola"

/clone libs"Pathogen-infected compatible 1 (PIC1)"
/note="Vector: pBluescript II SK(-) from Lambda Zap II;
Site 1: XhoI; Site 2: EcoRI; Four-week-old sorghum
seedlings were sprayed with spore suspension prepared from
seedlings were sprayed with spore suspension prepared from
3-week-old FRM42I, a sorghum isolate of the anthracenose
pathogen Colletotrichum graminicola. Inoculated plants
were kept in a 25 C dark growth chamber with 100% relative
humidity for 24 hr, followed by 12/12 hr of light/dark
cycle at 25 C with 90% relative humidity for another 24
hr. All leaves were harvested and quick frozen with liquid
nitrogen and stored in a -80 C freezer. The library was
made from poly-A RNA in the cloning vector lambda ZhP II.
Clones to be sequenced were prepared by mass excision.
WARNING: While most or all ESTs are expected to derive
from the host plant, no effort was made to eliminate ESTs
deriving from the pathogen."
        çi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                    tissue_type="Leaves"/dev_stage="4-week-old seedlings infected with
                                                                                                                                                                                                                                                                                                                                                                                                                                     cultivar="BTx623"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Sorghum bicolor"
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                                                               1 (bases 1 to 744)
Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Penton,R.D., Han Anderson,O.D., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T., P.S., Hsia,C.C., Kang,Y., Tong,J.C. and Zhang,D. Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
The structure and function of the expressed portion of the wheal cenomes - Normalized shoot cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                 BQ281359 744 bp mRNA linear EST 13-MAY-200 WHE3020_D06_H12ZS Wheat unstressed seedling shoot normalized cDNA library Triticum aestivum cDNA clone WHE3020_D06_H12, mRNA
Unpublished
Contact: Olin Anderson
US Department of Agriculture, Agriculture
West Area, Western Regional Research Cente
                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
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Sequences have been trimmed to remove vector
quality sequence with phred score less than
Seq primer: SK primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAACACGCACCACATCGCCTGCAACAGCCTGGACCATGACCCGGACCTCCAGCACATGCC
                                          CCCGTTGCTGGTGGCTTCCCCTGCCGAATTGGTGGGAGAGGGTCGCGTTTTGTGCTTTTCAG
                                                                                                                                     AAAGAAGGTGCGGCAGCGTTGGCTGGAGATCGCCGGAGTTGCAGCGTTCTGGGTTTGGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: Lambda Uni-ZAP XR, excised phagemid pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were surface-sterilized, germinated and grown aseptically in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Roots were harvested. The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made in the Total State and Control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control o
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cDNA library"
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/lab_host="E. coli DH10B"
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/tissue_type="Etiolated shoot"
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cultivar="Chinese Spring'
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0; Mismatches 133;
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Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 3529 1 45 1 row: B co
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1abs Zea mays cDNA, mRNA s

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Stanford University
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
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l (bases 1 to 585)
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                                                                                                                                      118
                                                           Conservative
                                                                                                                                  /note="Organ: ear; Vector: PAD-GAL4-2.1; Site 1: Ecor. Site 2: XhoI; RNA isolated by Hake lab. 1 million pfu amplified. Ampicillin is the selection marker."

151 c 167 g 146 t 3 others
                                                                                                                                                                                                /dev_stage="2 mm"
/lab_host="E. coli XLOLR"
/clone_lib="3529 - 2 mm ea
                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/cultivar="B73"
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/tissue_type="ear"
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                                                                                                                                      TIGR
9712 Medical Center Drive,
Tel: 301-838-5843
Fax: 301-838-0208
                                                                                                                                                                                                                                    Zea mays

Zea mays

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Wagnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 497)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.

Consortium for Maize Genomics
                                                                                                                                                                                                                                                                                                                                                                                                             BZ730988
OGEDJ37TC ZM_0.7_1.5_KB OGEDJ37TC zmrvey sequence.
                                                                                                                                                                                                   Unpublished
Other_GSSs: OGEDJ37TM
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                          BZ730988.1
                                                                                                              Seq primer: TF
Class: sheared
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                                                                                                                                     whitelaw@tigr.org
                                                                                                              sheared ends.
                                          /organism="Zea mays"
/mol_type="genomic DI
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBMa0237H02"
/clone_lib="ZM_0.7_1.5_KB"
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TITLE
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                                                                              Unpublished
Contact: Walbot V
Department of Biological Sciences
Stanford University
                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 499)
                                                                                                                                                                                                                                                                                CD484486 499 bp mRNA linear EST 04-TUN-201
3529 1115 1 A01.x 1 3529 - 2 mm ear tissue from Schmidt and Hake
labs Zea mays cDNA, mRNA sequence.
CD484486
 Email: walbot@stanford.edu
Plate: 3529 1 115 1 row: A
Location/Qualifiers
                                         855 California Ave,
Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                 Walbot, V.
Maize ESTs from
                                                                                                                                                                                                                             Zea mays
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3529 1 115 1 A01.y 1 3529 - 2 mm ear tit
labs Zea mays cDNA, mRNA sequence.
CD484487 CD484487.1 GI:31405755
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 497)

Walbot, V.

Maize ESTs from various cDNA libraries sequenced at Stanford
                                                                      Zea mays
                                                                                    Zea mays
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Similarity 99.6%;
94; Conservative
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/lab_host="E. coli XLOLR"
/clone_lib="3529 - 2 mm ea
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/mol_type="mRNA"
/cultivar="B73"
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Pred. No. 5.4e-76;
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Stanford University
855 California Ave, Palo Alto, CA
Tel: 650 723 2227
Fax: 650 725 8221
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Plate: 3529_1_115_1 row: A
Location/Qualifiers
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                                                                                                                       CCGCTCTTTGCCGTCTCCCCCAAGCTGTTCGGCAACATATGGTCCTACTTCTACCAACGG
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Site 2: XhoI; RNA isolated by Hake lab. 1 million
amplified. Ampicillin is the selection marker."
197 c 123 g 99 t
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/lab_host="E. coli XLOLR"
/clone lib="3529 - 2 mm ear tissue from labs"
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Pred. No. 8.3e-75;
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High quality sequence stop: 489.
Location/Qualifiers
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Fax: 314 615 5975
Email: jbedell@oriongenomics.
Plate: fzmb013f038 row: h c
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4041 Forest Park Ave,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 489)
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                        GGTGGCTTCCCTGCCGAATTGGTGGGAGAGGGTCGCGTTTGTGCTTTTCAGCTTCACCAT
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/note="Organ: leaf; Vector: BBCSK(-); Site 1: HincII; DNA
prepared from purfied nuclei was randomly sheared,
end-repaired, size fractionated to enrich for the 0.5 to
5 kb fraction, ligated into HincII-digested pBCSK(-)
vector and electroporated into E. coli cells."
a 156 c 130 g 116 t
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/clone="fzmb013f038h11"
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/cultivar="MO17"
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Pred. No. 9.1e-71;
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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
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Hordeum vulgare subsp. vulgare
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: 81-559-81-6855
GCCTGCAACAGCCTGGACCATGACCCGGACCCTCCAGCACATGCCGCTCTTTGCCGTCTCC
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/mol_type="mRNA"
/cultivar="Haruna Nijo"
/db_xref="taxon:112509"
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/clone_lib="K. Sato unpublished
Nijo germination shoots"
224 c 183 g 165 t
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The University of Georgia, Department of Plant Biology,
Plant Sciences Building, Rm. 2502, Athens, GA 30602-72.
Tel: 706 542 1860
Fax: 706 583 0210
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Cordonnier-Pratt, M.-M., Wentzel, V., Suzuki, Y.,
Cordonnier-Pratt, Sun, F., Sullivan, R., Shah, M.,
, R.R., Liang, C., Sun, F., Sullivan, R., Shah, M.,
, A. and Pratt, L.H.
An EST database from Sorghum: salt-stressed se
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Seq primer: Sug3 (CGACCTGCAGCTCGAGCACA)
POLYA=Yes.
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Other_ESTs: SS1_43_D08.g1_A012
Contact: Cordonnier-Pratt MM
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/db xref="taxon:4558"
/clone="SS1 43 D08 A012"
/lab_host="DH10B-TI phage-resistant E. coli"
/lab_host="DH10B-TI phage-resistant E. coli"
/clone lib="Salt-stressed seedlings"
/clone lib="Salt-stressed seedlings"
/note="Vector: pME18S-FL3; Site 1: XhoI; Site 2: XhoInote="Vector: pME18S-FL3; Site 1: XhoI; Site 2: XhoInote="Vector: pME18S-FL3; Site 1: XhoInote="Vector: pME18S-FL3; Site 1: XhoInote="Vector: pME18S-FL3; Site 1: XhoInote="Vector: pME18S-FL3; Site 1: XhoInote="Vector: pME18S-FL3; Site 1: XhoInote="Vector: pME18S-FL3; Site 1: XhoInote="Vector: pmE18S-FL3; Site 1: XhoInote="Vector: pME18S-FL3; Site 1: XhoInote="Vector: pME18S-FL3; Site 1: XhoInote="Vector: pME18S-FL3; Site 1: XhoInote="Vector: pME18S-FL3; Site 1: XhoInote="Vector: pME18S-FL3; Site 1: XhoInote="Vector: pME18S-FL3; Site 1: XhoInote="Vector: pME18S-FL3; Site 1: XhoInote="Vector: pME18S-FL3; Site 1: XhoInote="Vector: pME18S-FL3; Site 1: XhoInote="Vector: pME18S-FL3; Site 1: XhoInote="Vector: pME18S-FL3; Site 1: XhoInote="Vector: pME18S-FL3; Site 1: XhoInote="Vector: pME18S-FL3; Site 1: XhoInote="Vector: pME18S-FL3; Site 1: XhoInote="Vector: pME18S-FL3; Site 1: XhoInote="Vector: pME18S-FL3; Site 1: XhoInote="Vector: pME18S-FL3; Site 1: XhoInote="Vector: pME18S-FL3; Site 1: XhoInote="Vector: pME18S-FL3; Site 1: XhoInote="Vector: pME18S-FL3; Site 1: XhoInote="Vector: pME18S-FL3; Site 1: XhoInote="Vector: pME18S-FL3; Site 1: XhoInote="Vector: pME18S-FL3; Site 1: XhoInote="Vector: pME18S-FL3; Site 1: XhoInote="Vector: pME18S-FL3; Site 1: XhoInote="Vector: pME18S-FL3; Site 1: XhoInote="Vector: pME18S-FL3; Site 1: XhoInote="Vector: pME18S-FL3; Site 1: XhoInote="Vector: pME18S-FL3; Site 1: XhoInote="Vector: pME18S-FL3; Site 1: XhoInote="Vector: pME18S-FL3; Site 1: XhoInote="Vector: pME18S-FL3; Site 1: XhoInote="Vector: pME18S-FL3; Site 1: XhoInote="Vector: pME18S-FL3; Site 1: XhoInote="Vector: pME18S-FL3; Site 1: XhoInote="Vector: pME18S-FL3; Site 1: XhoInote="Vector: pME18S-FL3; Site 1: XhoInote="Vector: pME18S-FL3; Site 1: XhoInote="Vector: pME18S
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/mol_type="mRNA"
/cultivar="IS3620C"
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                              CCTATCACGGTAACTATATGAT 1705
                                                                                                                                                 --TATTGATCATTCAACCTGCCTGAGTCAGGTTGGAATTTTCGTGTTTGACAAGTGGCTGT
                                                                                                                                                                                                               TTCTGGTGTTCAGCTTGGTGCCCATGTGATTGTCTGGATGCCTTTCAGTTATTTAGAGA- 1565
                                                                                                                                                                                                                                                                              TATGGGAGGCTGTGAACACCCATGGATAAATGGGATGA--AGATACGGGCTAATGGCAAC
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                                                                                              CTATCCAGTTGGAGAGTTCATGCTTCAATAGTCTGGTTGTTCACGGGATGTTCTGTTCTC 1683
                                                                                                                                ACTATTGATCATTTAACCCGACTGAGTCGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seedlings grown in hydroponic culture. Seedlings were transferred to a 150 mM NaCl solution and harvested at 3, 6, 12 and 24 hr following transfer. Roots and leaves were pooled from all time points and RNA isolated. Double-stranded cDNA was cloned unidirectionally into different DralII sites of the pME18S-FL3 vector (5-prime DraIII site is CACTGTGTG, 3-prime DraIII site is CACCATGTGTG.
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Pred. No. 9.6e-70;
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 562
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KEYWORDS
SOURCE
ORGANISM
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VERSION
                                                                                                                                                                                                                                                                              RESULT 14
BQ788546
                                                                REFERENCE
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                                                AUTHORS
1 (bases 1 to 679)

Anderson,O.D., Akhunov,E., Chao,S., Crossman,C.,
Lazo,G.R., Rausch,C.J., Wilson,C. and Woo,J.
                                                                                                                                                                                                                       BQ788546 679 bp mRNA linear WHE4151_B02_C03ZS Wheat CS whole plant cDNA library aestivum cDNA clone WHE4151_B02_C03, mRNA sequence.
                                                                                                                                                                                       aestivum cDNA clone WHE
BQ788546
BQ788546.1 GI:21997018
                                                                               Spermatophyta; Magnoliophyta; Triticeae; Triticum.
                                                                                                                                                                      EST
                                                                                                                    Eukaryota; Viridiplantae;
                                                                                                                                     Triticum aestivum
                                                                                                                                                        Triticum aestivum (bread
                                                                                                                                                        wheat)
                                                                                                  Streptophyta; Embryophyta; Tracheophyta;
yta; Liliopsida; Poales; Poaceae; Pooideae
            portion
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Triticum
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Unpublished
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: oandersn@pw.usda.gov
Sequences have been trimmed to remove vector sequence
quality sequence with phred score less than 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: 5105595818
TCCGCATGATCTCCACCAAGGAGCTGCAGGCGCACGCCGCGGACGACCTCTGGATCT
                                                                                                                                                                                                                                                                                                                        CAACGGCGCCGGAAGCCCAATGCCGGCCGCCAGCAA-----GGACGCCGCCGACG
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                                                                               TCCCGCTCATCACCCTCGCCGGCCAGGACGCCACCGACGCCTTCATGGCCTACCACCCGC
                                                                                                                                                                 TCCCGCTTCTCACCCTGGCGGGGCAGGACGCCACCGACGCCTTCGCCGCCTACCACCCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Wheat CS whole plant cDNA library"
/clone="Vector: Lambda Uni-ZAP XR, excised phagemid
/note="Vector: Lambda Uni-ZAP XR, excised phagemid
pBluescript SK(-); Site_1: EcoRi; Site_2: XhoI; plant
tissues from wheat cv. CS grown to full tilpering stage in
greenhouse were collected at University of California,
Davis (Jan Dvorak's lab, K. Deal and E. Akhunov). Total
RNA was prepared from leaves (young leaf and third leaf),
whole roots, crown, steam and sheath tissues, and then
equal quantities of RNA were pooled from the these
samples. PolyA was purified from the pooled RNA, a cDNA
library was made, and the cDNA clones were in vivo excised
to give pBluescript SK(-) phagemids in J Dvorak's lab (E.
Akhunov, J. Dvorak) at the University of California,
Davis. Colony plating, plasmid DNA preparations and DNA
sequencing were performed in the OD Anderson lab (all
other authors)."

107 t 1 others
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/db xref="taxon:4455"
/db xref="taxon:4455"
/clone="WHE4151_B02_C03"
/tissue_type="Roots, leaves, crown, stem and sheath"
/dev_stage="Adult"
/lab_host="E._coli_SOLR"
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81.4%;
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REFERENCE
AUTHORS
TITLE
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Matches 441; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 650 723 2227 Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stanford University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Walbot V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AI691910.1 GI:4967237
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  855 California Ave,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Department of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Walbot,V.
Maize EST8 from various cDNA libraries
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 CGTCCGCGACCTTTGCAAGAAGCATGGGCTCACTTATTCTGCAGCCACATTNTGGGGTGC
                   CGTCCGCGACCTTTGCAAGAAGCATGGGCTCACTTATTCTGCAGCCACATTCTGGGGTGC 1365
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                                                                                                                                        180
                                                               Conservative
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                                                                                                                                                                                                           /tissue_type="mixed"
/dev_stage="ear length from 0.5 cm - 2.0 cm"
/lab_host="XLOLR (Stratagene)"
/clone_lib="606 - Ear tissue cDNA library from Schmidt
                                                                                                                                                                                                                                                                                         /organism="Zea mays"
/mol_type="mRNA"
/cultivar="Ohio43"
                                                                                                                                                               /note="Organ: immature ear; Vector: pBK-CMV; Site_1: EcoRI
.Site_2: XhoI; Mixed ear tissue cDNA library from Schmidt
                                                                                                                                                                                                     lab"
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Location/Qualifiers
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99.8%;
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                                                            0
                                                          Score 441; DB 9;
Pred. No. 5.4e-67;
0; Mismatches 1
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cDNA library from Schmidt lab Zea
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US-08-831-570-1
US-08-315-570-1
US-08-366-779-4
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US-09-313-294A-1966
US-09-313-294A-3256
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8894.970 Million cell updates/sec
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## ALIGNMENTS

US-08-934-254-26

Sequence 26, Application US/08934254 Patent No. 6355861 GENERAL INFORMATION:

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; NAME/KEY:
; LOCATION:
US-08-934-254-26
Query Match
Best Local Similarity
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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION NUMBER: US/08/934,254
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NAME/KEY:
LOCATION:
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 8383ZYXWVU
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Thomas, Terry L.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID
TITLE OF INVENTION: DELTA 6-DESATURASE
NUMBER OF SEQUENCES: 27
                                                                                                             FEATURE:
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LENGTH: 1702 base pairs
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CITY: Garden City
STATE: New York
COUNTRY: United St.
ZIP: 11530
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RESULT 2
US-08-831-570-1
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                                                                                                                                                                                                                                                  CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 1054)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEPAX: (516) 743-4366
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application Patent No. 5959175
  Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                            MOLECULE TYPE:
FEATURE:
NAME/KEY: CD:
LOCATION: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Thomas, Terry L.
APPLICANT: Numberg, Andrew N.
APPLICANT: Beremand, Phillip D.
TITLE OF INVENTION: A SUNFLOWER ALBUMIN 5' REGULATORY REGION
TITLE OF INVENTION: FOR THE MODIFICATION OF PLANT SEED LIPID
TITLE OF INVENTION: COMPOSITION
                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1684 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/831,570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Garden City
STATE: New York
  Local Similarity
                                                                                                                                                           STRANDEDNESS: don TOPOLOGY: linear
                                                                                                                                                                                               TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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Matches
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Patent No.
                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/831,575
FILING DATE: 09-APR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGIO, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10203
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                    TELEFAX: (516) 742-436 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Thomas, Terry L.

APPLICANT: Li, Zhongsen
TITLE OF INVENTION: AN OLEOSIN 5'REGULATORY REGION FOR THE
TITLE OF INVENTION: MODIFICATION OF PLANT SEED LIPID COMPOSITION
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1684 base pair
                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                              LENGTH: 1684 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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ZIP: 11530
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5977436
                                                                                    Similarity
 ATTACCTCAGATGAACTCAAGAACCACGATAAACCCCGGAGATCTATGGATCTCGATTCAA
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/ 742-4366
/ NO: 1:
                                                                  Score 365.4; DB 2;
Pred. No. 1.2e-69;
0; Mismatches 581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Version #1.30
                                                                                                    Length 1684;
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                                                                           GGCCTGCAGTTCCAGATTGAGCACCATCTGTTTTCCCCGCCTACCTCGGTGCCACCTTCGC
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                                             GGATTGCAATTCCAAATTGAGCATCATTTGTTTCCCAAGATGCCTAGATGCAACCTTAGG
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US-08-366-779-4
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TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENCTH: 1685 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
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                                                                                                                              Query Match 20.7%;
Best Local Similarity 55.8%;
Matches 740; Conservative
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APPLICANT:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 83
TELECOMMUNICATION INFORMATION
TELEPHONE: (516) 742-4343
TELEPHX: (516) 742-4366
                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
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CORRESPONDENCE ADDRESS:
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CITY: Garden City
STATE: New York
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Nuccio, Michael
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                                                                                                                              Score 365.4; DB 1;
Pred. No. 1.2e-69;
0; Mismatches 581;
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TYPE: nucleic acid;
STRANDENESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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                                                                                                                           Query Match
Best Local Similarity
Matches 740; Conserv
                                                                                                                                                                                                                                                                                                        TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 1
FILING DATE: 28-JAN-
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (516) 742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/3-
FILING DATE: 30-DEC-1994
ATTORNEY/AGENT INFORMATION:
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APPLICANT: Numberg, Andrew N.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID
TITLE OF INVENTION: DELTA 6-DESATURASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (516)
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    Application

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GGGAAAGCCTATGATGTTTCGGATTGGGTGAAAGACCATCCAGGTGGCAGCTTTCCCTTG
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                                                                ATTACCTCAGATGAACTCAAGAACCACGATAAACCCCGGAGATCTATGGATCTCGATTCAA
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Reddy, Avutu S.
Nuccio, Michael
                                                                                                                            Conservative
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Pred. No. 1.2e-69;
                                                                                                                            Mismatches 581;
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                                      AAGGTTGCACCGGCCGTCCGCGACCTTTGCAAGAAGCATGGGCTCACTTATTCTGCAGCC 1351
                                                                                                                              GGCCTGCAGTTCCAGATTGAGCACCATCTGTTTTCCCCGCCTACCTCGGTGCCACCTTCGC
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AAAATCTCGCCCTACGTGATCGAGTTATGCAAGAAACATAATTTGCCTTACAATTATGCA
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                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 838:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEFX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                              Query Match
Best Local Similarity 55.8
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APPLICANT: Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Thomas, 7
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION: NAME: Presser, Leopold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 400 Garden
CITY: Garden City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Presser, Leopold REGISTRATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: United States
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                                                                        GCCACGTGTACGACGTCACGCCCTGGCTCCCCCACCACCGGGCGACCTCCCGCTT
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400 Garden City Plaza
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PRODUCTION OF GAMMA LINOLENIC ACID BY
DELTA 6-DEGATURASE
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                                                                                                                                                                                                                                           Score 365.4; DB 4; Pred. No. 1.2e-69; 0; Mismatches 581;
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                                  AGGACCGCTACAAGTGGTGGTGCTCCGAAGAATTTGGTATGGGAGGCTGTGAACACCCAT 1471
                                                                                           TCTTTCTCCAAGGCCAATGAAATGACACTCAGAACATTGAGGAACACAGCATTGCAGGCT
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  -GATATAACCAAGCCGCTCCCGAAGAATTTGGTATGGGAAGCTCTTCACACTCAT
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APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLY
FILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
SEQ ID NO 3256
LENGTH: 266
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US-09-313-294A-1966
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NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6476212 700551823H1
NAME/KEY: unsure
LOCATION: 256
OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-1966
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APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Lieura Y.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
SQC ID NO 1966
LENGTH: 291
TYPE: DNA
                                                                                                                                                                                           Sequence 3256, Application US/09313294A Patent No. 6476212 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1966, Application US/09313294A Patent No. 6476212
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                ACCATCTGTTTCCCCGCCTACCTCGGTGCCACCTTCGCAAGGT 1296
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Pred. No. 1.5e-50;
                                                                                                                              AND POLYPEPTIDES
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HOTICK, Robert
TITLE OF INVENTION: METHOD FOR MAINTENANCE AND
FILE REFERENCE: 0867/0D905
CURRENT APPLICATION NUMBER: US/09/249,585A
CURRENT FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 18
SOFTMARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 1926
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NAME/KEY: misc feature

NAME/KEY: unsure

LOCATION: 262

OTHER INFORMATION: a, t, c, 9

US-09-313-294A-3256
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US-09-249-585A-4
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                                                                                                                           Query Match 6.8%;
Best Local Similarity 48.4%;
Matches 333; Conservative
                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09249585A Patent No. 6417002
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 240;
                                                                                                                                                                            TYPE: DNA
ORCANISM: Epstein Barr Virus
FEATURE:
NAME/KEY: misc feature
LOCATION: (1). (1926)
OTHER INFORMATION: template strand of EBNA-1 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Zea mays
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                     TGCAGGCCAGGACCGCTACAAGTG 1427
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ACCTTCGCAAGGTTGCACCGGCCGTCCGCGACCTTTGCAAGAAGCATGGGCTCACTTATT
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                                                                                                                            Score 120; DB 4;
Pred. No. 6.1e-17;
0; Mismatches 359
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Horlick, Robert A.
APPLICANT: Damaj, Bassam B.
APPLICANT: Damaj, Bassam B.
TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Genes
TITLE OF INVENTION: From Multiple Transfected Episomes
FILE REFERENCE: 0867/1D903US1
CURRENT APPLICATION NUMBER: US/09/130,114
CURRENT FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 1931
                                                                                                                                                          ; LENGTH: 1931
; TYPE: DNA
; ORGANISM: EBNA
US-09-130-114-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-130-114-2
                                                                                             Query Match
Best Local Similarity
Matches 333; Conser
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                                                                                             Score 120; DB 2;
Pred. No. 6.1e-17;
0; Mismatches 355
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APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT
NUMBER OF SEQUENCES: 52
                                                                                                                                                                    ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                            APPLICATION NUMBER: EP 9: FILING DATE: 26-AUG-1991 ATTORNEY/AGENT INFORMATION: NAME: BENT, Stephen A.
                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE:
                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & I
STREET: 1800 Diagona
NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768 REFERENCE/DOCKET NUMBER: 30
                                                                                                                                               FILING DATE
                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                    CITY: Alexandria
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  30472/114 IMMU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 14
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
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CLONE: pTZgpt-
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                          GTCCTGATGGCCGTCCTCTTCTACGCCGCGCTGTACCTCGTCCTCGCA
                                                      GTTGGCCGCCTCTCTGACTACGCCGTCTCCCCCGCGTCCGCCGACTACCGCCGCCTCCTC
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US-08-343-428-1
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GENERAL INFORMATION:
APPLICANT: Nakamu
APPLICANT: Tsuzuk
                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                               APPLICANT:
APPLICANT:
           SOFTWARE: WordPerfect 5.0 CURRENT APPLICATION DATA:
                                                           ZIP: 10020-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                      TITLE OF INVENTION: NO NUMBER OF SEQUENCES: 4 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                         APPLICANT:
                                                                                                             CITY: New York
STATE: New Tork
                       COMPUTER: IBM Compatible OPERATING SYSTEM: MS Dos 5.0 SOFTWARE: WordPerfect 5.0
                                                                                                                                               STREET:
                                                                                                     COUNTRY:
                                                                                                                                                          ADDRESSEE:
APPLICATION NUMBER:
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                                                                                                                      New York
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                                                                                                        USA
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Teraoka, Hiroshi
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Kitadokoro, Kengo
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 30-APR-1
APPLICATION NUMBER: (

30-APR-1993

JAPAN 4-126511 PCT/J93/00592 CLASSIFICATION:

18-NOV-1994

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Best Local Similarity
Matches 394; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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ORIGINAL SOURCE:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 19-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Haley, Jr., James F.
REGISTRATION NUMBER: 27794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDENTIFICATION METHOD:
NAME/KEY: -10 signal
LOCATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: doubl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 435..1505
IDENTIFICATION METHOD:
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NAME/KEY: CDS
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AGGTCGCCGCCTCGACGGCGCGCGTCAGCGTCACCCGCGTCCCCGGCGTGTTCCAGC
                           ACCGGATCGCCGTGGAGGCCGACTCCTCCGTCTCCGCCCCCCCGACCTGGCCCCGGCTCCGCA 879
                                                                                      TCTCTGACTACGCCGTCTCCCCCGCGGCCGCCGACTACCGCCGCCTCCTCGCGCAGCTAT 428
                                                                                                                  CCGCCCTGGAGGCACGGCCAAGATCCCCGGCACCTCGTGGGGGCTGGACCCGCGCACCA
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Pred. No. 9.7e-08;
0; Mismatches 508;
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RESULT 13
5212296-16
;Patent No. 5212296
;Patent No. 5212296
; APPLICANT: DEAN, CAROLINE;HARDER, PATRICIA A.;LETO,
;J.; O'KEEFE, DANIEL P.;OMER, CHARLES A.;ROMESSER, JAMES
.TEDPERMAN, JAMES M.
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; TITLE OF INVENTION: EXPRESSION OF HERBICIDE METABOLIZING
                                                                                                                                                                                                                                                                                                                                                                  ;SEQ ID NO:16:
                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                           Query Match
Best Local
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APPLICATION NUMBER: 464,499
FILING DATE: 12-JAN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 19
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 405,605
FILING DATE: 11-SEP-1989
                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/
FILING DATE: 23-AUG-1990
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CTTCGCCGCCTACCACCCGCCCTCGGCGCGCCCCCCTCCGCCGCCTTCTTCGTTGGCCG
                                                                                                                                                                                           CCCCGAGGTCGAGGAGGTGCTCCACGACGAGATGCTGGCCGCCGGCCCGAC
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                                                        CGGCGTGCCCTACGCCGACCACGAGTTCTTCCAGGACGCGAGCAAGCGGCTGGTGCAGTC
                                                                                      CCACCACCGGGCGGCGACCTCCCGCTTCTCACCCTGGCGGGGCAGGACGCCACCGACGC
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                                                                                                                                                                                                                                                             Score 75.6; DB 6;
Pred. No. 1.9e-07;
0; Mismatches 399;
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RESULT 14
5212296-5
; PATENT NO. 5212296
; PATENT DEAN, CAROLINE; P
; J.; O'KEEFE, DANIEL P.; OMER, CI
TEDDERMAN, JAMES M.
TEDDERMAN, JAMES M.
                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/07/569,781
; FILING DATE: 23-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 464,499
; FILING DATE: 12-JAN-1990
; APPLICATION NUMBER: 405,605
; FILING DATE: 11-SEP-1989
; SEQ ID NO:5:
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                                                                                                                                                                                                                                                       Query Match 4.3
Best Local Similarity 44.1
Matches 315; Conservative
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1879
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CTTCGCCGCCTACCACCCGCCCTCGGCGCGCCGCTCCTCCGCCGCTTCTTCGTTGGCCG
                                                                    CGCCGACCTGGTCAGTCAGTTCGCGCTGCCGGTGCCCTCCATGGTGATCTGCCGACTCCT
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                                                                                                                                                                                                                                                                       4.3%;
                                                                                                                                                                                                                                                     Score 75.6; DB 6;
Pred. No. 2.1e-07;
0; Mismatches 399;
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APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DAN SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILLING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOPTWARE: PATENTIN VET. 2.1
SEQ ID NO 1
LENGTH: 4411529
TYPE: DNA
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US-09-103-840A-1/c
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GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FTETT OWEN R.
                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 279; Conserv
                                                                                                                                                                                                                                                                                           ORGANISM: Mycobacterium tuberculosis OTHER INFORMATION: H37Rv
                                                         1218087
                                                                                                                             1218147 CGTACAGCCACCCCCGGTGGCGCCCTTGCCGCCATTGCCGCCATTGCCGCCGTTGCCGC
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205 CTCCATCTCCGGCGACGTGTACGACGTCACGCCCTGGCTCCCCCACCACCACCCGGGCGGA 264
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                                                         CGCAATGCCGCCCTCTGTCGATGCAATGCCGGCCCCCCGGCGACGCCGCGGGGCGCCGGCGA 144
                                                                                         CGTGCGCATGATCTCCTCCAAGGAGCTCCGCGCTCACGCTTCCGCCGACGACCTCTGGAT
                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                     4.1%;
                                                                                                                                                                                                  Score 72.8; DB 3;
Pred. No. 5.8e-06;
0; Mismatches 322;
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                                                                          1217607 CCCCACCGGCCCGGCGGCCACCGGCACCGCCGCCGCCGCTGCTGACGCCATTAC 1217548
                                                                                                                                                                                                                                                                                                                                         445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         622 CATCACCGGCCATCCGGTCCTCGACCGCGTCGTGCAGGTGCTCTCCGGGAAACTGCCTCAC 681
                                                                                                                                                                               562 TCTCATTGGCTTCGGGATCCAGTCCGGCTGGATGGGCCACGACTCGGGGCCACCACCAC 621
                                      682 CGGC 685
                                                                                                                                                                                                                                                   CGCCGCGCTGTACCTCGTCCTCGCATGCGCCAGCGCCTGGGCGCACCTCCTCCTCGCGGGGGG 561
                                                                                                                                                                                                                                                                                                                                     CGAACGCGTCGGCCCACCCCCAAGGTCCAGCT---CGTCCTGATGGCCGTCCTCTTCTA 501
                                                                                                                                                                                                                                                                                                                                                                                                                   CTCCCCCGCGTCCGACTACCGCCGCCGCCTCCTCGCGCAGCTATCCTCCGCGGGCCTCTT 444
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Search completed: January 1, 2004, 00:05:24 Job time : 99.5326 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
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13877.414 Million cell updates/sec
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1764
                                         Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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4: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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			6.5	6.5	6.8	6.8	7.3	8.5	8.6	11.6	13.5	13.5	20.7	24.9	27.8	Query Match
	12733	1380	263	480	9025608	1095	476	1098	287	657	265	265	1685	1350	1702	Query Match Length DB
	15	10	10	10	8 1:	15	9	12	10	9	12	9	14	10	14	
	US-10-032-393-47	US-09-967-477B-7	US-09-878-574-9255	US-09-924-035A-370	5 US-10-156-761-1	US-10-156-761-2285	US-09-770-444-39	US-10-369-493-27824	US-09-878-574-3260	US-09-770-149-494	US-09-923-876-5116	US-09-923-876-5116	US-10-029-756-4	US-09-938-842A-558	US-10-029-756-26	ID
# P		Sequence 7, Appli	Sequence 9255, Ap	Sequence 370, App	Sequence 1, Appli	Sequence 2285, Ap	Sequence 39, Appl	Sequence 27824, A	Sequence 3260, Ap	Sequence 494, App	Sequence 5116, Ap	Sequence 5116, Ap	Sequence 4, Appli	Sequence 558, App	Sequence 26, Appl	Description

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15	15 10 12 14	3 9 11 11 11 11 11 11 11 11 11 11 11 11 1	13 13 13	13 13 13
US-09-967-4778-3 US-10-156-761-1188 US-10-156-761-3949 US-10-156-761-5034	-10-16 -09-80 -10-32 -10-21 -10-10	US-09-769-863-28 US-10-054-534B-28 US-10-431-952-28 US-09-758-269-13 US-09-923-876-3376	-09-769-863 -10-054-534E -10-431-952- -10-292-798- -10-017-161-	US-10-156-761-1580 US-10-292-798-1513 US-10-017-161-1857 US-10-017-161-1813 US-10-017-161-1483 US-10-292-798-1141 US-10-292-798-1141
Sequence 3, Appli Sequence 1188, Ap Sequence 3949, Ap Sequence 5034, Ap	e 29, e 11, e 74,	28, 28, 3376	Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Sequence 1189, Ap Sequence 1481, Ap	Sequence 1513, Ap Sequence 1513, Ap Sequence 1857, Ap Sequence 1191, Ap Sequence 1191, Ap Sequence 1141, Ap Sequence 1141, Ap

## ALIGNMENTS

RESULT 1

LENGTH: 1702 base pairs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity Matches 832; Conserv
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LOCATION:
CAGACCTTTTTATTGCTCCTCACCAGGCGCGACGTCCCTGACCGCGCTCTAAACTTAATG
                            CAGTCCGCCCTGTTCGTTCTCACGGAGAAGAGGGTGCCGCAGCGGTTGCTTGAGATCGCG
                                                          AGCTACCAGCACTGGACCTACTACCCGGTCATGATCTTCGGCCGAGTCAACCTCTTCATC
                                                                          AGCTACCAGCACCTGGACCTTCTACCCCGGTAATGTGCATCGCCCAGGATAAATCTTCTCGCG
                                                                                                                                                  ATATEGT CCTACTTCTACCAACGGACCCTGGCGTTCGATGCCGCCTCGAAATTCTTCATC
                                                                                                                                                                                                                CATGACCCGGACCTCCAGCACATGCCGCTCTTTGCCGTCTCCCCCCAAGCTGTTCGGCAAC
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                                                                                                                    ATCACCTCGGTCTTCTATGGCCGAGTCCTGAAATTCGACGAAGTGGCACGGTTCCTAGTC
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STRANDEDNESS: both
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GENERAL INFORMATION:

APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Dr. STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-06-22
PRIOR FILING DATE: 2001-06-22
                                                                                                                                                       NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 558
LENGTH: 1350
TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 558, Application US/09938842A Patent No. US20020160378A1
                                                    Matches
                                                                                            Query Match
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189 CCGACGACCTCTGGATCTCCATCTCCGGCGACGTGTACGACGTCACGCCCTGGCTCCCCC
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                                                 Score 439.2; DB 10;
Pred. No. 4.4e-110;
0; Mismatches 513;
                                                                                            Length 1350,
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                                                 CTCGCTTACCTCGTTGCCATCTCCGGAAAGTTTCTCCGGTGGTTCAAGAGCTTTGCAAGA
                                                                            CCCGCCTACCTCGGTGCCACCTTCGCAAGGTTGCACCGGGCCGTCCGCGACCTTTGCAAGA 1325
                                                                                                                                                      GATCATACATGGATTGGTTCTTTGGTGGATTACAGTTTCAGCTTGAGCATCATTTGTTCC 1141
                                                                                                                                                                                             CTCCTTGGATGGATTGGTTCCACGGTGGCCTGCAGTTCCAGATTGAGCACCATCTGTTTC
                                                                                                                                                                                                                                                         CACCCACCGGTAGCGACTGGTTCGAGAAGCAAGCGGCGGGAACAATCGATATCTCTTGTA 1081
                                                                                                                                                                                                                                                                                                                CGGCGCTTCAACACACTTCAATTCACGCTTAACCATTTCGCTGCTGATGTCTACGTTGGTC
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US-10-029-756-4
(S-quence 4, Application US/10029756
; Publication No. US20020108147A1
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MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID
US-10-029-756-4
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Best Local Similarity
Matches 740; Conserv
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TELEPAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 4:
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FILING DATE: 21-Dec-2001
CLASSIFICATION: <URKnown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/934,254
FILING DATE: <UNKnown>
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 8383ZYXWVU
TELECHNUMICATION INFORMATION:
TELECHNOWICKETON INFORMATION:
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,

CURRENT APPLICATION DATA:
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TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID
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CITY: Garden City
STATE: New York
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                                                                                                                                                                ATCTCCTCCAAGGAGCTCCGCGCTCACGCTTCCGCCGACGACCTCTGGATCTCCATCTCC 214
                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1685 base pairs
TYPE: nucleic acid
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                                                                      GGGAAAGCCTATGATGTTTCGGATTGGGTGAAAGACCATCCAGGTGGCAGCTTTCCCCTTG
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                                    ACATTCTGGGGTGCAAATGTGCTTACATGGAAGACACTCAGGGCTGCTGCATTGCAGGCC 1411
                                                                                                          AAGGTTGCACCGGCCGTCCGCGACCTTTGCAAGAAGCATGGGCTCACTTATTCTGCAGCC
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RESULT 5 US-09-923-876-5116

Sequence 5116, Application US/09923876
Publication No. US20030237110A9
GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Kamigaki, Laura Y. (Ito)
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED
FILE REFERENCE: PL-0012-1 CON
CURRENT APPLICATION NUMBER: US/09/923,876
CURRENT FILING DATE: 2001-08-06

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US-09-923-876-5116
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GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Vamicaki, Laura Y. (Ito)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/085,331
PRIOR FILING DATE: 1998-05-05
NUMBER OF SEQ ID NOS: 6332
SOFTWARE: PERL PROGRAM
SEQ ID NO 5116
LENGTH: 265
                                                                                                                                                                                                                                                                                                                                   Matches 248;
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Best Local :
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CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/298,329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Kamigaki, Laura Y. (Ito)
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYMUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: PL-0012-1 CON
                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Incyte ID No. US20020013958A1 700456385H1
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                   CAGCGGTTGCTTGAGATCGCGGGGG
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CAGCGGCTGCTTGAGATCGCCGGTG
                                                                GCCAGGATAAATCTTCTGGCGCAGTCCGCTGTCTTCGTCCTGACCGAGAAGAGGGTGCCG
                                                                                   GCCGCCTCGAAATTCCTCATCAGCTACCAGCACTGGACCTTCTACCCGGTAATGTGCATC
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93.6%;
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Pred. No. 4.6e-55;
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APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
PAPULCANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2024 (PARA-013PRV)
CURRENT APPLICATION NUMBER: US/09/770,149
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,506
PRIOR FILING DATE: 2000-01-27
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FASESEQ for Windows Version 4.0
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US-09-770-149-494/c
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PRIOR FILING DATE: 1998-05-05
NUMBER OF SEQ ID NOS: 6332
SOFTWARE: PERL Program
SEQ ID NO 5116
LENGTH: 265
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Best Local Similarity
Matches 248; Conserv
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APPLICANT: Gorlach
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PRIOR FILING DATE: 1999-04-21
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OTHER INFORMATION: Incyte ID No. US20030237110A9 700456385H1
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ORGANISM: Zea mays
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Ledford, Brooke L.
Woessner, Jeffrey P.
Haas, William David
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Hamilton, Carol I
Price, Jennifer I
                                                                                                                                                                                                              Kricker, Maja
Slader, Ted
                                                                                                                                                                                   Davis, Keith R.
Allen, Keith
                                                                                                                                                                                                                                                     Garcia, Carlos A.
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eaka, Joshua G.
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Pred. No. 4.6e-55;
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; SEQ ID NO 3260 ; LENGTH: 287 ; TYPE: DNA

ORGANISM: Glycine

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RESULT 7
US-09-878-574-3260
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                                                                                                                                                                         Sequence 3260, Application Upparent No. US20020110548A1
GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 338; Conserv
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules .
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 199-06-14
NUMBER OF SEQ ID NOS: 15775
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Pred. No. 1.5e-45;
0; Mismatches 202;
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; ORGANISM: Neurospora crassa
US-10-369-493-27824
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Chen, Marry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION (
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/03-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 27824
LENGTH: 1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 27824, Application US/10369493 Publication No. US20030233675A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                             Matches 436; Conservative
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Best Local Similarity 50.4%;
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OTHER INFORMATION: unsure
OTHER INFORMATION: Clone I
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                                         ACCATGACCCGGACCTCCAGCACATGCCGCTCTTTGCCGTCTCCCCCAAGCTGTTCGGCA
                                                                                                                      CGCACCATTTCCATGTCGATACTGTCATCGGCATCATCATTGCCGACTTCATCGGTGGTC
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LIB3028-013-Q1-B1-H6
                                                                                                                                                                                                                                                                                                           Score 150.2; DB 12;
Pred. No. 9.6e-31;
0; Mismatches 408;
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Sequence 39, Application US/09770444
Patent No. US20020023280A1
GENERAL INFORMATION:
APPLICANT: Gorlach, Jorn
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APPLICANT:
APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2027 (PARA-016PRV)
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                                                                                          Garcia, Carlos A.
Kricker, Maja
Slader, Ted
Davis, Keith R.
Allen, Keith
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Ledford, Brooke L.
Woessner, Jeffrey P.
Haas, William David
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Hamilton, Carol M.
Price, Jennifer L.
                                                                                                                                                                                                                                                                         Page, Amy
                                                                                                                                                                                                                                                                                     Yu, Yang
Rameaka, Joshua G.
                                                                                                                                                                                                                                                                                                                             Raines, Tracy M.
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Sequence 2285, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: INFORMATION:
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/770,444
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,502
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 39
LENGTH: 476
                                                                                                                                                                                                                                                                                                                                 RESULT 10
US-10-156-761-2285
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NAME/KEY: misc_feature
LOCATION: (1)...(476)
OTHER INFORMATION: n = A,T,C or
US-09-770-444-39
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ilarity 55.8%;
Conservative
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LENGTH: 1095
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Best Local Similarity
Matches 457; Conserv
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                                       CCACGGTGGCCTGCAGTTCCAGATTGAGCACCATCTGTTTCCCCCGCCTACCTCGGTGCCA 1284
                                                                                                 GAAGACGGCCGTCCTGTCCATCGCCCAGGGCAAGACCAAGCGCCCCCGTCCTGGAGTCGTT
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       CTACGGCGGCCTCAACTACCAGGTCGAGCACCACCTGTTCCCGGCCATGCCCCAGAAGAA
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; PEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t,
US-10-156-761-1
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US-10-156-761-1/c
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APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, WASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
CURRENT FILING DATE: 2002-05-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 46.8%;
Matches 457; Conservative
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PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 90
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                                     GGACCATGACCCGGACCTCCAGCACATGCCGCTCTTTGCCGTCTCCCCCAAGCTGTTCGG
                                                                                                                                                      GTTCCGCAGCAAGAAGGCCGCCTCCGCCGTCGGATACTTCCACGCCAACCTCGTCAACGG
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                                                                                                       CCTCAGCATCGCCTGGTGGAAGTGTTAACCACAACACGCACCACACATCGCCTGCAACAGCCT
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RESULT 12

US-09-924-035A-370/c

Sequence 370, Application US/09924035A

Patent No. US20020142319A1

GENERAL INFORMATION:

APPLICAMT: Griach, Jrn

ITILE OF INVENTION: Expressed Sequences of Ara

FILE REFERENCE: 2011US

CURRENT APPLICATION NUMBER: US/09/924,035A

CURRENT FILING DATE: 2000-08-11

PRIOR APPLICATION NUMBER: US 60/148,784

PRIOR APPLICATION NUMBER: US 60/148,784

PRIOR FILING DATE: 1999-08-13

INMBER OF SEQ ID NOS: 900

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 370

LENGTH: 480

TYPE: DNA

ORGANISM: Arabidopsis thaliana

US-09-924-035A-370
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Best Local Similarity 61.0%;
                                                                                                                                                        1191 TCGACATCCTGTGCTCCCTTGGATGGATTGGTTCCACGGTGGCCTGCAGTTCCAGATTG 1250
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                                              AGCACCATCTGTTTCCCCGCCTACCTCGGTGCCACCTTCGCAAGGTTGCACCGGCCGTCC 1310
                                                                                                      TCGATATCTCTTGTAGATCATACATGGATTGGTTCTTTGGTGGATTACAGTTTCAGCTTG
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                                                                                                                                                                                                                                     Score 115.2; DB 10;
Pred. No. 2.8e-21;
                                                                                                                                                                                                               Mismatches 128;
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RESULT 14
US-09-967-477B-7
; Sequence 7, Application US/09967477B
; Patent No. US20020156254A1
; GENERAL INFORMATION:
; APPLICANT: Xiao Qiu
; APPLICANT: Haiping Hong
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; ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: 701102270H1
US-09-878-574-9255
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US-09-878-574-9255
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER: 09255
LENGTH: 263
TWYDE: NAM.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                             TTCACATTCTACCC
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Pred. No. 4.6e-21;
0; Mismatches 80;
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; CURRENT APPLICATION NUMBER: US/09/967,477B; CURRENT FILLING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: 60/236,303
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/297,562
; PRIOR APPLICATION NUMBER: 60/297,562
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; SEQ ID NO 7
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; NAME/KEY: CDS
; LOCATION: (1)...(1380)
US-09-967-477B-7
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Best Local Similarity 47.0%;
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TYPE: DNA
ORGANISM: Thraustochytrium
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TCGGCAACATATGGTCCTACTTCTACCAACGGACCCTGGCGTTCGATGCCGGCCTCGAAAT 860
                                                                                                                                 GCCTGGACCATGACCCGGACCTCCAGCACATGCCGCTCTTTGCCGTCTCCCCCAAGCTGT 800
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                                                                ACCTGCACAGCGCCAAGGACGAGGGCTTCATCGGCGACCCGGACATCGACACCATGCCGC
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FAD4, FAD5, FAD5-2, AND FAD6, NOVEL FATTY ACID DESATURASE FAMILY MEMBERS AND
Score 112; DB 10;
Pred. No. 3.3e-20;
                 Length 1380;
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APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Gross, Molly
ITITLE OF INVENTION: BACTERIAL PROMOTERS AND METHODS OF
FILE REFERENCE: ELITRA.010A
CURRENT APPLICATION NUMBER: US/10/032,393
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 00/259,434
PRIOR FILING DATE: 2000-12-27
PRIOR APPLICATION NUMBER: 09/948,993
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
SEQ ID NO 47
TENGTH: 12733
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US-10-032-393-47/c
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                                                                                                               ; FEATURE:
; OTHER INFORMATION: Vector peref14
US-10-032-393-47
                                        Query Match
Best Local Similarity
Matches 359; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 47, Application US/10032393 Publication No. US20030027286A1 GENERAL INFORMATION:
                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                   TYPE: DNA
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  4 CGAGCTCCCTCTCTCCCCAATCCTCCCCGCCTCCCCCTACCAAATCAGCACCACCCAA 63
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                                    Score 100.4; DB 15;
Pred. No. 1.3e-16;
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Search completed: January 1, 2004, 05:19:13
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4004	Result No.
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US-09-857-524B-3 US-10-612-783-1024 US-10-219-999-27869 US-10-425-114-14218	sult Query No. Score Match Length DB ID Description
Sequence 3, Appli Sequence 1024, Ap Sequence 27869, A Sequence 14218, A	Description

1 GCACGAGCTCCCTCTCTCCCCAATCCTCCCCGCCTCCCCCTACC		LENGTH: TYPE: DN ORGANISM 09-857-52	PRIOR FILING DATE: 1984-12-03 PRIOR FILING DATE: 1984-12-03 NUMBER OF SEQ ID NOS: 17 SOFTWARE: Microsoft Office 97 SEQ ID NO 3	857,524B	APPLICANT: Rebecca E. Cahoon APPLICANT: William D. Hitz APPLICANT: Anthony J. Kinney TITLE OF INVENTION: Membrane-Bound Desaturases	US-09-857-524B-3 ; Sequence 3, Application US/09857524B ; GENERAL INFORMATION: APPLICANT. Edgar R. Cahoon	ALIGNMENTS RESULT 1	452 25.6 1465 39 US-09-335-625-19394 445 25.2 1650 22 US-09-513-996A-68612	453.8 25.7 110149 23 US-09-534-859-381 453.8 25.7 110149 34 US-09-803-736-381 453.8 25.6 1465 22 US-09-513-996A-34823 452 25.6 1465 31 US-09-513-996A-34823	2 27.6 1828 52 US-10-425-114-14869 2 27.6 1940 52 US-10-424-599-36789 2 27.2 1940 52 US-10-424-599-36789 3 US-09-857-5248-7 4 26.3 615 36 US-09-855-4194-52475	491.2 27.8 1702 30 US-09-685-775-26 491.2 27.8 1702 44 US-10-029-756-26 486.6 27.6 514 65 US-60-110-784-6 486.7 27.6 1828 48 US-10-219-089-15694	602 34.1 1207 52 US-10-425-114-28231 539.4 30.6 684 28 US-09-654-617-452235 539.4 30.6 684 30 US-09-684-016-452235 539.4 30.6 684 30 US-09-684-016-452235	609.6 34.6 1967 48 US-10-219-999-12725 609.6 34.6 1967 52 US-10-425-114-14991 609.6 34.5 2236 52 US-10-425-299-124471 600 34.5 2236 52 US-10-424-599-124471	891.4 50.5 1408 52 US-10-425-114-17460 891.4 50.5 1485 94 US-60-391-781-446 845.4 47.9 1069 65 US-60-110-784-8 829.8 47.0 1302 53 US-60-110-784-8	973.6 55.2 14392 34 US-09-815-264-72548 973.6 55.2 14581 27 US-09-620-392-30987 891.4 50.5 1407 86 US-60-312-544-3168 891.4 50.5 1408 48 US-10-219-099-13422	12 1175 66.6 1448 30 US-09-684-016-265928 13 1091.4 61.9 1972 35 US-09-857-524B-9 14 1000.6 56.7 1944 53 US-10-437-593-83761 15 973.6 55.2 14392 31 US-09-702-114-25614	1333.8 75.6 2054 2 PCT-US03-07858A-288 1333.8 75.6 2054 51 US-10-389-566-288 1337.6 2054 53 US-10-389-586-288 1337.6 2054 53 US-10-61-520-288	3.8 75.6 2054 1 PCT-US03-07858-288 S 3.8 75.6 2054 1 PCT-US03-07858A-288 S 3.8 75.6 2054 2 PCT-US03-07858-288 S
60	1764; Qy 0: Gans 0: Db	Оу Db	Oy Db	Oy Db	Qy dd	Oy Db	Oy Db	equence 1921, Ap equence 19394, A Qy equence 68612, A Db	equence 381, App equence 381, App equence 381, App equence 34823, A Db	Sequence 14869, A Sequence 36789, A Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli	equence 26, Appl Qy equence 26, Appl equence 26, Appl equence 6, Appl equence 6, Appl equence 1264pl equence 1264pl	25.55.65	12725, 14991, 1494471,	equence 17460, A equence 17460, App equence 446, App equence 8, Appli equence 8, Appli equence 8, Appli onence 8759 A	equence 72548, A Qy equence 30987, A equence 3168, Ap Db	Sequence 9, Appli Sequence 9, Appli Sequence 83761, A Db	288	equence 288, App equence 288, App Db
1081 CATCTGCGGGATTCAGCACGTCCAATTCTGCCTGAACCACTTCTCGTCCGACGTGTATGT 1140	1021 GCTGGTGGCTTCCCTGCCGAATTGGTGGGAGAGGGTCGCGTTTGTGCTTTTCAGCTTCAC 1080	961 GGTGCCGCAGCGGTTGCTTGAGATCGCGGGGGTCGCCACATTCTGGGCTTGGTACCCGTT 1020 	901 GTGCATCGCCAGGATAAATCTTCTCGCGCAGTCCGCCCTGTTCGTTC	841 GTTCGATGCCGCCTCGAAATTCTTCATCAGCTACCAGCACTGGACCTTCTACCCGGTAAT 900	781 TGCCGTCTCCCCCAAGCTGTTCGGCAACATATGGTCCTACTTCTACCAACGGACCCTGGC 840	721 GCACCACATCGCCTGCAACAGCCTGGACCATGACCCGGACCTCCAGCACATGCCGCTCTT 780	661 GCTCTCCGGGAACTGCCTCACCGGCCTCAGCATCGCCTGGTGGAAGTGTAACCACAACAC 720	601 CCACGACTCGGGCCACCACCGCATCACCGGCCATCCGGTCCTCGACCGCGTCGTGCAGGT 660	541 GGCGCACCTCCTCGCGGGGGGTCTCATTGGCTTCGTCTGGATCCAGTCCGGCTGGATGGG 600	481 CCTGATGGCCGTCCTCTTCTACGCCGCGCTGTACCTCGTCCTCGCATGCGCCAGCGCCTG 540	421 GCAGCTATCCTCCGCGGGCCTCTTCGAACGCGTCGGCCCCACCCCCAAGGTCCAGCTCGT 480	361 TGGCCGCCTCTCTGACTACGCCGTCTCCCCCGCGTCCGCCGACTACCGCCGCCTCCTCGC 420	301 CGACGCCTTCGCCGCCTACCACCCGCCCTCGGCGCGCCCCCTCCTCCGCCGCTTCTTCGT 360	241 GCTCCCCACCACCAGGGGGGGGACCTCCCGCTTCTCACCCTGGCGGGGCAGGACGCCAC 300	181 CGCTTCCGCCGACCTCTGGATCTCCATCTCCGGCGACGTGTACGACGTCACGCCCTG 240	121 CGGCGACGCCGGGCGCCCGGCGACGTGCGCATGATCTCCTCCAAGGAGCTCCGCGCTCA 180	61 CAAGGCGCATCCGAGCCACGGCCGCCAATGCCGCCCTCTGTCGATGCAATGCCGGCCCC 120	1 GCACGAGCTCCCTCTCTCCCCAATCCTCCCCGCCTCCCCCTACCAAATCAGCACCACC 60

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Sequence 1024, Application US/10612783
; GEQUERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules And
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53373)A
CURRENT APPLICATION NUMBER: US/10/612,783
CURRENT FILING DATE: 2003-07-02
NUMBER OF SEQ ID NOS: 7098
SEQ ID NO 1024
LENGTH: 2067
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4577_136:
US-10-612-783-1024
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US-10-612-783-1024
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Best Local Similarity 90.2%;
Matches 1588; Conservative
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                                                                Clone ID: PAT_MRT4577_136542C.1
        Score 1406.4; DB 53; Length 2067; Pred. No. 3.1e-252; O; Mismatches 151; Indels 21;
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US-10-219-999-27869

Sequence 27869, Application US/10219999

GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Edgerton, Michael D
APPLICANT: Hinkle, Gregory J.
APPLICANT: Kovalic, David K.
                                                             APPLICANT: Liu, Jingdong
APPLICANT: Stein, Joshua
ITITLE OF INVENTION: CDNA SEQUENCES AND USES FOI
FILE REFERENCE: 38-10(52726)C
CURRENT APPLICATION NUMBER: US/10/219,999
CCURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/324,109
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: US 60/312,544
PRIOR FILING DATE: 2001-08-15
IPRIOR APPLICATION NUMBER: US 60/312,544
PRIOR FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 63520
SEQ ID NO 27869
LENGTH: 1541
                  ORGANISM: Zea mays FEATURE:
                                                    TYPE: DNA
 NAME/KEY: CDS
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                                  CACCGGCCGTCCGCGACCTTTGCAAGAAGCATGGGCTCACTTATTCTGCAGCCACATTCT
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Sequence 288, Application PC/TUS0307858
GENERAL INFORMATION:
APPLICANT: Monsanto Technology, LLC
APPLICANT: Laurie, Cathy C
TITLE OF INVENTION: Nucleic Acid Molecules Ass
FILE REFERENCE: 38-77(590) D
CURRENT APPLICATION NUMBER: PCT/US03/07858
CURRENT FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: US 60/365,301
PRIOR FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 60/391,786
PRIOR APPLICATION NUMBER: US 60/391,786
PRIOR APPLICATION NUMBER: US 60/392,018
PRIOR APPLICATION NUMBER: US 60/392,018
PRIOR FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: US 60/392,018
PRIOR FILING DATE: 2002-06-26
NUMBER OF SEQ ID NOS: 2459
SOFTWARE: Patentin version 3.2
SEQ ID NO 288
LENGTH: 2054
TYPE: DNA
CRGANISM: Zea mays
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CGACTCGGGCCACCACCGCATCACCGGCCATCCGGTCCTCGACCGCGCTCGTGCAGGTGCT
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Sequence 288, Application PC/TUS0307858A

GENERAL INFORMATION:

APPLICANT: Monsanto Technology, LLC

APPLICANT: Monsanto Technology, LLC

APPLICANT: Monsanto Technology, LLC

ITITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants

FILE REFERENCE: 38-77(52901)

CURRENT APPLICATION NUMBER: PCT/US03/07858A

CURRENT APPLICATION NUMBER: US 60/365,301

PRIOR APPLICATION NUMBER: US 60/365,301

PRIOR APPLICATION NUMBER: US 60/391,786

PRIOR APPLICATION NUMBER: US 60/391,786

PRIOR APPLICATION NUMBER: US 60/392,018

PRIOR APPLICATION NUMBER: US 60/392,018

PRIOR FILING DATE: 2002-06-25

PRIOR FILING DATE: 2002-06-25

SOFTWARE: Patentin version 3.2

SEQ ID NOS: 2459

LENGTH: 2054

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438 CCGCCTCTCCGACTACACCGCCTCCGCCCCCCCCCACCCCCAGCTCCGCCACCCCCAGCTCCCCCCCAGCTCCCCCCCAGCTCCCCCCAGCTCCCCCCCAGCTCCCCCCCAGCTCCCCCCCC	Db 318 TĊĊĊĂĊĊĂĊĊĂĠĠĠĠĠĠĠĂĠĊŢĊĊĠĠĠŢĊĂŢĠĂĠĠĠĠĠĠĠĠ	184 TICCGCCGACGACCTCTGGATCTCCATCTCCGGCGACGTGTACGACGTCACGCCCTGGCT 24	Qy  138 CACCCATAGGGGCCACGGCCAATGCCGCTCTGCCCAAGGAGCTCCGCGCTCACGC 183  Qy  124 CGACGCCGCGGCGACGCGACGCATGCCGCTCCCAAGGAGCTCCGCGCTCACGC 183  Qy  125 CGACGCCGCGGCCGACGGCGACGCTCACGCTCCAAGGAGCTCCGCGCTCACGC 183  180 CGACGCCGCGCGGCCGACGGCTGACGCTCCAAGGAGCTCCGCGCTCACGC 183  198 AGACGCCGCGCGGCCGACGACGTCGCGTTGATCTCCTCCAAGGAGCTCCGCGCTCACGC 257	4 CGAGCTCCCTCTCTCCCCAATCCTCCCCGCCTCCCAAATCAGCACCACCCAA 63	ery Match st Local Si tches 1558;	; SEQ 1D NO 288 ; LENGTH: 2054 ; TYPE: DNA ; TYPE: DNA ; ORGANISM: Zea mays PCT-HSO3-07858-288	E C F	FILING DATE: 2002-03-15 APPLICATION NUMBER: US FILING DATE: 2002-06-25	NCE: 38-77(52900)D  LICATION NUMBER: PCT/US03/07858  LING DATE: 2003-03-14  CAPTION NUMBER: 05-14	ENERAL INFORMATION: APPLICANT: MONGANTO Techn APPLICANT: Laurie, Cathy APPLICANT: Laurie, Cathy	RESULT 7 PCT-US03-07858-288 • Senience 288 Application BC/THISD207858	Qy 1719 TTAATTCATGAACACTTGTTTCA 1741	Qy 1666 ACGGGATGTTCTGTTCTCCCTATCACGGTAACTATGATGATGATGATCCTTGCT 1718
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1518 ĠAATTTGGTCTGGAGĠCATTGAACACCCATGGATAAACGĠACGAGĠATATGGCTG 1577  1495 -GCTAATGGCAACTTCTGGTG-TTCAGCTTGGTGCCCATGTGATTGTCTGGATGC 1547	GACACTCAGGGCTGCTGCATTGCAGGCCAGGACCGCTACAAGTGGTGGTGGTGCTCCGAA	1264 TCCCCGCCTACCTCGGTGCCACCTTCGCAAGGTTGCACCGGCCGTCCGCGACCTTTGCAA 1323	1218 GCCACCCAAGGGCAACGACTGGTTCGAGAAGCAGACGCAGGCAG	1084 CTGCGGGATTCAGCACGTCCAATTCTGCCTGAACCACTTCTCGTCCGACGTGTATGTCGG 1143	GGTGGCTTCCCTGCCGAATTGGTGGGAGAGGGTCGCGTTTGTGCTTTTCAGCTTCACCAT	964 GCCGCAGCGGTTGCTTGAGATCGCCGGGGGTCGCCACATTCTGGGCTTGGTACCCGTTGCT 1023	904 CATCGCCAGGATAAATCTTCTCGCGCAGTCCGCCCTGTTCGTTC	844 CGATGCCGCCTCGAAATTCTTCATCAGCTACCAGCACTGGACCTTCTACCCGGTAATGTG 903	784 CGTCTCCCCCAAGCTGTTCGGCAACATATGGTCCTACTTCTACCAACGGACCCTGGCGTT 843	724 CCACATCGCCTGCAACAGCCTGGACCATGACCCGGACCTCCAGCACATGCCGCTCTTTGC 783	664 CTCCGGGAACTGCCTCACCGGCCTCAGCATCGCCTGGTGGAAGTGTAACCACAACACGCA 723	604 CGACTCGGGCCACCACCGCATCACCGGCCATCCGGTCCTCGACCGCGTCGTGCAGGTGCT 663	544 GCACCTCCTCGCGGGGGGGTCTCATTGGCTTCGTCTGGATCCAGTCCGGCTGGATGGGCCA 603

438 CCGCCTCTCCGACTACACCGTCTCCCCCGCGTCCGCCGACTACCGCCCTCCTGGCGCA 424 GCTATCCTCCGCGGGCCTCTTCGAACGCGCCGCCCACCCCCAAGGTCCAGCTCCTCCT []	Qy 304 CGCCTTCGCCGCCTACCACCCGCCCTCGGCGCGCCTCCTCCGCCGCTTCTTCGTTGG 363	Qy 244 CCCCCACCACCCGGGCGGCGGCGCTCCCCGCTTCTCACCCTTGGCGGGGCAGGACGCCACCGA 303	Qy 184 TTCCGCCGACGACCTCTGGATCTCCATCTCCGGCGACGTGTACGACGTCACGCCCTGGCT 243	QY 124 CGACGCCGGCGGCGACGGCGGATGATCTCCTCCAAGGAGCTCCGCGCTCAACGC 183		GARGICCCICTCTCCCCAATCCTCCCCGGCTCCCCCTACCAAATCAGCACCJ	Query Match 75.6%; Score 1333.8; DB 2; Length 2054; Best Local Similarity 88.4%; Pred. No. 1.1e-238; Matches 1558; Conservative 0; Mismatches 177; Indels 28; Gaps 9;	LENGTH: TYPE: DN ORGANISN	PRIOR FILING DATE: 2002-06-26  NUMBER OF SEQ ID NOS: 2459 SOFTWARE: Patentin version 3.2 SEQ ID NO 288	PRIOR FILING DATE: 2002-03-15  PRIOR APPLICATION NUMBER: US 60/391,786  PRIOR FILING DATE: 2002-06-25  PRIOR FILING DATE: 2002-06-25	FILE REFERENCE: 38-77(52900)D  FILE REFERENCE: 38-77(52900)D  CURRENT PILICATION NUMBER: PCT/US03/07858A  CURRENT FILING DATE: 2003-05-09  PRIOR APPLICATION NUMBER: NE 60/365 301	Page Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant of the Constant	RESULT 8 PCT-USO3-07858A-288 ; Sequence 288, Application PC/TUSO307858A	QY 1719 TTAATTCATGAACACTTGTTTCA 1741	QY 1666 ACGGGATGTTCTGTTCTCCTATCACGGTAACTATATGATGATGATGATCCTTGCT 1718	Db 1698 TGTTGACAAGTGACCGTCTATCCAGTTGAAGAGTTCATGCTTCAATTGTCTGGGTTGTTC 1757
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1518 GAATTTGGTCTGGGAGGCATTGAACACCCATGGATAAACGGGACGAGGATATGGCTG 1577  1495 -GCTAATGGCAACTTCTGGTG-TTCAGCTTGGTGCCCATGTGATTGTCTGGATGC 1547	GACACTCAGGGCTGCCGCATTGCAGGCCAGGAGCGCCACAGGCGGCGCGCGC	1324 GAAGCATGGGCTCACTTATTCTGCAGCCACATTCTGGGGTGCGAATGTGCTTACATGGAA 1383	TCCCGCCTACCTCGGTGCCACCTTCGCAAGGTTGCACCGGCCGTCCGCGACCTTTGCAA		GCCACCCAAGGGCAATGACTGGTTTGAGAAGCAGACGGCAGGCA	1084 CTGCGGGATTCAGCACGTCCAATTCTGCCTGAACCACTTCTCGTCCGACGTGTATGTCGG 1143	1024 GGTGGCTTCCCTGCCGAATTGGTGGGAGAGGGTCGCGTTTGTGCTTTTCAGCTTCACCAT 1083	964 GCCGCAGCGGTTGCTTGAGATCGCGGGGGTCGCCACATTCTGGGCTTGGTACCCGTTGCT 1023	904 CATCGCCAGGATAAATCTTCTCGCGCAGTCCGCCCTGTTCGTTC	844 CGATGCCGCCTCGAAATTCTTCATCAGCTACCAGCACTGGACCTTCTACCCGGTAATGTG 903	784 CGTCTCCCCCAAGCTGTTCGGCAACATATGGTCCTACTTCTACCAACGGACCCTGGCGTT 843	724 CCACATCGCCTGCAACAGCCTGGACCATGACCCGGACCTCCAGCACATGCCGCTCTTTGC 783	.664 CTCCGGGAACTGCCTCACCGGCCTCAGCATCGCCTGGTGGAAGTGTAACCACACACA	604 CGACTCGGGCCACCGCATCACCGGCCATCCGGTCCTCGACCGCGTCGTGCAGGTGCT 663	544 GCACCTCCTCGCGGGGGGTCTCATTGGCTTCGTCTGGATCCAGTCCGGCTGGATGGGCCA 603	

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304 CGCCTTCGCCGCCTACCACCCGCCCTCGGCGCCCCCCCCC	244 CCCCCACCACCCGGGCGACCTCCCCGCTTCTCACCCTGGCGGGGCACGACGACGACGA 303	184 TTCCGCCGACGACCTCTGGATCTCCATCTCCGGCGACGTCTACGACGTCACGCCCTGGCT 243	124 CGACGCCGCGGGGGCGACGTGCGCATGATCTCCTCCAAGGAGCTCCGCGCTCACGC 183	64 GGCGCATCCGAGCCACGGCCGCGCAATGCCGCCCTCTGTCGATGCAATGCCGGCCCCCGG 123	CCCCTACCAATCAGCACC!	Query Match  75.6%; Score 1333.8; DB 53; Length 2054; Best Local Similarity 88.4%; Pred. No. 1.1e-238; Matches 1558; Conservative 0; Mismatches 177; Indels 28; Gaps 9;	LENGTH: 2054 TYPE: DNA ORGANISM: Zea mays 0-613-520-288	PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26  PRIOR FILING DATE: 2002-06-26	R FILING DATE: 2003-03-14  R FILING DATE: 2003-03-14  R FILING DATE: US 60/391,786  R FILING DATE: 2002-06-25  D ADDITION NUMBER: US 60/392 018	CONTRINT REFLICATION NUMBER: 03/10/013,320  CURRENT FILING DATE: 2003-07-02  PRIOR APPLICATION NUMBER: US 60/365,301  PRIOR FILING DATE: 2002-03-15  PRIOR PRICE 3002-03-15	ICANT: Maclong, Lu  B OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants REPERSICE: 38-77 (52900)E REPERSICE: 38-77 (52900)E	GENERAL INFORMATION: APPLICANT: Monsanto Technology, LLC APPLICANT: Laurie, Cathy C APPLICANT: Wi Wei	SULT 10 -10-613-520-288 Sequence 288. Application US/10613520	1719 TTAATTCATGAACACTTGTTTCA 1741	1666 ACGGGATGTTCTGTTCTCCCTATCACGGTAACTATATGATGATGATGATGCTTGCT 1718	1607 TGTTGACAAGTGGCTGTCTATCCAGTTGGAGAGTTCATGCTTCAATAGTCT-GGTTGTTC 1665	1548 CTTTCAGTTATTAGA-GATATTGATCATTCAACCTGCTGAGTCAGGTTGGAATTTTCG 1606
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Sequence 265928 Application US/09654617
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
TITLE OF INVENTION:
FILE REFERENCE: 38-21(15097)B
CURRENT APPLICATION NUMBER: US/09/654,617
CURRENT FILING DATE: 2000-09-05
NUMBER OF SEQ ID NOS: 463173
SEQ ID NO 265928
LENGTH: 1448
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US-09-654-617-265928
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Best Local Similarity
Matches 1187; Conserv
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APPLICANT: Kovalic, David K.
APPLICANT: Liu, Jingdong
FIITLE OF INVENTION: 38-21(15097)D
CURRENT APPLICATION NUMBER: US/09/684,016
CURRENT FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US 09/654,61
PRIOR FILING DATE: 2000-09-05
NUMBER OF SEQ ID NOS: 463173
SEQ ID NO 265928
LENGTH: 1448
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US-09-684-016-265928
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milarity 98.3%;
Conservative
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Pred. No. 4.5e-209;
0; Mismatches 20;
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Sequence 9, Application US/09857524B
GENERAL INFORMATION:
APPLICANT: Edgar B. Cahoon
APPLICANT: Rebecca E. Cahoon
APPLICANT: William D. Hitz
APPLICANT: Anthony J. Kinney
TITLE OF INVENTION: Membrane-Bound Desaturases
FILE REFERENCE: BB1264
CURRENT APPLICATION NUMBER: US/09/857,524B
CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/110,784
PRIOR APPLICATION NUMBER: 60/110,784
PRIOR FILING DATE: 1998-12-03
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Microsoft Office 97
SEQ ID NO 9
LENGTH: 1972
TYPE: DNA
ORGANISM: Triticum aestivum
US-09-857-524B-9
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US-09-857-524B-9
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Best Local Similarity
Matches 1355; Conserva
CCCCCGCGTCCGCCGACTACCGCCGCCCTCCTCGCGCAGCTATCCTCCGCGGGGCCTCTTCG 446
                                                                                                                                     TCCCGCTCATCACCCTCGCCGGCCAGGACGCCACGACGCCTTCATGGCCTACCACCCGC
                                                                                                                                                          TCCCGCTTCTCACCCTGGCGGGGCAGGACGCCACCGACGCCTTCGCCGCCTACCACCCGC
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                                                                                                                                                                                                                                            CAATGCCGCCCTCTGTCGATGCAATGCCGGCCGCCCCGGCGACGCCGCGGCGGCGACGC
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                                                                                 TCCGCATGATCTCCACCAAGGAGCTGCAGGCGCACGCTGCCGCGGACGACCTCTGGATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGATTA 1747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGAGATATTGATCATCCAGCCTGACCTGAGTCAGGTTGGAATTTTCGTGTTGACAAGTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.9%;
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CTCATGGATGACTGGGATCAGGACTGGAGTATGAGACAATTGTAAGCGTCGAGCCTTGCG
                                    CCCATGGATAAATGGGATGAAGATACGGGCTAATGGCAACTTCTGGTGTTCAGCTTGGTG
                                                                                                  AGGCCAGGACCGCTACAAGTGGTGGTGCTCCGAAGAATTTGGTATGGGAGGCTGTGAACA
                                                                                                                                                                                                CAGCCACATTCTGGGGTGCAAATGTGCTTACATGGAAGACACTCAGGGCTGCTGCATTGC
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RESULT 14
US-10-437-963-83761
US-10-437-963-83761
; Sequence 83761, Application US/10437963
; GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT FILING DATE: 2003-05-14
UNMBER OF SEQ ID NOS: 204966
; SEQ ID NO 83761
LENGTH: 1944
; TYPE: DNA
; ORGANISM: OTyza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_83060C.1
US-10-437-963-83761
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                         GTATGGGAGGCTGTGAACACCCCATGGATAAATGGGATGAAGATACGGGCTAATGGCAACT
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       GTTTGGGAAGCTGTGAACACTCATGGATGAATTGGA---
                                                                            TTGAGGGCTGCTGCATTGCAGGCCAGGAAAGCCACTAGTGGTGCTGCGCCAAAGAATTTG
                                                                                                                                                    CATGGGCTGCCTTATGCCGCCGCCTCGTTCTGGCAGGCTAATGTGTTGACATGGAAGACA
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APPLICANT: Cao, Yongwei
APPLICANT: Kovalic, David K.
APPLICANT: Liu, Jingdong
APPLICANT: McIninch, James
APPLICANT: McIninch, James
APPLICANT: Wu, Wei
FILE OF INVENTION: Plant Genome Sequence and Uses Thereof
FILE REFERENCE: 38-21(51237)F
CURRENT APPLICATION NUMBER: US/09/702,134
CURRENT APPLICATION NUMBER: US/09/702,134
CURRENT FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 52202
FILE OF SEQ ID NOS: 52202
FILENCTH: 14392
TYPE: DNA
ORGANISM: Oryza Bativa
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Pred. No. 2.6e-171;
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1566 6730	GCCTTTCAGTTATTTAGAGAT
1506 6778	447 GGTATGGGAGGCTGTGAACACCCATGGATAAATGGGATGAAGATACGGGCTAATGGCAAC
1446 6827	7 ACTCAGGGCTGCTGCATTGCAGGCCAGGACCGCTACAAGTGGTGGTGGTGCTCCGAAGAATTT
1386 6887	27 GCATGGGCTCACTTATTCTGCAGCCACATTCTGGGGTGCAAATGTGCTTACATGGAAGAC
1326 6947	267 CCGCCTACCTCGGTGCCACCTTCGCAAGGTTGCACCGGCCGTCCGCGACCTTTGCAAGAA
1266 7007	207 TCCTTGGATGGATTGGTTCCACGGTGGCCTGCAGTTCCAGATTGAGCACCATCTGTTTCC
1206 7067	147 ACCCAAGGGCAATGACTGGTTTGAGAAGCAGAGGGAGGCACGCTCGACATCCTGTGCTC
1146 7127	CCTGAACCACTTCTCGTCCGACGTGTATGTCGGGCC
1086 7187	27 GGCTTCCCTGCCGAATTGGTGGGAGAGAGGTCGCGTTTGTGCTTTCAGCTTCACCATCTG
1026 7247	67 GCAGCGGTTGCTTGAGATCGCGGGGGTCGCCACATTCTGGGCTTGGTACCCGTTGCTGGT
966 7307	7 CGCCAGGATAAATCTTCTCGCGCAGTCCGCCCTGTT
906 7367	47 TGCCGCCTCGAAATTCTTCATCAGCTACCAGCACTGGACCTTCTACCCC
846 7427	87 CTCCCCCAAGCTGTTCGGCAACATATGGTCCTACTTCT/ 
786 7484	7 CATCGCCTGCAACAGCCTGGACCATGACCCGGACCTCCAC
726 7544	67 CGGGAACTGCCTCACCGGCCTCAGCATCGCCTGGTGGAAGTGTAAC
666 7604	07 CTCGGGCCACCACCGCATCACCGGCCATCCGGTCCTCGACCGCGTC
606 7664	47 CCTCCTCGCGGGGGGTCTCATTGGCTTCGTCTGGATCCAGTCCGGCTGG
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Search completed: January 1, 2004, 04:20:52 Job time: 3937.96 secs

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Scoring table:
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Perfect score:
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IDENTITY_NUC
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1764
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                                                       GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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Minimum DB seq length: 0
Maximum DB seq length: 200000000 Total number of hits satisfying chosen parameters: 8967382

4483691 segs, 1203673480 residues

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : Pending_Patents_NA_New:*

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8: /cgm2_6/ptodata/1/pna/US10_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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76.4	79.4	80.2	80.2	83.6	89	100.4	103	194	213.6	273.8	337.6	365.4	385.2	439.2	452.2	453.8	459	486.2	491.2	602	609.6	891.4	1349	Score
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560 560	616	85692	85692	1215	1455	340	262	626	663	1071	966	1685	1719	2144	1341	1389	1953	1828	1702	1207	1967	1408	1541	Length
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US-10-417-700A-138 US-10-425-114A-13841	US-10-425-114A-5327	PCT-US03-19069-1	PCT-US03-18787-1	US-09-897-516A-4197	US-10-425-114A-5694	US-10-680-765-11214	US-10-680-765-14762	US-10-425-114A-10881	US-10-425-114A-14800	US-10-425-114A-10518	US-10-425-114A-6172	US-10-702-777-4	US-10-425-114A-10327	US-10-425-114A-15122	US-60-496-751-2	US-60-496-751-3	US-60-496-751-1	US-10-425-114A-14869	US-10-702-777-26	US-10-425-114A-28231	US-10-425-114A-14991	US-10-425-114A-17460	US-10-425-114A-14218	ID
Sequence 138, App	Sequence 5327, 1	Sequence 1, Appli	۲	419	Sequence 5694, 1		Sequence 14762,	Sequence 10881,		10518,				Sequence 15122,	Sequence 2, App	Sequence 3, App						Sequence 17460,	Sequence 14218,	Description

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	?4, Appl	l6, Appl	193, App	119, App	35258, A	562, App	523, App	15517, A	16902, A	17564, A	23176, A	123, App	11904, A	2, Appli	2, Appli	l6, Appl	34, Appl	li, Appl	11, Appl	28252, A

## ALIGNMENTS

Qy 639 TCCTCG         Db 241 TCCTCG	Qy 579 GGATCC        Db 181 GGATCC	Qy 519 TCCTCG	Qy 459 CCACCC        Db 61 CCACCC	Qy 399 CCGACT	Query Match Best Local Similarity Matches 1349; Conser	RESULT 1  US-10-425-114A-14218  Sequence 14218, Application US GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Liu, Jingdong APPLICANT: Kovalic, David K. APPLICANT: Screen, Steven E APPLICANT: Tabaska, Jack E APPLICANT: Tabaska, Jack E APPLICANT: TOABASKA, Jack E APPLICANT: TOABASKA, Jack E APPLICANT: OF INVENTION: Nucleic A TITLE OF INVENTION: Nucleic A TITLE OF INVENTION: Nucleic A TITLE OF INVENTION: Number: US-1128 CURRENT APPLICATION NUMBER: U CURRENT APPLICATION NUMBER: U CURRENT FILING DATE: 2003-04 NUMBER OF SEQ ID NOS: 73128 SEQ ID NO 14218 LENGTH: 1541 TYPE: DNA TYPE: DNA GRANISM: Zea may8 FEATURE: OTHER INFORMATION: Clone ID: US-10-425-114A-14218
TCCTCGACCGCGTGCTGCAGGTGCTCTCCGGGAACTGCCTCACCGGCCTCAGCATCGCCT 698	GGATCCAGTCCGGCTGGATGGGCCACGACTCGGGCCACCACCGCATCACCGGCCATCCGG 638	TCCTCGCATGCGCCAGCGCCTGGGCGCACCTCCTCGCGGGGGGGTCTCATTGGCTTCGTCT 578	CCACCCCAAGGTCCAGCTCGTCCTGATGGCCGTCCTCTTCTACGCCGCGCTGTACCTCG 518	CCGACTACCGCCGCCTCCTCGCGCAGCTATCCTCCGCGGGGCCTCTTCGAACGCGTCGGCC 458	76.5%; Score 1349; DB 7; Length 1541; larity 100.0%; Pred. No. 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	14218, Application US/10425114A NPORMATION: T: Liu, Jingdong T: Zhou, Yihua T: Kovalic, David K. T: Kovalic, David K. T: Screen, Steven E T: Tabaska, Jack E T: Cao, Yongwei INVENTION: Nucleic Acid Molecules and Other Molecules Associated With INVENTION: Plants and Uses Thereof for Plant Improvement ERENCE: 38-21(5313)B RAPPLICATION NUMBER: US/10/425,114A FILING DATE: 2003-04-28 F SEQ ID NOS: 73128 1141 NA M: Zea mays 1541 NA M: Zea mays 1647-14218

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Sequence 17450, Application US/10425114A

GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Tabbaska, Jack E
APPLICANT: Tabbaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT FILING DATE: 2003-04-28
INUMBER OF SEQ ID NOS: 73128
SEQ ID NO 17460
LENGTH: 1408
TYPE: DNA
ORGANISM: Zea mays
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; OTHER INFORMATION:
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Pred. No. 2.1e-225;
0; Mismatches 116;
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US-10-425-114A-14991  US-10-425-114A-14991  Sequence 14991, Application US/10425114A  GENERAL INFORMATION:  APPLICANT: Liu, Jingdong APPLICANT: Shou, Yihua  APPLICANT: Socreen, Steven E APPLICANT: Socreen, Steven E APPLICANT: Gao, Yongwei  ITILE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With ITILE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With ITILE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With ITILE OF INVENTION: Plants and Uses Thereof for Plant Improvement  CURRENT FILING DATE: 2003-04-28  ICURRENT FILING DATE: 2003-04-28  ICURRENT FILING DATE: 2003-04-28  INVESE OF SEQ ID NOS: 73128  SEQ ID NO 14991  ORGANISM: Glycine max  FEATURE:  ORGANISM: Glycine max  FEATURE:  ORGANISM: Glycine max  FEATURE:  ORGANISM: Glycine ID: LIB3049-020-H4_FLI  US-10-425-114A-14991  OUBLY Match B96; Conservative 0; Mismatches 429; Indels 9; Gaps 2;  OUBLY Match B96; Conservative 0; Mismatches 429; Indels 9; Gaps 2;  OUBLY Match B96; Conservative 0; Mismatches 429; Indels 9; Gaps 2;  OUBLY Match B96; Conservative 0; Mismatches 429; Indels 9; Gaps 2;  OUBLY Match B96; Conservative 0; Mismatches 429; Indels 9; Gaps 2;  OUBLY Match B96; Conservative 0; Mismatches 429; Indels 9; Gaps 2;  OUBLY Match B96; Gaps 2;  OUBLY Match B96; Gaps 2;  OUBLY Match B96; Gaps 2;  OUBLY Match B96; Gaps 2;  OUBLY Match B96; Gaps 2;  OUBLY Match B96; Gaps 2;  OUBLY Match B96; Gaps 2;  OUBLY Match B96; Gaps 2;  OUBLY Match B96; Gaps 2;  OUBLY Match B96; Gaps 2;  OUBLY Match B96; Gaps 2;  OUBLY Match B96; Gaps 2;  OUBLY Match B96; Gaps 2;  OUBLY Match B96; Gaps 2;  OUBLY Match B96; Gaps 2;  OUBLY Match B96; Gaps 2;  OUBLY Match B96; Gaps 2;  OUBLY Match B96; Gaps 2;  OUBLY Match B96; Gaps 2;  OUBLY Match B96; Gaps 2;  OUBLY Match B96; Gaps 2;  OUBLY Match B96; Gaps 2;  OUBLY Match B96; Gaps 2;  OUBLY Match B97; Match B97; Match B97; Match B97; Match B97; Match B97; Match B97; Match B97; Match B97; Match B97; Match B97; Match B97; Match B97; Match B97; Match B97; Match B97; Matc	Db 663 GTGCCCTCCTTGGATTGGTTCCATGGGGGCCTGCAGTTCAGATTGAGCACCATCT 722  Qy 1261 GTTTCCCCGCCTACCTCGGTGCCACCTTCGGAAGGTTCCAGATTGAGCACCATCT 722  Qy 1261 GTTTCCCCGCCTACCTCGGTGCCACCTTCGGAAGGTTCCAGATTGAGCACCATCT 722  Qy 1271 CAAGAAGCATGGGCTCACCTTATTCTGCAGCCGCACCTTCGGGGTGCAAATGTGCTTACATG 1380  Db 783 CAAGAAGCATGGGCTGACCTATTCTGCAGCCCACTTCTGGGGTGCAAATGTGCTTACATG 1380  P3 CAAGAACACTCAGGCTGGTGCATTCCAGCCCACCTCCTTCTGGAAACCAAATGTGCTTACATG 842  Qy 1435 TCCGAAGAATTTGGTATGGAAGCACCCATGAGTGGATGAAGATA 1491  Db 903 TCCGAAGAATTTGGTATGGAAGCACTGAACCCCATGGATAAATGGGATGAAGATA 1491  Db 903 TCCGAAGAATTTGGTATGGAAGCACTTGAACACCCATGGAACGAAAACGGAAGAATA 1491  Db 904 TCCGAAGAATTTGGTATGGAAGCACTTGAACACCCATGGAACGAAAACGGAAGAATA 1491  Db 905 TCCGAAGAATTTGGTATGGAACACCCATGAACCCATGGAAAACGGAAGAATA 1491  Db 906 TCCGAAGAATTTGGTATGGAACACTTCTGGTG-TCAGCTTGGTGCCAAATGGATGAAGATA 1600  P1492 CGGGCTAATGGCAACCTTCTGGTG-TCAACCCCATGGATGAAAACGGAACGAAGATA 1600  P1547 CCTTTCAGTTATTACA-CAATATTAATCAACCCTTCTAGTCCAACGCAACCCAAGTTGCTCAATATTCTGGAACACCCAACCCAACCCAACCCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCCAACCAACCCAACCCAACCCAACCCAACCCA
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US-10-425-114A-28231
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APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 28231
LENGTH: 1207
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Best Local :
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ORGANISM: Zea mays
FEATURE:
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                                                           GCCGCCTCTCCGACTACACCGTCTCCCCCGCGTCCGCCGACTACCGCCGCCTCCTGGCGC
                                                                                 GCCGCCTCTGACTACGCCGTCTCCCCCGCGTCCGACTACCGCCGCCTCCTCGCGC
                                                                                                                                                              TTCCCCACCACCCGGGCGGCGACCTCCCGCTCATCACCTTGGCGGGGCAGGACGCCACCG
                                                                                                                                                                                                                        TCCCCCACCACCCGGCGACCTCCCGCTTCTCACCCTGGCGGGGCAGGACGCCACCG
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Pred. No. 7.9e-149;
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Sequence 26, Application US/10702777

GENERAL INFORMATION:

APPLICANT: Thomas, Terry L.

APPLICANT: Thomas, Terry L.

TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID
LOCATION: 48.14
SEQUENCE DESCRIPTION: US-10-702-777-26
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FILLING DATE: 19-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 8383ZYXWVU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4346
TELEFAX: (516) 742-4366
TELES: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US/10/702,777
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
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ADDRESSEE: Scully,
                                                                            FEATURE:
                                                                                                                                 FEATURE:
                                                                                                                                             MOLECULE TYPE:
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TYPE: nucleic acid
STRANDEDNESS: both
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STATE: New York
COUNTRY: United States
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                                                        NAME/KEY: CDS
                                                                                            LOCATION:
                                                                                                             NAME/KEY:
                                                                                                                                                               TOPOLOGY:
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            TGCCTGAACCACTTCTCGTCCGACGTGTATGTCGGGCCACCCAAGGGCAATGACTGGTTT
                                                        GAGAGGGTCGCGTTTTGTGCTTTTCAGCTTCACCATCTGCGGGATTCAGCACGTCCAATTC
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ilarity 62.0%;
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0; Mismatches 498;
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 GTGTCCAAAGACTACAGAAAGCTTGCATCTGAGTTCTCAAAATTGGGTCTTTTTGACACC
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US-10-425-114A-14869
; Sequence 14869, Application US/10425114A
; GENERAL INFORMATION:
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; OTHER INFORMATION: Clone
US-10-425-114A-14869
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APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwel
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated 1
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TILE REFERENCE: 38-21(53313)B
CURRENT PILING DATE: 2003-04-28
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 14869
LENGTH: 1828
TYPE: DNA
ORGANISM: Glycine max
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Best Local Similarity
Matches 820; Conserv
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                                                                                 CGCCCGCTCCTCCGCCGCTTCTTCGTTGG----CCGCCTCTCTGACTACGCCGTCTCCCCC
                                                                                                                                                     TCAAACCTTGCTGGCCAGGATGTCACTGATGCATTCATAGCATACCATCCTGGCACAGCA
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                                                 TGGTCACACCTTGACAAATTCTTCACTGGCTACCACCTCAGTGACTTCAAGGTCTCTGAG
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Pred. No. 4.5e-118;
0; Mismatches 513;
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                                                                                               AGGACCGCTACAAGTGGTGGTGCTCCGAAGAATTTGGTATGGGAGGCTGTGAACACCCAT
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                                             GGATAAATGGGATGAAGAT 1490
                                                                            AGGGACTTGACAA---ACCCTGCCCCTAAGAATTTGTTGTGGGAAGCTGTTAATACCCCAT 1488
                                                                                                                                        TCATTTTGGGAGGCCAATCAGTGGACAATTAGGACCCTCAGGACTGCTGCCCTACAGGCT 1431
                                                                                                                                                                                                    AACATTTCGCCTTTGGTCAGTGACCTTTGCAAGAAGCATAATTTGCCTTATAGGAGCTTG
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Sequence 1, Application US/60496751
; GENERAL INFORMATION:
; APPLICANT: Urein, Virginia
; APPLICANT: Urein, Virginia
; APPLICANT: Froman, Byron
; APPLICANT: Gonzales, Jennifer
; TITLE OF INVENTION: Fatty Acid Desaturases if
; FILE REFERENCE: MONS: 044USP1
; CURRENT APPLICATION NUMBER: US/60/496,751
; CURRENT APPLICATION NUMBER: US/60/496,751
; CURRENT FILING DATE: 2003-08-21
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin version 3:1
; SEQ ID NO 1
; LENGTH: 1953
; TYPE: DNA
; ORGANISM: Primula juliae
US-60-496-751-1
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US-60-496-751-3
; Sequence 3, Application US/60496751
; GENERAL INFORMATION:
; APPLICANT: Ursin, Virginia
; APPLICANT: Groman, Byron
; APPLICANT: Gonzales, Jennifer
; TITLE OF INVENTION: Fatty Acid Desaturases from the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the following form of the f
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                   CCCTGAGAAACACAGCCATTGAGGCTCGGGACCTCTC---TAATCCGATCCCAAAGAATA 1357
                                                                                                                                                                                      CGCGGATGCCTAGGGGTCAGTTTCGGAAGATTTCTCCTTTTGTGAGGGATTTGTGTAAGA
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APPLICANT: Froman, Byron

APPLICANT: Gonzales, Jennifer

APPLICANT: Gonzales, Jennifer

TITLE OF INVENTION: Fatty Acid Desaturases from Primula

FILE REFERENCE: MONS:044USP1

CURRENT APPLICATION NUMBER: US/60/496,751

CURRENT FILING DATE: 2003-08-21

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PatentIn version 3.1

SEQ ID NO 2

LENGTH: 1341

TYPE: DNA

COGGANISM: Primula juliae

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Pred. No. 3.8e-109;
0; Mismatches 498;
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APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE OF INVENTION: Nulleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53313)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 15122
LENGTH: 2144
TYPE: DNA
OPCANITY: NAMER OF SEQ ID NOS: 73128
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                                                                                                            ; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3051-045-B9_FLI
US-10-425-114A-15122
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                                      Conservative
                                                        24.9%;
59.0%;
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                                    Score 439.2; DB 7;
Pred. No. 1.4e-105;
0; Mismatches 543;
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; OTHER INFORMATION: US-10-425-114A-10327
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US-10-425-114A-10327
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APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 10327
LENGTH: 1719
TYPE: DNA
TYPE: DNA
ORGANISM: Glycine max
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Best Local Similarity 62.1%;
Matches 625; Conservative
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Kovalic, David K.
Screen, Steven E
Tabaska, Jack E
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                                                                                 TCTCCCCCAAGCTGTTCGGCAACATATGGTCCTACTTCTACCAACGGACCCTGGCGTTCG
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Pred. No. 2.4e-91;
0; Mismatches 378;
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RESULT 12
US-10-702-777-4
; Sequence 4, Application US/10702777
; GENERAL INFORMATION: Terry L.
; APPLICANT: Thomas, Terry L.
; TITLE OF INVENTION: PRODUCTIO)
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COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/10/702,777
FILING DATE: 06-Nov-2003
CLASSIFICATION ATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/934,254
FILING DATE: 19-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
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ADDRESSEE: SCULIY, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
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COUNTRY: United States
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Best Local Similarity
Matches 740; Conserv
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TELEPAX: (516) 742-436
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 4:
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LENGTH: 1685 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
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TELECOMMUNICATION INFORMATION:
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516) 742-4366
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Pred. No. 4.1e-86;
0; Mismatches 581;
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APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21 (53313)B CURRENT APPLICATION NUMBER: US/10/425,114A CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NO5: 73128 SEQ ID NO 6172 LENGTH: 966
                                                                                                                                  Query Match
Best Local Similarity
Matches 503; Conserv
                                                                                                                                                                                                                                               ORGANISM: Glycine FEATURE:
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                                                                                                                              Score 337.6; DB 7;
Pred. No. 6.9e-79;
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                                                      ; OTHER INFORMATION: US-10-425-114A-10518
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APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 10518
                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10518, Application US/10425114A
 Query Match
Best Local Similarity
                                                                                                             TYPE: DNA
ORGANISM: Glycine max
                                                                                           FEATURE:
                                                                                                                                                LENGTH: 1071
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                                                                          Clone ID:
 15.5%;
                                                                        700942135_FLI
 Score 273.8; DB 7
Pred. No. 5.6e-62;
                   Length
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661

601

541

481 1210 421

361

1030

970 181 910

301

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Sequence 14800, Application US/10425114A

GENERAL IMPORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 14800
LENGTH: 663
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US-10-425-114A-14800
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; OTHER INFORMATION: Clone ID: LIB3028-013-H6_FLI
US-10-425-114A-14800
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                                                          Query Match 12.:
Best Local Similarity 66.:
Matches 322; Conservative
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                                                                                                                                                                                      TYPE: DNA
ORGANISM: Glycine max
1001 TTCTGGGCTTGGTACCCGTTGCTGGTGGCTTCCCTGCCGAATTGGTGGGAGAGGGTCGCG 1060
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                                                        Score 213.6; DB 7;
Pred. No. 3.7e-46;
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                                GGAT 1484
                                                                                                                                                                                                                      CCGGCCGTCCGCGACCTTTGCAAGAAGCATGGGCTCACTTATTCTGCAGCCACATTCTGG 1360
                                                                                               ACAAGTGGTGGTGCTCCGAAGAATTTGGTATGGGAGGCTGTGAACACCCATGGATAAATG 1480
                                                                                                                                                   GGTGCAAATGTGCTTACATGGAAGACACTCAGGGCTGCTGCATTGCAGGCCAGGACCGCT 1420
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                                                                 CTCAGTAACCCTTCTTCCCAGAATTTGTTGTGGGAAGCTTTTAACACTCATGGTTGATTT
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 GGAT 482
                                                                                                                                  GAGGCCAATCTTTGGACTCTTAAGACCCTTAGGACTGCTGCTCCCAGGCCAGGA---AT
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Search completed: January 1, 2004, 04:50:00 Job time: 449.364 secs

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Result
No.
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Maximum DB
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      4001004
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                    1484
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Match
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1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
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Listing first 45 summaries
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Copyright (c) 1993 - 2004 Compugen Ltd.
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B. napus sld1 prot
Sphingolipid desat
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P. tricornutum D6	ABG73600	23	477	۲.	535
•	AAB46440	22	520	۲	552
	AAB46436	22	8	2	564.5
<ul> <li>purpureu</li> </ul>	AAB46435	22	483	2	564.5
rolegnia	AAE31900	24	453	ν.	571
dınd	AAB46439	22	178	Ψ	597
Pythium irregulare	AAE22063	23	459	.4	612
Soybean sphingolip	AAY71553	21	253	7.	688.5
Protein d52pu with	AAY51352	21	222		771
Protein d51pu with	AAY51350	21	224		795
Desaturase enzyme	AAW84141	19	252		881
Protein b51bo with	AAY51351	21	284	9.	
Arabidopsis thalia	AAG53863	21	326	5	1133.5
Arabidopsis thalia	AAG07393	21	353	٥.	1163
Arabidopsis thalia	AAG53862	21	353	٥.	1168
Arabidopsis thalia	AAG29291	21	326	7.	N.
Florida bitterbush	AAY71551	21	448	51.4	1295.5
rose	ABG73418	24	450	ω.	1358
satur	AAW85122	20	446	4.	1370
Borage delta-6-des	ABG73417	24	448	٠.	1376
primrose	ABG73416	24	452	٠.	1379
rimrose	AAU79851	23	452	۰.	1379
abidopsis thali	AAG07391	21	517	۵.	1382
abidopsis thal	AAG07392	21	449	٠.	1382
aliana sldl	AAY51334	21	449	5	1387
idopsis thal	AAG53861	21	449	5	1387
e delta-6-de	30	24	4	55.0	w
orago officinalī	U7983	23		5	
Sunflower HADES pr	AAY51349	21	448	55.2	1391

## ALIGNMENTS

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RESULT 1
AAY71552
Corn; sphingolipid desaturase; membrane-bound desaturase; transgenic plant; fatty acid.
                                                                                                       08-JUN-2000
                                                                                                                                                                          Corn sphingolipid desaturase.
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                                                                                                                                                                                                        AAY71552;
                                                                                                                                                                                                                       AAY71552 standard; Protein; 462
                     WPI; 2000-412336/35.
N-PSDB; AAD01350.
                                           Cahoon EB, Cahoon RE,
                                                                          03-DEC-1998;
                                                                                         02-DEC-1999;
                                                                                                                      WO200032790-A2
                                                                                                                                     Zea mays.
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                                           Hitz WD,
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                                            Kinney AJ;
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Polynucleotide encoding delta-6 desaturase enzyme useful for producing transgenic plants and for producing antibodies specific to which is

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RESULT 2
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Matches 462;
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                                                                                                                                                                                                                                        Wheat; sphingolipid desaturase; membrane-bound transgenic plant; fatty acid.
                                          02-DEC-1999;
                                                                                            08-JUN-2000.
                                                                                                                                                                                           Triticum aestivum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GVATFWAWYPLLVASLPNWWERVAFVLFSFTICGIQHVQFCLNHFSSDVYVGPPKGNDWF
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Pred. No. 1.4e-251;
Mismatches 0;
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Soybean sphingolipid desaturase

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12-OCT-2000

(first

entry)

AAY71554

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Protein;

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Best Local S
Matches 372
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The present sequence is useful for producing transgenic plants having altered levels of sphingolipid desaturase which in turn would alter the fatty acid composition. The enzyme is also useful for producing polyclonal or monoclonal antibodies. The polynucleotide is useful as primer or probe for screening cDNA libraries to isolate desired full-length cDNA clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polynucleotide encoding delta-6 desaturase enzyme useful for procuransgenic plants and for producing antibodies specific to which useful for screening cDNA expression libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                               QTAGTLDILCSPWMDWFHGGLQFQIEHHLFPRLPRCHLRKVAPAVRDLCKKHGLTYSAAT
                                                                                                                  ATFWAWYPLLVASLPNWWERVAFVLFSFTICGIOHVOPCLNHFSSDVYVGPPKGNDWPEK 362
                                                                                                                                                                    SYFYQRTLAFDAASKFFISYQHWTFYPVMCIARINLLAQSALFVLTEKRVPQRLLEIAGV
                                                                                                                                                                                                                       PVLDRVVQVLSGNCLTGLSIAWWKCNHNTHHIACNSLDHDPDLQHMPLFAVSPKLFGNIW
                                                                                                                                                                                                                                                                                                             ITLAGQDATDAFMAYHPPSVRPLLRRFFVGRLSDYTVPPASADFRRLLAQLSSAGLFERV
                                                                                                                                                                                                                                                                                                                         LTLAGQDATDAFAAYHPPSARPLLRRFFVGRLSDYAVSPASADYRRLLAQLSSAGLFERV
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                                                                                                     AAFWVWYPLLVSCLPNWWERVAFVLASFVITGIQHVQFCLNHFSSAVYVGPPKGNDWFER
                                                                                                                                                      SVCYERTLAFDAISKFFVSYQHWTFYPVMGFARINLLVQSIVFLITQKKVRQRWLEIAGV
                                                                                                                                                                                                           PALNRLLQVVSGNCLTGLGIAWWKFNHNTHHISCNSLDHDPDLQHLPLFAVSTKLFNNLW
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                                                 QTAGTLDIKCSPWMDWFHGGLQFQVEHHLFPRLPRCHYRMVAPIVRDLCKKHGLSYGAAT
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polynucleotide encoding delta-6 desaturase enzyme useful for producing transgenic plants and for producing antibodies specific to which is useful for screening cDNA expression libraries -
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QARDL'TN-PAPKNLLWEAVN'THG
             QARTATSGGAPKNLVWEAVNTHG
                                                FGGLQFQLEHHLFPRLPRCQLRKISPLVSDLCKKHNLPYRSLSFWEANQWTIRTLRTAAL
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                                                                                               PERVMFVLASFAVCSIQHIQFCLNHFAANVYVGPPSGNDWFEKQTSGTLDISCASSMDWF
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This invention describes a novel sphingolipid desaturase that selectivel introduces a double bond into the sphingolipid separation or sphingolipid and capnoids. A DNA sequence encoding the sphingolipid desaturase, or a vector containing the DNA sequence, can be used to produce transgenic plants, especially crop plants, with an increased or decreased delta-8-unsaturated long-chain base content or an altered delta-8-unsaturated long-chain base chair, especially to compensate for a delta-8-unsaturated long-chain base in increase tolerance or resistance to soil salinity, ion stress or toxicity, drought, wet conditions, cold or frost and/or phytopathogenic microorganisms, or to alter size growth and flowering time. Cells, transgenic organisms or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-127549/12.
N-PSDB; AAZ44832.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transgenic plant; crop plant; delta-8-unsaturated long-chain base; tolerance; resistance; soil salinity; ion stress; toxicity; drought; cold; frost; phytopathogenic microorganism; flowering time; cosmetic; pharmaceutical; food; chemical raw material.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B. napus sld1 protein.
                                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New sphingolipid desaturase that selectively introduces double bond
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Best Local Similarity
Matches 254; Conserv
                                                                                                                                                                                                                                                                                                                         Sphingolipid desaturase; sld1; sphingobase; ceramide; capnoid; transgenic plant; crop plant; delta-8-unsaturated long-chain base; tolerance; resistance; soil salinity; ion stress; toxicity; drought; cold; frost; phytopathogenic microorganism; flowering time; cosmetic; pharmaceutical; food; chemical raw material.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plants containing the DNA sequence can be used to produce sphingolipids and capnoids with unsaturated sphingobases. The sphingolipids or capnoid can be used in cosmetics, pharmaceuticals and foods and as chemical raw materials. This sequence represents the Brassica napus sphingolipid desaturase sld1 protein described in the method of the invention.
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                                                                                                                                                                                                                                                                               Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sphingolipid desaturase protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VVYGVVACTSIWAHLISAVLIGILWIQSAYVGHDSGHYNVTSTKPCNKLVQLLSGNCITG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALYLVLACASAWAHLLAGGLIGFVWIQSGWMGHDSGHHRITGHPVLDRVVQVLSGNCLTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WERVAFVLFSFTICGIQHVQFCLNHFSSDVYVGPPKGNDWFEKQTAGTLDILCSPWMDWF
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Pred. No. 1.1e-138;
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RESULT 7
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Best Local S
Matches 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     desaturates, or a vector containing the DNA sequence, can be used to produce transgenic plants, especially crop plants, with an increased or decreased delta-8-unsaturated long-chain base content or an altered delta-8-unsaturated long-chain base cis/trans ratio, especially to compensate for a delta-8-unsaturated long-chain base deficiency, to exclude production of delta-8-unsaturated bases, to increase tolerance or resistance to soil salinity, ion stress or toxicity, drought, wet conditions, cold or frost and/or phytopathogenic microorganisms, or to alter size growth and flowering time. Cells, transgenic organisms or plants containing the DNA sequence can be used to produce sphingolipids and capnoids with unsaturated sphingobases. The sphingolipids or capnoids can be used in cosmetics, pharmaceuticals and foods and as chemical raw materials. This sequence represents a sphingolipid desaturase protein described in the method of the invention.
                       AAR98455
                                                 AAR98455 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel sphingolipid desaturase that selectively introduces a double bond into the sphingobase of the ceramide residue of sphingolipids and capnoids. A DNA sequence encoding the sphingolipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 15; 62pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New sphingolipid desaturase that selectively introduces double bond
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                                                                                                                                                                                                                                                                                                                               179 TRGWNKFAGIFIGNCITGISIAWWKWTHNAHHIACNSLDYDPDLQHLPMLAVSSKLFNSI
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                                                                                                                                                                                                                                                                                                                                                                                                                                    59 INLAGODVTDAFTAFHPGTAWKHLDKLFTGYHLKDYQVSDISRDYRKLASEFAKAGMFEK
                                                                                                                                                                                                                                             VATFWAWYPLLVASLPNWWERVAFVLFSFTICGIQHVQFCLNHFSSDVYVGPPKGNDWFE
                                                                                                                                                                                                                                                                                         WSYFYQRTLAFDAASKFFISYQHWTFYPVMCIARINLLAQSALFVLTEKRVPQRLLEIAG
                                                                                                                                          TFWGANVLTWKTLRAAALQARTATSGGAPKNLVWEAVNTHG 462
                                                                                                                                                                                                                                                                                                                                             HPVLDRVVQVLSGNCLTGLSIAWWKCNHNTHHIACNSLDHDPDLQHMPLFAVSPKLFGNI
                                                                                                                                                                                                                                                                                                                                                                                                          VGPTPKVQLVLMAVLFYAALYLVLACASAWAHLLAGGLIGFVWIQSGWMGHDSGHHRITG
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTLAGQDATDAFAAYHPPSARPLLRRFFVG-RLSDYAVSPASADYRRLLAQLSSAGLFER
                                                                                                                 SFYDANVTTLKTLRTAALQARDLTN-PAPQNLAWEAFNTHG
                                                                                                                                                                     KQTRGTIDIACSSWMDWFFGGLQFQLEHHLFPRLPRCHLRSISPICRELCKKYNLPYVSL
                                                                                                                                                                                              KQTAGTLDILCSPWMDWFHGGLQFQIEHHLFPRLPRCHLRKVAPAVRDLCKKHGLTYSAA 421
                                                                                                                                                                                                                        TLIFWTWFPLLVSRLPNWPERVAFVLVSFCVTGIQHIQFTLNHFSGDVYVGPPKGDNWFE
                                                                                                                                                                                                                                                                            TSVFYGROLTFDPLARFFVSYOHYLYYPIMCVARVNLYLOTILLISKRKIPDRGLNILG
                                                                                                                                                                                                                                                                                                                                                                                KGHGVIYSLCFVSLLLSACVYGVLYSGSFWIHMLSGAILGLAWMQIAYLGHDAGHYQMMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSIEVLNSIADGK-----KYITSKELKKHNNPNDLWISILGKVYNVTEWAKEHPGGDAPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                               Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56.6%; Score 1427.5; DB 2: 55.1%; Pred. No. 1.7e-138; tive 77; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          capnoids
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Expression of the desaturase in transgenic plants, esp. sunflower, soybean, maize, tobacco, peanut, carrot or oilseed rape, results in increased GIA produ. Alteration of the plant membrane lipids as a result of expression of the desaturase may also result in increased
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       resistance to chilling.
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ty acid; octadecatetraeonic acid;
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tive 73; Mismatche
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                       Query Match
Best Local Similarity
Matches 247; Conserv
                                                                                                                                                     This sequence corresponds to the borage (Borago officinalis) desaturase enzyme. The encoding lipid metabolism gene is an of a heterologous gene which can be expressed at high levels seed-specific manner in transgenic plants, when placed under of the sunflower albumin gene 5' regulatory region (AAV34397)
                                                                                                                                                                                                                                                                                         Example 2; Fig 1; 38pp; English.
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                                                                 Li Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Delta-6 desaturase; borage; oleosin; AtS21; promoter; transgenic plant; seed; lipid; fatty acid; oilseed; v gamma-linolenic acid; octadecatetraenoic acid.
WPI; 1999-180333/15
N-PSDB; AAX24917.
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Matches 247
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Sphingolipid desaturase; sld1; sphingobase; ceramide; capnoid; transgenic plant; crop plant; delta-8-unsaturated long-chain b tolerance; resistance; soil salinity; ion stress; toxicity; dr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid containing oleosin 5'-regulatory region - useful for modulating fatty acid synthesis and lipid metabolism in plants, particularly to increase content of gamma-linolenic acid
                                                                                                              27-APR-2000
                                                                                                                                                                                     AAY51349 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200 LSIAWWKCNHNTHHIACNSLDHDPDLQHMPLFAVSPKLFGNIWSYFYQRTLAFDAASKFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 ALYLVLAÇASAWAHLLAGGLIGFVWIQSGWMGHDSGHHRITGHPVLDRVVQVLSGNCLTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 RMISSKELRAHASADDLWISISGDVYDVTPWLPHHPGGDLPLLTLAGQDATDAFAAYHPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                 HGGLQFQIEHHLFPRLPRCHLRKVAPAVRDLCKKHGLTYSAATFWGANVLTWKTLRAAAL
                                                                                                                                                                                                                                                                                                                                                                                                                     GERIMFVIASLSVTGMQQVQFSLNHFSSSVYVGKPKGNNWFEKQTDGTLDISCPPWMDWF
                                                                                                                                                                                                                                                                                                                                                                                                                                         WERVAFVLFSFTICGIQHVQFCLNHFSSDVYVGPPKGNDWFEKQTAGTLDILCSPWMDWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VSYQHWTFYPIMCAARLNMYVQSLIMLLTKRNVSYRAQELLGCLVFSIWYPLLVSCLPNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISYQHWTFYPVMCIARINLLAQSALFVLTEKRVPQRLLEIAGVATFWAWYPLLVASLPNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVYGVLFCEGVLVHLFSGCLMGFLWIQSGWIGHDAGHYMVVSDSRLNKFMGIFAANCLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STWKNLDKFFTGYYLKDYSVSEVSKDYRKLVFEFSKMGLYDKKGHIMFATLCFIAMLFAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SARPLLRRFFVG-RLSDYAVSPASADYRRLLAQLSSAGLFERVGPTPKVQLVLMAVLFYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KYITSDELKNHDKPGDLWISIQGKAYDVSDWVKDHPGGSFPLKSLAGQEVTDAFVAFHPA
                                                                                                                                                                                                                                                                            QARDITK-PLPKNLVWEALHTHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISIGWWKWNHNAHHIACNSLEYDPDLQYIPFLVVSSKFFGSLTSHFYEKRLTFDSLSRFF
                                                                           HADES
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                                                                                                              (first
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                                                                           protein.
                                                                                                                                                                                                                                                                                                                                              entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55.3%;
                                                                                                                                                                                     448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1393; DB 20;
Pred. No. 5.9e-135;
3; Mismatches 121;
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                                                                                                                                                                                                                                                                                                           462
 long-chain base;
toxicity; drought;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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cold; frost; phytopathogenic microorganism; flowering time; cosmetic;
pharmaceutical; food; chemical raw material.
                                                                                                                                                     27-JUN-1998;
                                                                                                                                                              30-DEC-1999
                                                                                                                                    (GVSE-) GVS
                                                                                                                          Zaehringer U,
                                                                                                                                    GES ERWERB & VERW LANDWIRTSCHAFTLICH
                                                                                                                                             98DE-1028850
                                                                                                                                                      98DE-1028850
                                                                                                                           Schmidt H,
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New sphingolipid desaturase that selectively introduces double bond TULO sphingolipids and capnoids

Disclosure; Page 33-34; 62pp; German

This invention describes a novel sphingolipid desaturase that selectively controduces a double bond into the sphingobase of the ceramide residue of sphingolipids and capnoids. A DNA sequence encoding the sphingolipid desaturase, or a vector containing the DNA sequence, can be used to produce transgenic plants, especially crop plants, with an increased or decreased delta-8-unsaturated long-chain base content or an altered compensate for a delta-8-unsaturated long-chain base content or an altered compensate for a delta-8-unsaturated long-chain base deficiency, to exclude production of delta-8-unsaturated bases, to increase tolerance or resistance to soil salinity, ion stress or toxicity, drought, wet conditions, cold or frost and/or phytopathogenic microorganisms, or to calter size growth and flowering time. Cells, transgenic organisms, or complete some soil swith unsaturated sphingobases. The sphingolipids or capnoids can be used in cosmetics, pharmaceuticals and foods and as chemical raw materials. This sequence represents a desaturase protein, HADES, isolated from Helianthus annuus (sunflower) which is used in the method of the invention.

Sequence 448 AA;

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Matches 247; Conserv
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307
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                                                                                                                                                                                                                    140 ALYLVLACASAWAHLLAGGLIGFVWIQSGWMGHDSGHHRITGHPVLDRVVQVLSGNCLTG
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                            WERVAFVLFSFTICGIOHVOFCLNHFSSDVYVGPPKGNDWFEKQTAGTLDILCSPWMDWF
                                                                                                                                               LSIAWWKCNHNTHHIACNSLDHDPDLQHMPLFAVSPKLFGNIWSYFYQRTLAFDAASKFF
                                                                                                                                                                                     SVYGVLFCEGVLVHLFSGCLMGFLWIQSGWIGHDAGHYMVVSDSRLNKFMGIFAANCLSG
                                                                                                                                                                                                                                                   STWKNLDKFFTGYYLKDYSVSEVSKDYRKLVFEFSKMGLYDKKGHIMFATLCFIAMLFAM 126
                                                                                                                                                                                                                                                                   SARPLLRRFFVG-RLSDYAVSPASADYRRLLAQLSSAGLFERVGFTPKVQLVLMAVLFYA 139
                                                                                                                                                                                                                                                                                                                KYITSDELKNHDKPGDLWISIQGKAYDVSDWVKDHPGGSFPLKSLAGQEVTDAFVAFHPA
                                                                                                                                                                                                                                                                                                                                      RMISSKELRAHASADDLWISISGDVYDVTPWLPHHPGGDLPLLTLAGQDATDAFAAYHPP
 GERIMFVIASLSVTGMQQVQFSLNHFSSSVYVGKPKGNNWFEKQTDGTLDISCPPWMDWF
                                                                                        ISYQHWTFYPVMCIARINLLAQSALFVLTEKRVPQRLLEIAGVATFWAWYPLLVASLPNW
                                                                                                                        ISIGWWKWNHNAHHIACNSLEYDPDLQYIPFLVVSCKFFGSLTSHFYEKRLTFDSLSRFF
                                                             VSYQHWTFYPI
                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                        55.2%; Score 1391;
55.8%; Pred. No. 9
tive 73; Mismatch
                                                                                                                                                                                                                                                                                                                                                                           Mismatches 121;
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                                                                                                                                                                                                                                                                                                                                                                                                          448;
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ARESULT 11
AAU79830
ID AAU79930
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  Query Match
Best Local Similarity
                                                                                                                                                   The invention describes an isolated nucleic acid encoding an evening primrose Delta6-desaturase. The nucleic acid and a vector expressing the nucleic acid are useful for producing a plant such as sunflower, soybean, maize, tobacco, peanut, carrot or oil seed rape plant, with increased gamma linolenic acid (GLA) content, and also for inducing or increasing production of GLA in a bacteria or plant deficient, lacking in or producing low levels of GLA. The nucleic acid is also useful for inducing chilling tolerance in plants. This is the amino acid sequence of the corage delta6 desaturase involved in the production of gamma linoleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel nucleic acid encoding evening primrose delta6-desaturase which converts linoleic acid to gamma linolenic acid useful for producing gamma linolenic acid in transgenic plant or bacteria -
                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                        Example 9; Column 31-34; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ABK49502
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10-OCT-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU79830;
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14-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-MAR-2002
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91US-0774475.
92US-0817919.
92US-0307382.
97US-0789936.
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372..377
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  55.0%;
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Pred.
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1387; DB 23;
No. 2.5e-134;
                     Length 448
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                                                     13-OCT-1992;
19-SEP-1997;
10-OCT-1991;
08-JAN-1992;
14-SEP-1994;
28-JAN-1997;
            Thomas TL;
                                                                                                                                                                                                                                                                                Delta-6-desaturase; enzyme; delta-12-desaturase; sunflower; soybean; maize; tobacco; peanut; carrot; oil seed rape; gamma-linolenic acid; octadecatetraenoic acid; alpha-linolenic acid; delta-15-desaturase;
                                                                                                                                                                                                                                                                                                                             Borage delta-6-desaturase
                                                                                                                                                           08-AUG-2002
                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                Borago
                                                                                                                                                                                                                                                                                                                                                    17-APR-2003
                                                                                                                                                                                                                                                                                                                                                                          ABG73095;
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                                  (THOM/) THOMAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISYQHWTFYPVMCIARINLLAQSALFVLTEKRVPQRLLEIAGVATFWAWYPLLVASLPNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSIAWWKCNHNTHHIACNSLDHDPDLQHMPLFAVSPKLFGNIWSYFYQRTLAFDAASKFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVYGVLFCEGVLVHLFSGCLMGFLWIQSGWIGHDAGHYMVVSDSRLNKFMGIFAANCLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALYLVLACASAWAHLLAGGLIGFVWIQSGWMGHDSGHHRITGHPVLDRVVQVLSGNCLTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SARPLLRRFFVG-RLSDYAVSPASADYRRLLAQLSSAGLFERVGFTFKVQLVLMAVLFYA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KYITSDELKNHDKPGDLWISIQGKAYDVSDWVKDHPGGSFPLKSLAGQEVTDAFVAFHPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RMISSKELRAHASADDIWISISGDVYDVTPWLPHHPGGDLPLITLAGQDATDAFAAYHPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QARTATSGGAPKNLVWEAVNTHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HGGLQFQIEHHLFPRLPRCHLRKVAPAVRDLCKKHGLTYSAATFWGANVLTWKTLRAAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GERIMFVIASLSVTGMQQVQFSLNHFSSSVYVGKPKGNNWFEKQTDGTLDISCPPWMDWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VSYQHWTFYPIMCAARLNMYVQSLIMLLTKRNVSYRAQELLGCLVFSIWYPLLVSCLPNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISIGWWKWNHNAHHIACNSLEYDPDLQYIPFLVVSSKFFGSLTSHFYEKRLTFDSLSRFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STWKNLDKFFTGYYLKDYSVSEVSKDYRKLVFEFSKMGLYDKKGHIMFATLCFIAMLFAM 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                       QARDITK-PLPKNLVWEALHTHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HGGSQFQ1EHHLFPKMPRCNLRK1SPYV1ELCKKHNLPYNYASFSKANEMTLRTLRNTAL
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                                                                                                                                      2001US-0029756
                                                      92US-0817919.
94US-0307382.
97US-0789936.
                                  TL.
                                                                                       91US-0774475
                                                                                                   92US-0959952.
97US-0934254.
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AC AAG5:
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DT 18-0
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Best Local S
Matches 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a nucleic acid encoding an evening primrose delta-6-desaturase polypeptide. The nucleic acid, a vector comprising the nucleic acid or a nucleic acid encoding delta-12-desaturase, is useful for producing a plant (such as sunflower, soybean, malze, tobacco, peanut, carrot or oil seed rape plant) with increased gamma-linolenic acid (GLA) content by transforming a plant cell with the nucleic acid or vector and regenerating a plant with increased GLA content from the plant cell, for inducing or increasing production of GLA in an organism lacking in or producing low levels of GLA and for inducing production of octadecatetraenoic acid in at least one of a plant deficient or lacking in or producing low levels of octadecatetraenoic acid, a bacterium which produces alpha-linolenic acid or a bacterium which exhibits a delta-15-desaturase activity on a GLA substrate. This sequence represents
                           Arabidopsis thaliana protein fragment SEQ ID NO: 68613.
                                                               18-OCT-2000
                                                                                                                              AAG53861 standard; Protein; 449 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 borage delta-6-desaturase polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            el nucleic acid encoding evening primrose delta-6-desaturase, producing plant with increased gamma linolenic acid content, inducing octadecatetraenoic acid production in plant
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                                                                                                                                                                                                                                  QARTATSGGAPKNLVWEAVNTHG
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                                                                                                                                                                                                                                                                                                                                                                                                                VSYQHWTFYPIMCAARLNMYVQSLIMLLTKRNVSYRAQELLGCLVFSIWYPLLVSCLPNW
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; Pred. No. 2.5e-134;
73; Mismatches 122;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter
termination sequence.
                                      promoter;
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25-FEB-2000; 2000EP-0301439

08-APR-1999 16-APR-1999 99US-0126264. 99US-0126785. 99US-0127462. 99US-0130077 99US-0130449

99US-0130510. 99US-0130891. 99US-0131449. 99US-0132048.

30-APR-1999; 04-MAY-1999; 05-MAY-1999; 06-MAY-1999; 06-MAY-1999; 07-MAY-1999; 99US-0132407 99US-0132485 99US-0132485 99US-0132485 99US-0132487 99US-013263 99US-0134256 99US-0134218 99US-0134219 99US-0134219 99US-0134219 99US-0134219

99US-0134768 99US-0134941 99US-0135124

99US-0135353. 99US-013629. 99US-0136021. 99US-0136392. 99US-0137222. 99US-0137222. 99US-0137228.

08-JUN-1999 10-JUN-1999

-1999 99US-0137528.
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18-JUN-1999 18-JUN-1999 99US-0139460. 99US-0139462. 99US-0139463. 99US-0139750. 99US-0139750. 99US-0139817. 99US-0139817. 99US-0139899.

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5-0140354. 1040695. 10140823. 10140991. 10141287. 10141287. 10142154. 10142154. 10142154. 10142159. 10142159. 10142159. 10142159. 10142159. 10142159. 10142159. 10142159. 10142159. 10142159. 10142159. 10142159. 10142159. 101436. 101436. 101436. 10144005. 10144005.

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28-CT 1999
28-CT 1999
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07-SEP-1999;
10-SEP-1999;
13-SEP-1999;
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Pred. No. 2.5e-
59; Mismatches
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.5e-134;
les 125;
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                            Query Match
Best Local Similarity
Matches 247; Conserv
                                                                                                                                                                                                 desaturase, or a vector containing the DNA sequence, can be used to produce transgenic plants, especially crop plants, with an increased or decreased delta-8-unsaturated long-chain base content or an altered delta-8-unsaturated long-chain base catefolic especially to compensate for a delta-8-unsaturated long-chain base deficiency, to exclude production of delta-8-unsaturated bases, to increase tolerance or resistance to soil salinity, ion stress or toxicity, drought, wet conditions, cold or frost and/or phytopathogenic microorganisms, or to alter size growth and flowering time. Cells, transgenic organisms or plants containing the DNA sequence can be used to produce sphingolipids and capnoids with unsaturated sphingobases. The sphingolipids or capnoids can be used in cosmetics, pharmaceuticals and foods and as chemical raw materials. This sequence represents the Arabidopsis thaliana sphingolipid desaturase eld1 protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel sphingolipid desaturase that selectively introduces a double bond into the sphingobase of the ceramide residue of sphingolipids and capnoides. A DNA sequence encoding the sphingolipid desaturase, or a vector containing the DNA sequence, can be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sphingolipid desaturase; sld1; sphingobase; ceramide; capnoid; transgenic plant; crop plant; delta-8-unsaturated long-chain base; tolerance; resistance; soll salinity; ion stress; toxicity; drought; cold; frost; phytopathogenic microorganism; flowering time; cosmetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New sphingolipid desaturase that selectively introduces double into sphingolipids and capnoids -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pharmaceutical; food; chemical raw material.
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DB; AAZ44833.
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                               Conservative
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                                                           Score 1387; DB 21; Pred. No. 2.5e-134;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   termination sequence
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hybridisation assay; genetic mapping; gene expression control; promoter;
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1: pir1:*
2: pir2:*
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4: pir4:*
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                                            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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S68358

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linoleoyl-CoA desa linoleoyl-CoA desa linoleoyl-CoA desa linoleoyl-CoA desa Deltas fatty acid protein Ti3F2.1 [i Deltas fatty acid probable Deltas fatty acid probable Deltas fa linoleoyl-CoA desa nitrate reductase hypothetical prote omega-6 desaturase cytochrome b5 [imp cytochrome b5 [imp cytochrome b5 - co probable desA pronitrate reductase omega-3 fatty acid cytochrome b5 - wi nitrate reductase nitrate reductase probable heme bind nitrate reductase probable heme bind nitrate reductase probable heme bind nitrate reductase
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delta-8 sphingolip
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         당
      368 FGGLQFQLEHHLFPRLPRCHLRTVSPVVKELCKKHNLPYRSLSWWEANVWTIRTLKNAAI 427
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Regult No.

cytochrome b5, out	CBRT5M	35	Н	6.3	160	45
nitrate reductase	RDSPNH	26	9	6.4	161	44
nitrate reductase	T02240	39	8	6.4	161.5	43
conserved hypothet	B83034	70 2	ω	6.4	161.5	42
nitrate reductase	RDMUNH	17 1	بو	6.4	162	41
probable omega-6	T08136	13 2	4	6.4	162.5	40
cytochrome b5 At2g	T00796	34	<u>, , , , , , , , , , , , , , , , , , , </u>	6.5	163.5	39
nitrate reductase	S16292	32 1	9	6.5	164.5	38
nitrate reductas	T08108	<u>-</u> 2	9	6.5	164.5	37
nitrate reductas	E96807	17 2	9	6.6	166	36
nitrate reductase	S35228	17 2	9	6.6	166	35 5
phosphatidylchol	S43771	17 2	ń	6.6	166	34
nitrate reductas	852301	20 2	9	6.6	166.5	33
nitrate reductase	RDNTNS	)4 1	9	6.6	167	32
hypothetical prote	D85362	18 2	448	6.7	168.5	31
nitrate reductase	T08105	1 2	911	6.7	169.5	30

	36 164.5 6.5 38 164.5 6.5 38 164.5 6.5 39 163.5 6.4 40 162.5 6.4 41 165.5 6.4 42 161.5 6.4 43 161.5 6.4 44 165.6 6.3  RESULT 1 ARBA900  RESULT 1 ARBA900  RESULT 1 ARBA900  RESULT 1 ARBA900  RESULT 1 ARBA900  RESULT 1 ARBA900  RESULT 1 ARBA900  RESULT 1 ARBA900  RESULT 1 ARBA900  RESULT 1 ARBA900  RESULT 1 ARBA900  RESULT 1 ARBA900  RESULT 1 ARBA900  RESULT 1 ARBA900  RESULT 1 ARBA900  RESULT 1 ARBA900  RESULT 1 ARBA900  RESULT 1 ARBA900  RESULT 1 ARBA900  RESULT 1 ARBA900  RESULT 1 ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE 1-494 SCT  AFFETERE SEGUENCE: G CENTRAL RESULTS  AFFETERE SEGUENCE: G CENTRAL RESULTS  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA900  AFFETERE ARBA90  AFFETERE ARBA900  AFFETERE ARBA90  AFFETE	6.6 917 6.5 982 6.5 134 6.4 917 6.4 917 6.4 926 6.4 370 6.4 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 135 6.3 13	2093.	E96807 T708108 S16292 S16292 T700796 T700796 T700796 RDSPWH CBRT5M CBRT5M CBRT5M CBRT5M CBRT5M CBRT5M CBRT5M CBRT5M CBRT5M CBRT5M CBRT5M CBRT5M CBRT5M ALIGNMENTS ALIGNMENTS ALIGNMENTS ALIGNMENTS ALIGNMENTS O.; Shea, T.P.; in, L.A.; Shen, M. O.; Eisen, J.A.; of chromosome 2 of D:20083487; PMID:1 D:20083487; PMID:1	166 6.6 917 2 E96807  37 164.5 6.5 912 T S16292  38 164.5 6.5 982 1 S16292  39 163.5 6.5 982 1 S16292  39 163.5 6.4 44 2 TO0796  40 162.5 6.4 917 1 RDMUNH  41 161.5 6.4 917 1 RDMUNH  42 161.5 6.4 917 1 RDMUNH  43 161.5 6.4 917 1 RDMUNH  44 161.5 6.4 917 1 RDMUNH  45 160 6.3 135 1 CBRTSM  RESULT 1  AB4900  AB4900  AB4900  AB5900  AB6900  AB5900  AB5900  AB5900  AB5900  AB5900  AB5900  AB5900  AB6900  AB5900    AB590000  AB590000  AB590000  AB5900000  AB5900000  AB59000000  AB59000000  AB59000000  AB590000000  AB590000000  AB5900000000  AB59000000000000000000000000000000000000
	A;Accession: A84900 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-449 <sto> A;Cross-references: GB:AE002093; NID:g3702328; C;Genetics: A;Gene: At2946210 A;Map position: 2</sto>	inary inary ip some ies: GB:AE002	2093	, NID:g3702328, PI	IDN:AAC62885.1; GSPDB:GN00139
	Query Match 58.2%; Best Local Similarity 59.1%; Matches 262; Conservative 6  Matches 262; Conservative 7  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative 9  Matches 262; Conservative	58 CONSETVATION IISSKELRAHASA :: :: :	3.2% 9.1% 7e 10 10 10 10 10 10 10 10 10 10 10 10 10	Score 1466; DB 2; pred. No. 4.9e-119; 63; Mismatches 116; MISISGDVYDVTPWLPHHPGGD	S8.2%; Score 1466; DB 2; Length 449;  similarity 59.1%; Pred. No. 4.9e-119;  conservative 63; Mismatches 11; Indels 2; Gaps 2;  RMISSKELRAHASADDLWISISGDVYDVTPWLPHHPGGDLPLLTLAGQDATDAPAAYHPP 80    :-  :-
	Qy 81 SA 	RPLLRRFFVG-F   ;   WHHLEKLHNGYF	VRDI	YAVSPASADYRRLLAQLS :            :   HVSDVSRDYRRLAAEFS	SARPLLRRFFVG-RLSDYAVSFASADYRRLLAQLSSAGLFERVGFTFKVQLVLMAVLFYA 139 
	Qy 140 AI     Db 128 VI	YLVLACASAWAH              YGVLACTSIWAH	ILLAC	3GLIGFVWIQSGWMGHDS  :  :     ::     \VLLGLLWIQSAYVGHDS	ALYLVLACASAWAHLLAGGLIGFVWIQSGWWGHDSGHHRITGHPVLDRVVQVLSGNCLTG 199
	Qy 200 LS	SIAWWKCNHNTHI             SIAWWKWTHNAHI	IIACI	NSLDHDPDLQHMPLFAVS	LSIAWWKCNHNTHHIACNSLDHDPDLQHMPLFAVSPKLFGNIWSYFYQRTLAFDAASKFF 259 
	Qy 260 IS	SYQHWTFYPVMCJ           SYQHWTFYPVMCY	ARII	NLLAQSALFVLTEKRVPQ     :  : :::    	ISYQHWTEYPVMCIARINLLAQSALFVLTEKRVPQRLLEIAGVATEWAWYPLLVASLPNW 319 
	Qy 320 WE   Db 308 QE	RVAFVLFSFTIC         : RFIFVFVSFAVI	GIQI  - -  - -	IVQFCLNHFSSDVYVGPP 	WERVAFYLFSFTICGIQHYQFCLNHFSSDYYVGPPKGNDWFEKQTAGTLDILCSPWNDWF 379          :         ::
<u>.</u>	Оу 380 но     368 FG	GLOFOIEHHLFE      :      GLOFOLEHHLFE		RCHLRKVAPAVRDLCKKH        :  ::       RCHLRTVSPVVKBLCKKH	HGGLQFQIEHHLFPRLPRCHLRKVAPAVRDLCKKHGLTYSAATFWGANVLTWKTLRAAAL 439 

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delta 8 sphingolipid desaturase [imported] - rape
C;Species: Brassica napus (rape)
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_ch
C;Accession: T50555
R;Sperling, P.; Zaehringer, U.; Heinz, E.
J. Biol. Chem. 273, 28590-28596, 1998
A;Title: A sphingolipid desaturase from higher plants. Iden
A;Reference number: Z22986; MUID:99003197; PMID:9786850
A;Recession: T50555
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-449 <SPE>
A;Cross-references: EMBL:AJ224160; PIDN:CAA11857.1
A;Experimental source: cultivar Drakkar
C;Genetics:
A;Gene: s1d1
Delta8 sphingolipid desaturase (EC 1.14.99.-) [similarity] - (C;Species: Helianthus annuus (common sunflower) C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_chan; C;Accession: $68358 R;Sperling, P.; Schmidt, H.; Heinz, E. Sur. J. Biochem. 232, 798-805, 1995 A;Title: A cytochrome-b(5)-containing fusion protein similar A;Reference number: $68358; MUID:96028121; PMID:7588718 A;Accession: $68358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 RMISSKELRAHASADDLWISISGDVYDVTPWLPHHPGGDLPLLTLAGQDATDAFAAYHPP
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                                                                                                                                                                                                                                                                                                                                                                                                          HGGLQFQIEHHLFPRLPRCHLRKVAPAVRDLCKKHGLTYSAATFWGANVLTWKTLRAAAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WERVAFVLFSFTICGIOHVQFCLNHFSSDVYVGPPKGNDWFEKQTAGTLDILCSPWMDWF
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57.3%;
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-458 <SPE>
A;Cross-references: EMBL:X87143; NID:g1040728; PIDN:CAA60621.1; PID:g1040729
A;Cross-references: EMBL:X87143; NID:g1040728; PIDN:CAA60621.1; PID:g1040729
C;Superfamily: cytochrome b5 core homology
C;Keywords: heme; iron; metalloprotein; oxidoreductase
F;16-90/Domain: cytochrome b5 core homology <CB5>
F;16-90/Domain: cytochrome b5 core homology <CB5>
F;51,74/Binding site: heme iron (His) (axial ligands) #status predicted
                                                                                                                     A; Residues: 1-449 < DEH>
A; Cross references: EMBL:AL132962; PIDN:CAB71088.1
A; Experimental source: cultivar Columbia; BAC clone F2A:
A; Sperling, P; Zaehringer, U; Heinz, E.
J. Biol. Chem. 273, 28590-28596, 1998
A; Title: A sphingolipid desaturase from higher plants. 1
A; Reference number: Z22986; MUID:99003197; PMID:9786850
A; Accession: T51848
A;Status: preliminary; translated A;Molecule type: mRNA A;Residues: 1-449 <SPS: A;Cross-references: EMBL:AJ224161; A;Experimental source: Cultivar Co C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                      delta-8 sphingolipid desaturase (EC 1.14.99.-) [validated] - N;Alternate names: protein P2A19.180 (;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_chan C;Accession: T47950; T51848 R;De Haan, M.; Maarse, A.C.; Grivell, L.A.; Mewes, H.W.; Lemc submitted to the Protein Sequence Database, January 2000
                                                                                                                                                                                                                                                                                       A;Accession: T47950
A;Status: preliminary
A;Molecule type: DNA
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                       EMBL:AJ224161; PIDN:Ci
ce: cultivar Columbia;
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55.1%;
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Pred. No. 1.1e-
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                                        PIDN: CAA11858.1
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                 K.F.X.;
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mainly

green

parts,

some

flowers,

few

Quezi

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C;Species Mucor rouxii
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 03-Jun-2002
C;Accession: JC7556
R;Laoteng, K.; Mannontarat, R.; Tanticharoen, M.; Cheevadhanarak, S.
Biochem. Biophys. Res. Commun. 279, 17-22, 2000
A;Title: Delta6-desaturase of Mucor rouxii with high similarity to plant delta6-desatura
A;Reference number: JC7556; MUID: 20563795; PMID:11112411
A;Accession: JC7556
A;Molecule type: DNA
A;Residues: 1-523 <LAO>
A;Cross-references: GB:AF290983
A;Experimental source: strain ATCC 24905
C;Comment: This enzyme, a membrane-bound key enzyme, is responsible for the transformatic.
                                                                                                                                                                                                                                                                                                                                                                                                    linoleoyl-CoA desaturase (EC 1.14.19.3) - Mucor rouxii N; Alternate names: delta6-desaturase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Note: F2A19.180
C; Function:
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A; Map position:
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                                                                               MPPSVDAMPAPGDAAGAGDVRMISSKELRAH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QARD-VANPVVKNLVWEALNTHG
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                                                -AAD-RLLSSTSTRSSNIVTEEKFQELIKQGDSVFI-YEQKVYRV
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                                                                                                               77;
                                                                                                           Score 735; DB 2;
Pred. No. 1.2e-55;
77; Mismatches 177
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Pred. No. 3.4e-112;
9; Mismatches 125;
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A/Experimental Source: Clone W08D2
A/Experimental Source: Clone W08D2
B/Experimental S
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                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:AF031477; NID:g3088519; PIDN:AAC15586.1; F C;Genetics: A;Gene: CESD:W08D2.4 A;Map position: 4 A;Map position: 4 A;Introns: 13/3; 39/2; 234/3; 277/3; 378/1; 413/3 C;Superfamily: Caenorhabditis elegans Delta6 fatty acid desaturase C;Keywords: alternative splicing; oxidoreductase; unsaturated fatty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:Z70271; PIDN:CAA94233.1; GSPDB:GN00022;
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A; Residues: 1-473 <WIL>
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Best Local S
Matches 138
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                                                                                                                                   DGKWLYLSEEL-----VKKHPGGAVIEQYSIPPLNKNIETRGIITTRGSSNALDILYFY 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHLRKVAPAVRDLCKKHGLTYSAATFWGANVLTWKTLRAAALQ 440
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                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                             18.0%; Score 454.5; DB 1; 28.1%; Pred. No. 2e-31; ative 71; Mismatches 169;
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    LSDYAVSPAS
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Inolecyl-CoA desaturase (EC 1.14.19.3) [validated] - human
N;Alternate names: Delta6 fatty acid desaturase; protein DKFZp586C201.1
C;Species: Homo sapiens (man)
C;Date: 13-Aug-1999 #sequence revision 13-Aug-1999 #text_change 03-Jun-2002
C;Accession: T13155; T08765
R;Cho, H.P.; Nakamura, M.T.; Clarke, S.D.
J. Biol. Chem. 274, 471-477, 1999
A;Title: Cloning, expression, and nutritional regulation of the mammalian Delta-6 di
A;Reference number: Z17612; MUID:99085046; PMID:9867867
A;Accession: T13155
A;Accession: T13155
A;Molecule type: mRNA
A;Residues: 1-444 <CHO>
A;Cross-references: EMBL:AF126799; NID:94406527; PID:94406528; PIDN:AAD20018.1
R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, March 1999
A;Reference number: Z16471
A;Accession: T08765
A;Molecule type: mRNA
A;Residues: 'RTRG',138-428,'D',430,'M',432-444 <WAM>
A;Cross-references: EMBL:AL050118
A;Experimental source: adult uterus; clone DKFZp586C201
C;Genetics:
A;Cross-references: GDB:9956652
A;Note: DKFZp586C201.1
C;Superfamily: cytochrome b5 core homology
C;Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase; unsaturated: F;18-94/Domain: cytochrome b5 core homology
C;Keywords: chromoprotein; heme iron (His) (axial ligands) #status predicted
                                                                                                                                                       Query Match
Best Local S
Matches 122
                                                                                                                                                                                                                                                    Superfamily: cytochrome b5 core homology; Reywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase; unsaturated; 18-94/Domain: cytochrome b5 core homology <CB5>; 53,76/Binding site: heme iron (His) (axial ligands) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233 DKHNTHHAATNVIDHDGDIDLAPLFAFIP---GDLCKY----KASFEKAILKIVPYQHLY
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  ATDAFAAYHP-----PSARPLLRRFFVGRLS-----DYAV-SPASADYRRLLAQLSSA 116
                                                                                                     GDAAGAGDVRM---ISSKELRAHASADDLWISISGDVYDVTPWLPHHPGGDLPLLTLAGQD
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                                                     GEGAAEREVSVPTFSWEEIQKHNLRTDRWLVIDRKVYNITKWSIQHPGGQRVIGHYAGED
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                                                                                                                                                            Conservative
                                                                                                                                                                            16.2%; Score 408; DB 2; Length 444; 26.7%; Pred. No. 1.9e-27;
                                                                                                                                                            63;
                                                                                                                                                            Mismatches
                                                                                                                                                       172; Indels 100;
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                                                                                                                                                       Gaps
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A;Title: Molecular cloning and functional characterization of rat delta-6 fatty acid d A;Reference number: G00180; MUID:99160394; PMID:10049752
A;Accession: JG0180
A;Accession: JG0180
A;Status: preliminary
A;Molecule type: mRNA
A;Residuse: 1-444 <AKI'>
A;Cross-references: DDBJ:AB021980; NID:g4514721; PIDN:BAA75496.1; PID:g4514722
C;Superfamily: cytochrome b5 core homology
C;Superfamily: cytochrome b5 core homology <CB5-
F;18-94/Domain: cytochrome b5 core homology <CB5-
F;18-94/Domain: cytochrome b5 core homology <CB5-
F;53,76/Binding site: heme iron (His) (axial ligands) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 NLFK----TNHVFFLLLLAHIIALESIAWFTVFYFGNGWIPTLITAFVLATSQAQAGWLQ 179
  296 LLEIAGVATFWAWYPLLVASLPNWWERVAFVLFSFT-----
                                                                                                                                                                                                                                                                                                            133 MAVLFYAAL-YLVLACASAWAHLLAGGLIGFVWI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               292 VPQRLLEIAGVATFWAWYPLLVASL--PNW----WERVAFVLFSFT-----ICG----I 33
                                                                                                                                                                                                                                                                                                                                                               84 KFLKPLL----IGELAPEEPSLDRGKSSQITEDFRALKKTAEDMNLFK-----T 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 KELRAHASADDIWISISGDVYDVTPWLPHHPGGDLPLLTLAGQDATDAFAAYH-----P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 ATDAFRAFHPDLEFVGKFLKPLL----IGELAPEEPSQDHGKNSKITEDFRALRKTAEDM 123
                                                                                                                                                                                                                                                                                                                                                                                                                 80 PSARPLIRRFFVGRLSDY-----AVSPASADYRRLLAQLSSAGLFERVGPTPKVQLVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EFIQKHNLRTDRWLVIDRKVYNVTKWSQRHPGGHRVIGHYSGEDATDAFRAFHLDLDFVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLOFOIEHHLFPRLPRCHLRKVAPAVRDLCKKHGLTY 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QHVQFCLNHF------SSDVYVGPPKGNDWFEKQTAGTLDILCSPWMDWFHG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NFIRFLESHWFVWVTQMNHIVMEIDQEAY-----RDWFSSQLTATCNVEQSFFNDWFSG
                                                     ----W-----QPLEYGKKKLKYLPYNHQHEYFFLIGPPLLIPMYFQYQIIMTMIRR--RD
                                                                                                                                                            SVYKKSIWNHIVHKFVIGHLKGASANWWNHRHFQHHAKPNIFHKDPDIKSLHVFVLGE--
                                                                                                                                                                                                                                                               NHLFFFLLLSHIIVMESIAWFIL---SYFGNGWIPTVITAFVLATSQAQAGWLQHDYGHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HLNFQIEHHLFPTMPRHNLHKIAPLVKSLCAKHGIEY
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                                                                                                       FGNIWSYFYQRTLAFDAASKFFISY -- QHWTFYPVMCIARINLLAQSALFVLTEKRVPQR
                                                                                                                                                                                                    RITGHPVLDRVVQVLSGNCLTGLSIAWWKCNHNTHHIACNSLDHDPDLQHMPLFAVSPKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.9%; Score 400; DB 2; 26.4%; Pred. No. 9.6e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 166;
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     ----ICGIQHV--QFCLN 343
                                                                                                                                                                                                                                                                                                                  ---- QSGWMGHDSGHH 177
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C;Accession: T43319; T24875
R;Michaelson, L.V.; Napiter, J.A.; Lewis, M.; Griffiths, G. FEBS Lett. 439, 215-218, 1998
A;Title: Functional identification of a fatty acid delta5 A;Reference number: Z22422; MUID:99059458; PMID:9845325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Map position: 4
A;Introns: 43/3; 80/3; 197/3; 295/3; 318/2; 349/1; 384/3
A;Introns: 43/3; 80/3; 197/3; 295/3; 318/2; 349/1; 384/3
C;Superfamily: Caenorhabditis elegans Delta6 fatty acid desaturase
C;Keywords: oxidoreductase; unsaturated fatty acid biosynthesis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-197,'VSHIFNN',198-447 WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: A; Accession: T24875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, A; Reference number: Z19947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Swinburne, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: EMBL: AF078796; NID: g4003522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-447 < MIC>
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A;Accession: T43319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
T43319
Delta5 fatty acid desaturase (EC 1.14.99.-) T13F2.1 [validated] - Caenorhabditis
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Best Local Sim
Matches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cross-references: EMBL:Z81122; PIDN:CAB03352.1; GSPDB:GN00022; CESP:T13F2.1
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HFSSDVY-VGPPKGNDWFEKQTAGTLDILCSPWMDWFHGGLQFQIEHHLFPRLFRCHLRK
                                                             HYYDYYRNTAIYEQVGLSLHWAWSLGQLYFLPDWSTRIMFFLVSHLVGGFLLSHV-VTFN
                                                                                                                                                                                                                                                 GHHRITGHPVLDRVVQVLSGNCLTGLSIAWWKCNHNTHHIACNSLDHDPDLQHMPLFAVS
                                                                                                                                                                                                                                                                                                                              ERVGPTPKVQLVLMAVLF-----YAALYLVLACASAWAHLLAGGLIGFVWIQSGWMGHDS 174
                                                                                                                                                                                                                                                                                                                                                                                                              -PSARP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                               DGKWCQIDDAV-----LRSHPGGS-AITTYKNMDATTVFHTFHTGSKEAYQWLTELKKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DDLWISISGDVYDVTPWLPHHPGGDLPLLTLAGQDATDAFAAYHP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HFSSDVYVGPPKGNDWFEKQTAGTLDILCSPWMDWFHGGLQFQIEHHLFPRLPRCHLRKV
                                                                                                                                  AEHLNNYSQDSWVMTL-----FRWQHVHWTF--MLPFLRLSWLLQSIIFV---SQMPT
                                                                                                                                                                        PKLFGNIWSYFYQRTLAFDAASKFFISYQHWTFYPVMCIARINLLAQSALFVLTEKRVPQ
                                                                                                                                                                                                               AHHQLFKNRYYNDLASYFVGNFLQGFSSGGWKEQHNVHHAATNVVGRDGDLDLVPFYATV
                                                                                                                                                                                                                                                                                         Y----IRKILETIFTILFAFYLQYHTYYLPSAI-----LMGVAWQQLGWLIHEF
                                                                                                                                                                                                                                                                                                                                                                      CPTQEPEIPDIKDDPIKGIDDVNMGTFNISEKRSAQINKSFTDLRMRVRAEGLMDGSPLF
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                                                                                               -LLEIAGVATEWAWYPLLVASLPNWWERVAFVLFSFTICG--IQHVQFCLN
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26.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 370.5;
Pred. No. 3.
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3.5e-24;
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R;anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C elegans/ and www sanger.ac.uk/Projects/C elegans/
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: H88791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: T13F2.1
A;Map position: 4
C;Superfamily: Caenorhabditis elegans Delta6 fatty acid desaturase
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C; Genetics:
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Best Local Similarity
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401
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                                                                                                                                                      -- SOMPTHYYDYYRNTAIYEOVGLSLHWAWSLGOLYFLPDWSTRIMFFLVSHLVGGFLLS
                                                                                                                                                                                             TEKRVPQR------LLEIAGVATFWAWYPLLVASLPNWWERVAFVLFSFTICG--IQ 336
                                                                                                                                                                                                                                    VPFYATVAEHLNNYSQDSWVMTL-----FRWQHVHWTF--MLPFLRLSWLLQSIIFV-
                                                                                                                                                                                                                                                                       MPLFAVSPKLFGNIWSYFYQRTLAFDAASKFFISYQHWTFYPVMCIARINLLAQSALFVL 287
                                                                                                                                                                                                                                                                                                                  AHHOLFKURYYNDLASYFVGNFLQVSH1FNNGFSSGGWKEQHNVHHAATNVVGRDGDLDL
                                                                                                                                                                                                                                                                                                                                                     GHHRITGHPVLDRVVQVLSGNCL-----TGLSIAWWKCNHNTHHIACNSLDHDPDLQH
                                                                                                                                                                                                                                                                                                                                                                                            Y----IRKILETIFTILFAFYLQYHTYYLPSAI------LMGVAWQQLGWLIHEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CPTQEPEIPDIKDDPIKGIDDVNMGTFNISEKRSAQINKSFTDLRMRVRAEGLMDGSPLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VAPAVRDLCKKHGLTYSA----ATFW
PRHNLNTVMPLVKEFAAANGLPYMVDDYFTGFW
                                PRCHLRKVAPAVRDLCKKHGLTYSA----ATFW
                                                                          HV-VTFNHYSVEKFALSSNIMSNYACLQIMTTRNMRPGRFIDWLWGGLNYQIEHHLFPTM
                                                                                                               HVQFCLNHFSSDVY-VGPPKGNDWFEKQTAGTLDILCSPWMDWFHGGLQFQIEHHLFPRL
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25.8%;
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433
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Clare fatty acid desaturase (EC 1.14.99.-) [imported] - Synechocystis sp. C. Species: Synechocystis sp. C. Species: Synechocystis sp. C. Date: 19-Mar-1997 #sequence revision 19-Mar-1997 #text_change 20-Jun-2000 C. Accession: S35157; S76243
R;Reddy, A.S.; Nuccio, M.L.; Gross, L.M.; Thomas, T.L.

RESULT S35157

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C;Accession: T36617
R;Oliver, K.; Harris, D.; Bentley, S.D.;
submitted to the EMBL Data Library, June
A;Reference number: Z21610
A;Accession: T36617
                                                                                                                                                                                                                                        probable Delta6 fatty acid desaturase (EC 1.14.99.-) SCH35.42c C;Species: Streptomyces coelicolor C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Isolation of a Delta(6)-desaturase gene from the cyanobacterium Synechocystis A;Reference number: S35157; MUID:93283633; PMID:8389613
A;Accession: S35157
A;Status: preliminary
A;Molecule type: DNA
A; Gene:
                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-345 <OLI>A;Cross-references: EMBL:AL078610; PIDN:CAB44385.1; GSPDB:GN00070; SCOEDB:SCH35.42c
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Keywords: oxidoreductase; unsaturated fatty acid biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-359 <KAN>
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                                       A; Experimental source: strain A3(2)
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A;Experimental source: PCC 6803
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A; Title: Sequence
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                       Genetics:
SCOEDB: SCH35.42c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --LFIPF-YWFLYDV-------YLVLNKGKYHDHKIPPFQPLELASLLGIKLLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SKFFISYQHWTFYPVMCIARINLLAQSALFVLTEKRV------PQRLLEIAGVATFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FPVRLLGCMVLAIALAAFSFNVGHDANHNAYSSNPHINRVLGMTYD--FVGLSSFLWRYR 122
                                                                                                                                                                                                                                                                                                                                                                                                                                KHGLTYSA-ATFWGANVLTWKTLRA 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---NDWFEKQTAGTLDILC-SPWMDWFHGGLQFQIEHHLFPRLPRCHLRKVAPAVRDLCK 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGYVFGLPLALGFSIPEVLIGASVTYMTYGIVVCTI----FMLAHVLESTEFLTPDGESG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AWY----PLLVA-SLPN--WWERVAFVLESFTICGIQHVQFCLNHFSSDVYVGPPKG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---GLIGFVWIQ-----SGWMGHDSGHHRITGHPVLDRVVQVLSGNCLTGLSIAWWKCN
                                                                                                                                                                                                                                                                                                                                                                                           EFGVEYKVYPTFKAAIASNYRWLEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRRVLNORVDAYFAEHGLTQRDNPS-----MYLKTLIIVLWLFSAWAFVLFAPVI
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23.9%; Pred. No. 1.2e-13;
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                                                                                                                                                                                                                                                                                                                                                                                           354
                                                                                                                                                                                                    Parkhill, J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137;
                                                                                                                                                                                                                                            #text_change
                                                                                                                                                                                                      Barrell,
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                                                                                                                                                                                                      B.G.; Rajandream,
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Kamada, M.; Yasuda
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A;Status: preliminary
A;Molecule type: DNA
A;Moslecule type: DNA
A;Residues: 1-368 <TAS>
A;Cross-references: EMBL:X87094; NID:g809109; PIDN:CAA60573.1; C;Keywords: oxidoreductase; unsaturated fatty acid biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N;Alternate names: Delta6-desaturase
C;Species: Spirulina platensis
C;Date: 08-Jul-1995 #sequence_revisic
C;Accession: S54809
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                                            233
                                                                                                                                                                                                                                                                                                                                                                     166 QSGW-MGHDSGHHRITGHPVLDRVVQVLSGNCLT----GLSIAWWKCNHNT-HHIACNSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 RRLLAQLSSAGLFERVGPTPKVQ-LVLMAVLFYAALYLVLACASAWAHLLAGGLIGFVWI
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                                                                                                                                                                                                                                                                                                                                                                                                                              22 RRVNAYLEAENISPRONPPMYLKTAIILAWVVSAWTFVVFGPDVLWMKLLGCIVLGFGVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 LAVMYGQVALVAHDMAHRQVFRR----RRASELSGRIAGASIGMSYGWWQDKHTRHHANP 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 TPGS-DPARLSKKVADAGLLGRRPGYYTLRITAVTGLYAAGWAAFVLVGASWWTLAIAAF
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                                                                                                                                                                                                                                                                                                                                 AVGFNISHDGNHGGYSKY----OWVNYLSG--LTHDAIGVSSYLWKFRHNVLHHTYTNIL 135
SPWMDWFHGGLQFQIEHHLFPRLPRCHLRKVAPAVRDLCKKHGLTYSA-ATFWGANVLTW 431
                                                                                          V----AFVLFSFTICGIQHVQFCLNHFSSDV-YVGPPK---GNDWFEKQTAGTLDIL-C 372
                                                                                                                                                                                                                                                                                DHDPDLQHMPLFAVSPKLFGNIWSYFYQRTLAFDAASKFFISYQHWTF----YPVM-----C
                                            VIGASIVYMTHGLVAC----VVFMLAHVIEPAEFLDPDNLHIDDEWAIAQVKTTVDFAPN 288
                                                                                                                                         IADV----QTMLFKRQYHDHEIPSPTWVDIATLLAFKAFGVAVFLIIPIAVGYSP--LEA
                                                                                                                                                                                       IARINLLAQSALF -- VLTEKRVPQ-RLLEIAGVATFWAW ----- YPLLVASLPNWWER 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IEHHLFPRLPRCHLRKVAPAVRDLCKKHGLTYS 419
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24.3%; Pred. No. 1.7e-13
ative 55; Mismatches 15
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hypothetical protein TIK7.28 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C;Accession: A86390
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White,
Chin, C.W.; Chung, M.K.; Conn, L.;
Conway, A.B.; Conway, A.B.; Conway, A.R.; Creasy, T.H.
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, I
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Description: catalyzes the reduction of nitrate to nitrite
A;Description: catalyzes the reduction of nitrate to nitrite
C;Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 reduc;Superfamily: nitrate reductase (NADH); cytochrome b5 core homology cPCO>
F;36-425/Domain: molybdopterin-binding domain homology cPCO>
F;497-571/Domain: cytochrome b5 core homology cPBS>
F;613-864/Domain: cytochrome-b5 reductase homology cPCB>
F;139/Binding site: molybdopterin (Cys) (covalent) #status predicted
F;532,555/Binding site: heme iron (His) (axial ligands) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Gruber, H.; Goetinck, S.D.; Kirk, D.L.; Schmitt, R.
Gene 120, 75-83, 1992
A;Title: The nitrate reductase-encoding gene of Volvox carteri: Map location, sequence A;Reference number: JC1422, MUID:93013022; PMID:1398126
A;Accession: JC1422
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A;Reference number: A86141; MUID:21016719; PMID:11130712 A;Accession: A86390
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A;Introns: 183/3; 234/2; 295/1; 339/1; 372/1; 425/2; 521/3; 593/3; 677/3; 797/2
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A; Residues: 1-864 <GR2>
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36.4%; Pred. No. 7.9e-08;
tive 22; Mismatches 57
                                                                                                                                                                                                                                                                                                             R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso. Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.
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C;Superfamily: cytochrome b5; cytochrome b5 core homology
C;Keywords: heme; iron; metalloprotein
E;40,64/Binding site: heme iron (His) (axial ligands) #st
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                                  132 LMAVLF 137
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                                                                                                          PSARPLLRRFFVGRLSDYAVS--PASADYRRLLAQLSSAGLFER-----VGPTPKVQL-V
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                                                                                                                                                                                                                       7.3%; Score 184.5; DB 2.larity 36.5%; Pred. No. 1.1e-08; Conservative 23; Mismatches 48
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Search completed: January 1, 2004, 06:39:40 Job time : 18.3885 secs

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P40934 brassica ol
Q01170 chlorella v
P27968 hordeum vul
P11605 nicotiana t
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P46312 arabidopsis
P493101 cichorium i
P11832 arabidopsis
P39868 brassica na
P08619 nicotiana t
P43101 cichorium i
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P39869 brassica na
P08619 ratus norv
P48627 brassica na
P1035 arabidopsis
P49102 zea may9 (m
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5 phaseolus v
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## ALIGNMENTS

Query Match

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Score 424;

DB

Length 444;

27.7%;

Pred. No. 2.1e-27;

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28-FEB-2003
                                                                                                                                                                MEDIINE=97061201; PubMed=8905231;
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,
Yamada M., Yasuda M., Tabata S.;
"Sequence analysis of the genome of the unicellular cyanobacterium
Synechocystis sp. strain PCC6803. II. Sequence determination of the
entire genome and assignment of potential protein-coding regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reddy A.S., Nuccio M.L., Gross L.M., Thomas T.L.;
"Isolation of a delta 6-desaturase gene from the cyanobacterium
Synachocystis sp. strain PCC 6803 by gain-of-function expression
Anabaena sp. strain PCC 7120.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=93283633; PubMed=8389613;
Reddy A.S., Nuccio M.L., Gross L.
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Q08871;
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NCBI TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                   Res. 3:109-136(1996).
CATALYTIC ACTIVITY: Linoleoyl-CoA
linolenoyl-CoA + A + 2 H(2)O.
                                                               COFACTOR: IRON.
        SWISS-PROT
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A desaturase (EC 1.14.19.3) (Delt
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                                                                  STRAIN=f. Nagariensis / HK10;
MEDLINS=93013022; PubMed=1398126;
Gruber H., Goetinck S.D., Kirk D.L.,
"The nitrate reductase-encoding gene
sequence and induction kinetics.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
entitles requires a license agreement (See http://www.isb-
or send an email to license@isb-sib.ch).
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ProDom; PD001081; FA_desat_fam; 1.
Oxidoreductase; Iron; Complete pro
                                                        Gene 120:75-83(1992).
                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                   Eukaryota; Viridiplantae; Volvocaceae; Volvox.
                                                                                                                                                                                                             Volvox carteri.
                                                                                                                                                                                                                                           Nitrate reductase
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EMBL; D90914; BAA18502
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FUNCTION: Nitrate reductase is a key enzyme involved in step of nitrate assimilation in plants, fungi and bacte CAPTALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)0 = nitrate COPACTOR: EACH SUBUNIT OF THE ENZYME CONTAINS 1 EQUIVAL
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(Rel. 29, Last sequence update)
(Rel. 41, Last annotation update)
uctase [NADH] (EC 1.7.1.1) (NR).
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RESULT 4
FD61_SOYBN
ID FD61_SOY
AC P48630;
DT 01-FEB-1
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DT 28-FEB-2
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Matches 48
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Pfam; PF00174; oxidored molyb; 1.
Pfam; PF00174; oxidored molyb; 1.
PRINTS; PR00406; CYTBSTDTASE.
PRINTS; PR00363; CYTOCHROMEB5..
PRINTS; PR00407; EUMOPTERIN.
PRINTS; PR00407; EUMOPTERIN.
PRINTS; PR00317; FPNCR.
PRODOM; PE000612; CYE_B5; 1.
PRODOM; PE00191; CYTOCHROME_B5_1; 1.
PROSITE; PS00159; CYTOCHROME_B5_1; 1.
PROSITE; PS00259; CYTOCHROME_B5_2; 1.
PROSITE; PS00559; MOLYBDOPTERIN_BUK; 1.
Oxidoreductase; Plavoprotein; FAD; NAD; He
 01-FEB-1996
01-FEB-1996
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                         METAL
METAL
SEQUENCE
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InterPro; IPR00119; Cyt_B5.
InterPro; IPR001334; Cyt_B5 reductase.
InterPro; IPR000572; Euk_Mb_oxred.
InterPro; IPR001709; FPN cyt_redctse.
InterPro; IPR001066; Mo-Co_dimer.
InterPro; IPR001433; Oxred_FAD/NAD(P).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HEME IRON, AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS.
GROUP IS CALLED CYTOCHROME B-557.
-I- SUBUNIT: Homodimer (By similarity).
-I- INDUCTION: By nitrate.
-I- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASE:
N-TERMINAL DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF03404; Mo-c
Pfam; PF00175; NAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X64136; CAA45497.1; -. PIR; JC1422; JC1422.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Contains 1 cytochrome b5 heme-binding dor
SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES
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PF03404; Mo-co_dimer; 1.
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                                                                                                                                                                                                            AGQDATDAFAAYHPPSARPLLRRFFVGRL--SDYAVSPASADYRRLLAQLSSAGLFERV-
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Last sequence up
Last annotation
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IRON (HEME
IRON (HEME
                                                                                                                                                                                                                                                                                                           Score 185.5; DB 1;
Pred. No. 1.7e-07;
2; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLYBDENUM-PTERIN (POTENTIAL).
MOLYBDENUM-PTERIN (POTENTIAL).
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RON (HEME AXIAL LIGAND)
499529652CDDD1C7 CRC64
               update)
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Developmental and growth temperature regulation of two different microsomal omega-6 desaturase genes in soybeans.";

Plant Physiol. 110:311-319(1996)

-1- FUNCTION: ER (MICROSOMAL) OMEGA-6 FATTY ACID DESATURASE INTRODUCES THE SECOND DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE CYTOCHROME B5 AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS STERRIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L43920; AAB00859.1; -.
PIR; T07687; T07687.
InterPro; IPR005804; FA desat fam.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
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ProDom; PD001081; FA_desat_far
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Omega-6 fatty acid desaturase, endoplasmic reticulum isozyme (EC 1.14.19.-).
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                                                                                                                                                                                                                                                                  Similarity
GNIWSYFYORT-----LAFDAASKFFISY-QHWTFYPVMCIARINLL---AQSALFVLT
                                                 LTLHSTLL-VPYFSWKISHRRHHSNTGSLDRD-----EVFVPKPKSKVAWFSKYLNNPL
                                                                              VLSGNCLTGLSIAWWKCNHNTHHIACNSLDHDPDLQHMPLFAVSPKL--
                                                                                                                ATTYFHLLPQPFSLIAWPIYW--VLQSCLLTGVWV----IAHECGHHAFSKYQWVDDVVG
                                                                                                                                                                                  PNTKP---PFTVGQLK--KAIPPHCFQRSLLTSFSYV---
                                                                                                                                                                                                                                                   Conservative
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HISTIDINE
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Pred. No. 9.8e-08;
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ISTIDINE BOX-2.
ISTIDINE BOX-3.
49068805C21A1C31 CRC64;
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Q42342; Q9SB05;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 44, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Cytochrome b5 isoform 1.
ATSG53560 OR MNC6.10.
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid:
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cooke R., Laudie M., Raynal M., Delseny M.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.

-- FUNCTION: Membrane bound hemoprotein which function as an electorarier for several membrane bound oxygenases (By similarity).

-- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).

-- SIMILARITY: BELONGS TO THE CYTOCHROME B5 PAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=cv. Columbia;
MEDLINE=99097071; PubMed=9880378;
Fukuchi-Mizutani M., Mizutani M., Tanaka Y., Kus
"Microsomal electron transfer in higher plants:
heterologous expression of NADH-cytochrome beta5
Arabidopsis.";
Plant Physiol. 119:353-361(1999).
                                                         EMBL; AB007801; BAA74839.1; -.
EMBL; AB015476; BAB09732.1; -.
EMBL; F20001; CAA23377.1; -.
PIR; T52469; T52469.
                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Structural analysis of Arabidopsis thaliana chromosome Sequence features of the regions of 1,013,767 bp covered physically assigned P1 and TAC clones."; DNA Res. 5:297-308(1998).
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                                                                                                                                                                                                                             entities requires a license agreement (some send an email to license@isb-sib.ch).
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Nakamura Y., Sato S., Asamizu E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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IPR001199; Cyt_B5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Columbia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Columbia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Τ.,
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EMBL;

X68140; P04166; X71441;

CAA48240. 185M.

CAA50575.1; ALT_INIT.

(See http://www.isb-sib.ch/announce/

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Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYB5 TOP
P49098;
                                                                                                                                                                                                        PIANT MOLECULAR SECURITY: 537 (1994).

-!- FUNCTION: CYTOCHROME BS IS A MEMBRANE BOUND HEMOPROTEIN WHICH FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND OXYGENNASES. MAY PLAY A KEY ROLE IN THE MODIFICATION BY DESATURATION OF FATTY ACIDS IN THE ENDOPLASMIC RETICULUM, WHICH IN THE DEVELOPING SEED IS UTILIZED FOR MEMBRANE SYNTHESIS AND IN THE DEVELOPMENTALLY REGULATED PRODUCTION OF LARGE AMOUNTS OF STORAGE LIPIDS. IS INVOLVED IN THE REDUCTION OF CYTOCHROME P-450 AND MAY THEREFORE BE INVOLVED IN FLAVONOID BIOSYNTHESIS IN THE PETALS.
-!- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
-!- TISSUE SPECIFICITY: IS HIGHLY EXPRESSED IN DEVELOPING SEEDS, MODERATELY EXPRESSED IN FLOWERS, AND IS EXPRESSED AT LOW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nicotiana tabacum (Common tobacco).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00173; heme 1; 1
PRINTS; PR00363; CYTOCHROMEBS.
ProDom; PD000612; CYT B5; 1
PROSITS; PS00191; CYTOCHROME B5_1;
PROSITE; PS50255; CYTOCHROME B5_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94325476; PubMed=8049375; Smith M.A., Stobart A.K., Shewry P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last seq
28-FEB-2003 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                    Plant Mol.
                                                                                                                                                                                                                                                                                                                                                                                                               vitro protein targeting.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytochrome b5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Multigene family. TRANSMEM 107
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                                                                                                                                                                                                                                                                                                                                                                                                                               Smith M.A., Stobart A.K., Shewry P.R., "Tobacco cytochrome b5: cDNA isolation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               σ
                                                                                                                                                                                  SIMILARITY: BELONGS TO THE CYTOCHROME
                                                                                                                                                                                                  LEVELS IN THE LEAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 AA;
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64
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YTOCHROME_B5_2; 1.
Transmembrane; Heme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15084 MW;
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IRON (HEME AXIAL LIGAND)
MSS -> ARA (IN REF. 3).
; 9CC01C60F7C873FD CRC64;
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Pred. No. 5
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5.5e-08;
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                                                                                                                                                                                   B5
                                                                                                                                                                                   FAMILY.
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SIMILARITY).
                                                                                                                                        a collaboration -
MRL outstation -
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RESULT
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Best Local :
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EMBL; X84950; CAA59336.1; -.
PIR; S52857; S52857.
HSSP; P04166; IBUE.
InterPro; IPR001199; Cyt_B5.
InterPro; IPR001814; Cyt_B5 reductase.
InterPro; IPR000572; Euk_Mb_oxred.
InterPro; IPR001709; PPN Cyt_redctse.
InterPro; IPR005066; Mo-Co_dimer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P43100;
01-NOV-1995 (Rel. 3
01-NOV-1995 (Rel. 3
28-FEB-2003 (Rel. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BEABA
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CONFLICT
CONFLICT
                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatice Institute. There are no restrue by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                          Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BB147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Clavicipitaceae; Cordyceps.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Beauveria bassiana (Tritirachium shiotae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nitrate reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIA_BEABA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Electron transport; Transmembrane; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001199; Cyt_B5.
Pfam; PF00173; heme_1; 1.
ProDom; PB000612; Cyt_B5; 1.
PROSITE; PS00191; CYTOCHROME_B5_1;
PROSITE; PS50255; CYTOCHROME_B5_2;
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=176275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                               COFACTOR: REQUIRES FAD, A HEME GROUP (CI
AND ONE MOLYBDENUM ATOM.
SUBUNIT: Homodimer (By Similarity)
SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN
N. TERMINAL DOMAIN.
                                                                                                                                                                                                                                                                                                                     step of nitrate assimilation in plants, fungi and bacteria. CATALYTIC ACTIVITY: Nitrite + NADP(+) + H(2)O = nitrate + NCOFACTOR: REQUIRES FAD, A HEME GROUP (CALLED CYTOCHROME B-5
                                                                                                                                                                                                                                        SIMILARITY: Contains 1 cytochrome b5 heme-binding SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTA:
                                                                                                                                                                                                                             C-TERMINAL DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDVRMISSKELRAHASADDLWISISGDVYDVTPWLPHHPGGDLPLLTLAGQDATDAFA-A 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YHPPSARPLLRRFFVGRLSDYAVSPASADY 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GETKVFTLAEVSQHNNAKDCWLVISGKVYDVTKFLDDHPGGDEVLLSATGKDATDDFEDV
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107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32, Createa)
32, Last sequence update)
41, Last annotation updat
41, [NADPH] (EC 1.7.1.3) (NR)
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IRON (HEME AXIAL LIGAND) (BY SII
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MISSING (IN REF. 1; CAA48240).
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Matches 37
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PRINTS; PRO0363; CYTCCHROMEBS.
PRINTS; PRO0407; EUNOPTERIN.
PRINTS; PR00371; FPNCR.
PRO050m; PD000612; CYt_B5; 1.
PROSITE; PS00191; CYTCCHROME_B5_1; 1.
PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
                                                                                                                                                                                                                                                                                                                                                                                             P39863;

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01-FEB-1995 (Rel. 31, I

28-FEB-2003 (Rel. 41, I

28-FEB-2003 (Rel. 41, I
                                                                                                                                                                                                            MEDLINE=93380674; PubMed=8370541; Diolez A., Langin T., Gerlinger C., Brygoo Y., Daboussi M.-J "The nia gene of Fusarium oxysporum: isolation, sequence and development of a homologous transformation system."; Gene 131:61-67(1993).
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Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusari
NCBI_TaxID=5507;
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STRAIN=FOM24;
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                    This SWISS-PROT entry is copyright. It is produ between the Swiss Institute of Bioinformatics
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                                                                        COPACTOR: REQUIRES PAD, A HEMB GROUP (CALLED CYTOCHROME B AND ONE MOLYBDENUM ATOM.
SUBUNIT: Homodimer (By similarity).
SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES INTERMINAL DOWAIN.
SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN T
                                                                                                                                                                     FUNCTION: Nitrate reductase is a key enzyme involved in the first
step of nitrate assimilation in plants, fungi and bacteria.
CATALYTIC ACTIVITY: Nitrite + NADP(+) + H(2)O = nitrate + NADPH.
                                                                C-TERMINAL DOMAIN.
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MOLYBDENUM-PTERIN (POTENTI
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IRON (HEME AXIAL LIGAND) (
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ormatics and the EMBL outstation -
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SEQUENCE
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
eurosids II; Brassicales; Brassicaceae; Brassica.
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PROSITE; PS00191; CYTCHROME B5 1; 1

PROSITE; PS50255; CYTCHROME B5 2; 1

PROSITE; PS00559; MOLYBDOPTERIN EUK;
Oxidoreductase; Flavoprotein; FAD; N.
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Eukaryota; Viridiplantae;
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PRINTS; PR00363; CYTOCHROMEB
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PRINTS; PR00371; FPNCR.
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SEQUENCE FROM N.A., AN STRAIN=cv. Cauliflora;
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PF00175; NAD binding 1; 1.
PF00174; oxidored molyb; 1
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PF00970; FAD binding_6; 1.
PF00173; heme_1; 1.
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38; Conserv
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IPR001834; Cyt_B5_reductase.
IPR000572; Euk_Mb_oxred.
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31,
                                                                                                                                         (Cauliflower).
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230
428
620
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MOLYBDENUM-PTERIN (POTENTIAL).

MOLYBDENUM-PTERIN (POTENTIAL).

INTERCHAIN (POTENTIAL).

INTERCHAIN (POTENTIAL).

HEME-BINDING (BY SIMILARITY).

IRON (HEME AXIAL LIGAND) (BY SIMILARITY).

IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
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NADP (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
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                                                                                                                      Tracheophyta;
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RESULT 10
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Best Local S
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PRLNTS; PR0365; CYTOCHROMEB5.

PRODOM; PD000612; CYT B5; 1.

PROSITE; PS00191; CYTOCHROME B5 2; 1.

PROSITE; PS00295; CYTOCHROME B5 2; 1.

PROSITE; PS50255; CYTOCHROME B5 2; 1.

Electron transport; Transmembrane; He

TRANSMEM 107 127 POTENTII
                                                                                                                                                                                                                                   01-APR-1993
01-APR-1993
28-FEB-2003
                                                                                                                                                                                                                                                                     NIA CHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANT
SEQUENCE
                                                                                                                                                                                 Chlorella vulgaris.
Eukaryota; Viridiplantae;
Chlorellaceae; Chlorella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- FUNCTION: Membrane bound hemoprotein which function carrier for several membrane bound oxygenases.
-!- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO
                                   -:- FUNCTION: Nitrate reductase is a key enzyme involved in step of nitrate assimilation in plants, fungi and bacte -:- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate -:- COPACTOR: EACH SUBUNIT OF THE ENZYME CONTAINS 1 EQUIVAL
                                                                                      Biochem. J. 278:203-209(1991).
                                                                                               MEDLINE=91354204; PubMed=1883330; Cannons A.C., Iida N., Solomonson L.F. "Expression of a CDNA clone encoding Chlorella nitrate reductase.";
                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                        Nitrate reductase [NADH]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M87514; AAA32990.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright between the Swiss Institute of Bio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plant Physiol.
                                                                                                                                                                      NCBI_TaxID=3077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P00171; 1EHB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kearns E.V., Keck P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001199; Cyt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Brassica oleracea L.)."
GROUP IS SUBUNIT:
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                        HEME IRON,
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                                                                                                                                                                                                                                                                                                                                                                                                                                             34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      requires a license agreement
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                                                                                                                                                                                                       (Rel. 25, Creace, (Rel. 25, Last sequence update) (Rel. 41, Last annotation update) (Rel. 41, Last annotation update) (Rel. 41, Last annotation update) (Rec. 1.7.1.1) (NR) (Fragment).
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                        AND MOLYBDENUM-PTERIN AS
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5 K
15062 MW;
             CYTOCHROME
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                                                                                                                                                                                               Chlorophyta;
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Pred. No. 1
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764DC24A4CDDD591 CRC64;
             B-557
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                                                                                                             1 L.P.;
ling the
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                                                                                                                                                                                               Trebouxiophyceae;
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AXIAL LIGAND)
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                          PROSTHETIC GROUPS.
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.4e-07;
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RESULT 11

NIAT HORVU
ID NIAT 10 1-AL
DT 01-AL
DT 01-AL
DT 28-FF
GN NAR--
OS HORD
OC Trite;
OX NCBI
RN (1)
RC SIRA,
RX MIDAL
RA MATTH
RA WATTH
RA WATTH
RA MO11-
RL M01-
RC -1-
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Best Local S
Matches 38
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P27968;
01-AUG-1992
01-AUG-1992
28-FEB-2003
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Pfam; PF00173; heme 1; 1.
Pfam; PF03404; Mo-co dimer; 1.
PRINTS; PR0353; CYTOCHROMEB5.
PRINTS; PR00407; EUMOPTERIN.
PROMOBER CYT_B5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                           Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Stre
Spermatophyta; Magnoliophyta;
Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            METAL
NON_TER
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PROSITE; PS00191; CYTOCHROME_B5_1; 1.

PROSITE; PS50255; CYTOCHROME_B5_2; 1.

PROSITE; PS00559; MOLYBDOPTERIN_EUK; PARTIAL.

Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X56771; CAA40090.1; -. PIR; S17197; S17197. HSSP; P04166; 1B5M.
                                                      Miyazaki J.
Warner R.L.
                                                                             STRAIN=cv. Himalaya;
MEDLINE=91375416; PubMed=1896007;
                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                 Nitrate reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                          barley.";
                                                                                                                                  NCBI_TaxID=4513;
                                                                                                                                                                                                    NAR-7.
                                         "Characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON_TER
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N-TERMINAL DOWAIN.
SIMILARITY: CONTAINS 1 CYTOCHYO
SIMILARITY: TO FAD/NAD-BINDING
C-TERMINAL DOWAIN.
FUNCTION: Nitrate reductase
                                                                                                                                                                                                                                                                                                                                                                          62 LITLAGODATDAFAAYHPPSARPLIRRFFVGRLSDYAVSPASAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                         38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              assimilation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                 J., Juricek
                                                                                                                                                                                                                                                                                                                                                ILLVAGIDATDEFNAIHSLKAKKQLLEYYIGELAEEGQEAAASD
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IPR000572; Euk_Mb_oxred
IPR005066; Mo-co_dimer.
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                                                                                                                                                                                                                                                                                STANDARD;
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               228:329-334(1991).
                                                                                                                                                                                                            23, Created)
23, Last sequence update)
41, Last annotation update)
[NAD(P)H] (EC 1.7.1.2).
                                        and sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34830 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.8%;
                                                                 ₹
                                                                 Angelis K.,
                                                                                                                                                        Streptophyta; Embryophyta; Tracheophyta;
yta; Liliopsida; Poales; Poaceae; Pooidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                         17;
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-BINDING CYTOCHROME REDUCTASES
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IRON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 172.5;
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                                        of a
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key
                                        novel
                                                                 Schnorr K.M.,
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 enzyme
                                      nitrate
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involved in the first
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RESULT 12
NIA1_TOBAC
ID NIA1_TOBAC
AC P11605
DT 01-OCT

NIA1_TOBAC

STANDARD;

PRT;

904

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P11605; 01-OCT-1989 (Rel. 12, Created)

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PROVATOR; PSOVATO; CYTOCHROME B5_2; 1.

PROVATOR; PSOVATO; CYTOCHROME B5_2; 1.

PROVATOR; PSOVATO; PROVATOR; 1.

PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR; PROVATOR;
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Best Local
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Pfam; PF00173; heme 1; 1.
Pfam; PF03404; Mo-co dinex; 1.
Pfam; PF00175; NAD bInding 1; 1.
Pfam; PF00174; Oxidored moTyb; 1
PRINTS; PR00406; CYTBSRDTASB.
PRINTS; PR00363; CYTOCHROMEB5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001199; Cyt_B5.
InterPro; IPR001844; Cyt_B5_reductase.
InterPro; IPR0018572; Buk_Mb_oxred.
InterPro; IPR001572; Buk_Mb_oxred.
InterPro; IPR001709; FPN_cyt_redctse.
InterPro; IPR0015066; Mo-Co_dlimer.
InterPro; IPR001433; Oxred_FAD/NAD(P).
InterPro; IPR001221; Phe_hydroxylase.
Pfam; PR00970; FAD_binding_6; 1.
                                                                                                                                                                                                                                                                                                                                                 DISULFID
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                            Nitrate
METAL
                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                         METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                  METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oxidoreductase; Flavoprotein; FAD; NAD; NADP; Heme; Molybdenum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; S16895; RDBHNP.
HSSP; P17571; 2CND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X60173; CAA42739.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-TERMINAL DOMAIN.
SIMILARITY: Contains 1 cytochrome b5 heme-binding dom
SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INDUCTION: By nitrate. SIMILARITY: TO EUKARYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: Homodimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COFACTOR: EACH SUBUNIT OF THE ENZYME HEME IRON, AND MOLYBDENUM-PTERIN AS I GROUP IS CALLED CYTOCHROME B-557.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    step of nitrate assimilation in plants, fungi and bacteria.
CATALYTIC ACTIVITY: Nitrite + NAD(P)(+) + H(2)0 = nitrate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C-TERMINAL DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAD(P)H
582
                                            87
                                                                                                                                              27
                                                                                                                                                                                             l Similarity
37; Conserv
EMYRVGELIVTGNDYSPQSSNAD
                                            RRFFVGRL----SDYAVSPASAD 105
                                                                                                                               ELRAHASADDLWISISGDVYDVTPWLPHHPGGDLPLLTLAGQDATDAFAAYHPPSARPLL
                                                                                             EVRRHASKDSAWIVVHGHVYDCTAFLKDHPGGADSILINAGSDCTEEFDAIHSAKARGLL
                                                                                                                                                                                                                                                                                                891 AA;
                                                                                                                                                                                                                                                                                                                       168
221
406
550
573
                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES
                                                                                                                                                                                                                                                                                                                         168
221
406
550
573
                                                                                                                                                                                                                                                                                                98630 MW;
                                                                                                                                                                                                                       44.6%;
                                                                                                                                                                                                                                              6.7%;
                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                             MOLYBDENUM-PTERIN (POTENTIAL).
INTERCHAIN (POTENTIAL).
IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
, AA47EC52FC1EFD13 CRC64;
                                                                                                                                                                                                                       Score 170; DB 1;
Pred. No. 3.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                       MOLYBDENUM-PTERIN (POTENTIAL).
                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSTHETIC GROUPS. THE HEMB
                                                                                                                                                                                                32;
                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                 891;
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                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
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                                                                                                                                              86
                                                                                             581
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Ouery Match
Best Local
  Matches
                                                                                                                                                         PRINTS; PRO0406; CYTBSRDTASE.
PRINTS; PRO0363; CYTCCHROMEBS.
PRINTS; PRO0371; EVNOTERIN.
PRINTS; PRO0371; FPNCR.
PRODOM; PD000612; CYt_B5; 1.
PROSITE; PS00191; CYTCHROME_B5_1; 1.
PROSITE; PS00559; MOLYBDOPTERIN_BUK; 1.
PROSITE; PS00559; MOLYBDOPTERIN_BUK; 1.
                                                    METAL
SEQUENCE
                                                                               DISULFID
METAL
                                                                                                                                                                                                                                                                    Pfam;
Pfam;
                                                                                                                                                                                                                                                                                              Pfam;
Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a obstween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nicotiana tabacum (Common Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1989 (Rel. 12, Last
28-FEB-2003 (Rel. 41, Last
Nitrate reductase [NADH] 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                         METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  reductase genes."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vaucheret H.,
                                                                                                           METAL
                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP;
                                                                                                                                                                                                                                                                                                                   arPro; IPR001199; Cyt B5.

arPro; IPR001834; Cyt B5 reductase.

arPro; IPR000572; Euk mb oxred.

arPro; IPR001709; FPN cyt redctse.

arPro; IPR005066; Mo-co dImer.

arPro; IPR001433; Oxred FAD/NAD(P).

m; PF00970; FAD binding_6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-TERMINAL DOMAIN.
SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Step of nitrate assimilation in plants, fungi and bacteria. CATALYTIC ACTIVITY: Nitrite + NAD(+) + + (2)0 = nitrate + NACCPACTOR: EACH SUBUNIT OF THE ENZYME CONTAINS 1 EQUIVALENT HEME IRON, AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS. THE GROUP IS CALLED CYTOCHROME B-557.

ENZYME REGULATION: REGULATED BY THE NITROGEN SOURCE AND CONEY THE CIRCADIAN RHYTHM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: Homodimer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: Nitrate reductase is a key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C-TERMINAL DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                     S04838; RDNTNT.
                                                                                                                                                                                                                                                                    PF03404; Mo-co_dimer; 1.
PF00175; NAD_binding_1; 1.
PF00174; oxidored_molyb; 1.
                                                                                                                                                                                                                                                                                              PF03404; Mo-co_d:
                                                                                                                                                                                                                                                                                                                                                                                                                                               X14058; CAA32216.1;
  l Similarity
                                                                                                                              ductase; Flavoprotein; FAD; NAD; Heme; assimilation; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biol. 12:597-600(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xanthi; TISSUE=Leaf;
                                                                               183
237
422
566
  Conservative
                                                      $
                                                                               183
237
422
566
                                                      101907
             6.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence of
                                                                                                                                                                                                                                                                                                                                    o_dimer.
d_FAD/NAD(P).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tobacco)
                                                      WW;
  10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 annotation update) (EC 1.7.1.1) (NR1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence update)
Score 170; DB 1;
Pred. No. 3.4e-06;
.0; Mismatches 31
                                                   MOLYBDENUM-PTERIN (POTENTIAL)
INTERCHAIN (POTENTIAL).
IRON (HEME AXIAL LIGAND) (BY
IRON (HEME AXIAL LIGAND) (BY
9; 85642BDA723EE154 CRC64;
                                                                                                                      MOLYBDENUM-PTERIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rouze
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          enzyme involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 homeologous tobacco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OXIDOREDUCTASES
                                                                                                                                                Molybdenum;
                         Length 904;
                                                                                                                      (POTENTIAL).
                                                                                                         (POTENTIAL).
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             restrictions
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                                                                 SIMILARITY)
SIMILARITY)
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+ NADH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THE HEME
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 Gaps
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PR00406; CYTB5RDTASE.
PR00363; CYTOCHROWEB5.
PR00407; EUMOPTERIN.
PR00371; FPNCR.
PR00371; PPNCR.
PR00410; PHEHYDRXLASE.
PD000612; CYt_B5; 1.

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RESULT 13

RESULT 13

RESULT 13

RANA

ID NIAL BRANA

ID 101-FEB

DT 01-FEB

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                                                                                                                                                                 HSSP; P17571; 2CND.

InterPro; IPR001199; Cyt B5.

InterPro; IPR0011934; Cyt B5 reductase.

InterPro; IPR001834; Cyt B5 reductase.

InterPro; IPR001709; FNR cyt redctse.

InterPro; IPR001709; FNR cyt redctse.

InterPro; IPR001201; Phe hydroxylase.

InterPro; IPR001221; Phe hydroxylase.

Pfam; PF001721; Pheme 1; 1.

Pfam; PF003404; Mo-co dimer; 1.

Pfam; PF003404; Mo-co dimer; 1.

Pfam; PF00175; NAD binding 1; 1.

Pfam; PF00174; Oxidored molyb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-96222419; PubMed=9685274;

Fibuoda H., Ogawa T., Minami H., Yano H., Ohkawa Y.;

Fibuoda H., Ogawa T., Minami H., Yano H., Ohkawa Y.;

"Developmental stage-specific and nitrate-independent regulation of nitrate reductase gene expression in rapeseed.";

Plant Physiol. 111:39-47(1996).

-i- FUNCTION: Nitrate reductase is a key enzyme involved in the first step of nitrate assimilation in plants, fungi and bacteria.

-i- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.

-i- COPACTOR: REQUIRES FAD, A HEME GROUP (CALLED CYTOCHROME B-557)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a between the Swiss institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brassica napus (Rape).

Bukaryota; Viridiplante; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D38219; BAA07394.1; -. PIR; T08105; T08105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nitrate reductase
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28-FEB-2003
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01-FEB-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AND ONE MOLYBDENUM ATOM.

SUBUNIT: Homodimer (By similarity)
SIMILARITY: TO EUKARYOTIC MOLYBDOPY
N-TERMINAL DOMAIN.
SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C-TERMINAL DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: Contains 1 cytochrome b5 heme-binding dom
SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BRANA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 31, Last sequence update)
(Rel. 41, Last annotation update)
uctase [NADH], clone PBNBR1405 (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 31, Created)
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L outstation -
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RA Mayer K.F.X. Schueller C., Wambutt R., Murphy G., Volckaert G.,
Rohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,
RA Harris B., Ansorge W., Brandt P., Grivell L., Rieger M.,
RA Weichselgartner M., de Simone V., Obermater B., Mache R., Mueller M.,
RA Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T.,
RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
RA Reichert B., Fortetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
RA Reichert B., Fortetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
RA Reichert B., Fortetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
RA Reichert B., Fortetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
RA Reichert B., Forteren M., Wedler H., Ridley P.,
RA Langham S.-A., McCullagh B., Biham L., Robben J.,
RA Langham S.-A., McCullagh B., Biham L., Robben J.,
Vandenbussche F.,
RA Langham S.-A., McLijens I., Voet M., Bastiaens I., Aert R., Braun M.,
RA Weitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
RA Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
RA Holzer S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R.,
RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
RA Dose S., de Haan M., Maarse A., Schaefer M., Grimm M., Loehnert T.-H.,
RA Dose S., de Haan M., Maarse A., Schaefer M., Dauner D., Hezzl A.,
RA Neumann S., Argiriou A., Vitale D., Liguori R., Piravandi E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local :
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28-FEB-2003 (Rel. 41, Last annotation update)
Omega-6 fatty acid desaturase, chloroplast precursor (EC 1.14.19.-).
FAD6 OR FADC OR AT4G30950 OR F6II8.140.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magmoliophyta; eudicotyledons; core eudicots; Rosidae, eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Falcone D.L., Gibson S., Lemieux B., Somerville C.R.; "Identification of a gene that complements an Arabidopsis mutant deficient in chloroplast omega 6 desaturase activity."; plant physiol. 106:1453-1459(1994).
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SEQUENCE
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P46312; Q9M094;
01-NOV-1995 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=cv.
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PS50255; CYTOCHROME_B5_2; 1.
PS00559; MOLYBDOPTERIN_EUK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Columbia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32, Created)
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245
430
574
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Pred. No. 3.7e-06;
7; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IRON (HEME IRON (HEME
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nes 47;
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RA Schnabl S., Hiller K., Schmidt W., Lecharry A., Aubourg S., Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E., RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E., RA Gibbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A., RA Gibbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A., RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S., RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S., RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S., RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K., RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K., RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K., RA Schkon M., Murray J., Sheet P., Cordes M., Abu-Threideh J., Raschkon M., Murray J., Sheet P., Cordes M., Abu-Threideh J., RA Schkon M., Murray J., Sheet P., Cordes M., Abu-Threideh J., RA Liteille P., Courthey L., Cloud J., Abbott A., Scott K., Johnson D., RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K., RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K., RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K., RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K., RA Minx P., Berton T., Nyan B., Andrews S., Geisel C., Layman D., RA Minx P., Berton R., Vil D., Shekher M., Mattero A., Shah R., Swaby I.K., O'Shaugnessy A., Rodriguez M., Hoffman J., Till S., RA Chen E., Marra M., Martienssen R., McCombie W.R.;

PT "Commence and analysis of chromosome 4 of the plant Arabidopsis
Query Match
Best Local S
Matches 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AL022198; CAA18198.1;
EMBL; AL161578; CAB79813.1;
EMBL; AY045621; AAK73979.1;
EMBL; AY058078; AAL24186.1;
EMBL; AY058852; AAL24240.1;
                                                                                                                    DOMAIN
                                                                                                                                                                                 InterPro, IPR005804; FA_desat_fam.
Pfam; PF00487; FA_desat_trase; 1.
ProDom; PD001081; FA_desat_fam; 2.
Oxidoreductase; Fatty acid_biosynthesis; Chloroplast; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This
                                                                                    DOMAIN
                                                                                                                                                                                                                                      PIR; D85362; D85362.
InterPro; IPR005804; FA
                                                                                                                                                                                                                                                                                                                                                          EMBL; U09503; AAA92800.1; -.
                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 402:769-777(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         s SWISS-PROT entry is copyright. It is produced through a collab
ween the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                       peptide.
                                                                  367
448 AA;
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371
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                 6.7%;
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                                                                    W.
Score 168.5; DB
Pred. No. 2e-06;
4; Mismatches 1
                                                                                  CHLOROPLAST (BY SIMILARITY)
OMEGA-6 FATTY ACID DESATURA
HISTIDINE BOX-1.
HISTIDINE BOX-2.
HISTIDINE BOX-3.
                                                                    C3AC72FB28FBF287
                                                                                                                                                                                                                                                                                                                                                                                                         moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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                                                                                                                                     DESATURASE.
                                                                    CRC64;
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Similarity

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P08509;
01-AUG-1988
01-OCT-1989
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOBAC
                                                                                                                                                                                                                                                                                                                                                                      Calza R., Huttner E., Vincentz M., Rouze P., Galangau F., Vaucheret H., Cherel I., Meyer C., Kronenberger J., Caboche M.; "Cloning of DNA fragments complementary to tobacco nitrate reductase "RNA and encoding epitopes common to the nitrate reductases from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eu Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 171-724 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                     higher plants.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plant Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vaucheret H., Kronenberger J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=cv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nitrate reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete nucleotide sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4097;
                                                                                                                                  FUNCTION: Nitrate reductase is a key enzyme involved in the first step of nitrate assimilation in plants, fungi and bacteria.

CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)0 = nitrate + NADH.

COFACTOR: EACH SUBUNIT OF THE ENZYME CONTAINS 1 EQUIVALENT OF FAD, HEME IRON, AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS. THE HEME GROUP IS CALLED CYTOCHROME B-557.

ENZYME REGULATION: REGULATED BY THE NITROGEN SOURCE AND CONTROLLED BY THE CIRCADIAN RHYTHM.
SIMILARITY: Contains 1 cytochrome b5 heme-binding domain SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN 7 C-TERMINAL DOMAIN.
                                                                                         SUBUNIT: Homodimer.
SIMILARITY: TO EUKARYOTIC
                                                                   N-TERMINAL DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RLPRCHLRKVAPAVRDLCKKHGLTYSAATFWG--ANVLTW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIPSYNLRAAHESIQE-----NWGKYTNLATW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QHVQFCLNHFSSDVYVGPPKGNDW--FEKQTAGTLDILCSPWMDWFHGGLQFQIEHHLFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----SEVNRVKISLACVFAFMAVGWPLIVYKVGILGWVKFWLMPWLGYHFWMSTFTM----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VLTEKRVPQRLLEIAGVATFWA-WYPLLV--ASLPNW-----WERVAFVLFSFTICGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PVP----PEEFES--SPVMRKAIIFGYGPIRPWLSIAHWVNW-----HFNLKKFRA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HMPLFAVSPKLFGNIWSYFYQRTLAFD-AASKFFISYQHWTFYPVMCIARINLLAQSALF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVFEIDDLKALKSVLISVTSY-TLGLFMIAKSPWY-----LLPLAWAWTGTAITGFFVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genes.";
. Biol. 12:597-600(1989).
                                                                                                                                                                                                                                                                                                                                  Genet. 209:552-562(1987).
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(Rel. 12, Last sequence update)
(Rel. 41, Last annotation update)
uctase [NADH] 2 (EC 1.7.1.1) (NR2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Common tobacco)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -ADEWNAAQAQLNGTVHCDYPSWIEILCHDINVHIPHHISP
                                                                                         MOLYBDOPTERIN OXIDOREDUCTASES
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DISULFID
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Pfam; PF00173; heme 1; 1.
Pfam; PF03404; Mo-co_dimer; 1.
Pfam; PF00175; NAD binding_1; 1.
Pfam; PF00174; oxidored_molyb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                        ProDom; PD000612; Cyt_Bs; 1.
PROSITE; PS00191; CYTOCHROME_Bs_1; 1.
PROSITE; PS0255; CYTOCHROME_B5_2; 1.
PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;
Nitrate assimilation; Multigene family.
                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO0406; CYTOSHDASE.
PRINTS; PRO0363; CYTOCHROWEBS.
PRINTS; PRO0407; EUMOPTERIN.
PRINTS; PR00371; FPNCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001199; Cyt_B5.
InterPro; IPR001834; Cyt_B5_reductase.
InterPro; IPR000572; Euk_Mb_oxred.
InterPro; IPR001709; FPN_cyt_redctse.
InterPro; IPR005066; Mo-co_dImer.
InterPro; IPR001433; Oxred_FAD/NAD(P).
                                                                                                                                                                                                                                              METAL
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 592
                                                      532 KMYSMSEVRKHSSADSAWIIVHGHIYDATRFLKDHPGGTDSILINAGTDCTEEFDAIHSD
                         81
                                                                                 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P17571;
                                                                                                                             Similarity
                         SARPLLRRFFVGRL 94
                                                                                 RMISSKELRAHASADDLWISISGDVYDVTPWLPHHPGGDLPLLTLAGQDATDAFAAYHPP
KAKKLLEDFRIGEL
                                                                                                                                                                    183
237
422
566
589
904
                                                                                                               Conservative
                                                                                                                                                                       AA;
                                                                                                                             6.6%;
                                                                                                                                                                                    183
237
422
566
589
                                                                                                                                                                        101957 MW;
                                                                                                              10;
                                                                                                                           Score 167;
Pred. No. 5
                                                                                                                                                                       IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
4; 75196875A3561D69 CRC64;
                                                                                                                                                                                                              MOLYBDENUM-PTERIN (POTENTIAL).
MOLYBDENUM-PTERIN (POTENTIAL).
INTERCHAIN (POTENTIAL)
                                                                                                               Mismatches
                                                                                                                              DB 1;
5.9e-06;
                                                                                                               31,
                                                                                                                                          Length
                                                                                                               Indels
                                                                                                                                            904;
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                                                                                                               Gaps
                                                       591
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Search completed: January Job time: 11.1656 secs ۳ 2004, 06:30:54

5.1.6

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Result
No.
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
  1429
1427.5
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2521
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sp_mammal:*
sp_mhc:*
sp_organelle:*
sp_phage:*
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sp_bacteria:*
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sp_human:*
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sp_rodent:*
sp_virus:*
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(c) 1993 - 2004
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OBIId7 aquilegia v
Q9saus borago offi
O04353 borago offi
O92rp7 arabidopsis
Q81b96 arabidopsis
Q91r82 borago offi
Q81717 argania spi
Q9hdg8 mucor rouxi
Q8hdg8 mucor rouxi
Q8hdg9 saccharomyc
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8DIZ60 RESULT 1

Q9ZTU8; PRELIMINARY; Q9ZTU8; 1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-MAY-2003 (TrEMBLrel. 23,

Created)
Last sequence update)
Last annotation update)

469 ጅ

S276.

45	44	43	42	41	40	39	38	37	36	35	34	33	32	<u>u</u>	30	29	28	27	26	25	24	23	22	21	20	19	18	17
412	412.5	412.5	413	413.5	413.5	414	414.5	425	429	431.5	431.5	433	435	437	461.5	462.5	495.5	506.5	521	523	532	532	535	535	536	552	564.5	605.5
16.3	16.4	16.4	16.4	16.4	16.4	16.4	16.4		17.0	17.1	17.1	17.2	17.3	17.3	18.3	18.3	19.7	20.1	20.7	20.7	21.1	21.1	21.2	21.2	21.3	$\vdash$	22.4	4
444	449	449	444	449	449	501	444	454	454	445	445	454	357	452	443	443	525	467	457	457	457	457	477	457	457	520	483	573
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O60427 homo sapien	Bum	Bull	Q96i39 homo sapien		Q9jje7 mus musculu	OWO	Q96t10 homo sapien			Q8ay64 sparus aura	Q9y5q0 homo sapien	Q98sw7 oncorhynchu	Q9hdf4 mortierella	Q8uwm5 oncorhynchu	Q23221 caenorhabdi	O61388 caenorhabdi	Q9znw2 physcomitre	=	Q9hey4 mortierella	Q9uvv3 mortierella		Q9hey1 mortierella		Q9uvy3 mortierella	Q8x173 mortierella	Q91em9 ceratodon p	0	Q8nkg8 kluyveromyc

## ALIGNMENTS

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Query Match
Best Local Similarity
                                       Heme.
SEQUENCE
                                                                                                                                                            Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.

-- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.

EMBL; AF031194; AAD10250.1; --

HSSP; P00171; 115U.

InterPro; IPR001199; Cyt B5.

InterPro; IPR0010199; HA desat fam.

InterPro; IPR001092; HLH_basic.
                                                                                                                                                                                                                                                                                                                                       Triticum aestivum (Wheat).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Triticum.
NCBI_TaxID=4565;
                                                               ProDom; PD000612; Cyt B5; 1.
ProDom; PD001081; FA desat fam; 1.
PROSITE; PS50255; CYTOCHROME B5_2;
PROSITE; PS00038; HLH_1; 1.
                                                                                                                   Pfam; PF00487; FA_desaturase; 1. Pfam; PF00173; heme_1; 1. PFINTS; PR00363; CYTOCHROMEB5.
                                                                                                                                                                                                                                                          STRAIN-cv. ET3;

Belhalze E., Hebb D.M., Gardner R.C., Richards K.D.;

Paluminum tolerance in yeast conferred by over-expression

genes.";
                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                         469
                                       AA;
                                                             HLH_1; 1.
                                       52617 MW;
81.8%;
80.7%;
Score 2061; DB 10;
Pred. No. 5.8e-169;
                                       16F223CC1F79740D CRC64;
            Length 469;
                                                                                                                                                                                                                                                                         of wheat
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RESULT

OCCUPANT

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  Query Match
Best Local Similarity
                                                                                                            -!- SIMILARITY: BELONGS TO THE CYTOCHROME B5
EMBL; AF005096; AAD01240.1; -.
HSSP; PO0171; 115U.
InterPro; IPR001199; Cyt B5.
InterPro; IPR005804; FA_desat_fam.
Pfam; PF00487; FA_desaturase; 1.
Pfam; PF00173; heme_1; 1.
ProDom; PD000612; Cyt B5; 1.
ProDom; PD001081; FA_desat_fam; 1.
PROSITE; PS50255; CYTOCHROME_B5_2; 1.
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Q9ZTY9;
01-MAY-1999
                                                                         Heme.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                TISSUB-Seed endosperm;

MEDLINE=97268723; PubMed=9108131;

Sayanova O., Smith M.A., Lapinskas P., Stobart A.K., Dobson G.,

Christie W.W., Shewry P.R., Napier J.A.;

"Expression of a borage desaturase cDNA containing an N-terminal cytochrome b5 domain results in the accumulation of high levels delta6-desaturated fatty acids in transgenic tobacco.";

Proc. Natl. Acad. Sci. U.S.A. 94:4211-4216(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE=Seed endosp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=3988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATEWAWYPLLVASLPNWWERVAFVLFSFTICGIQHVQFCLNHFSSDVYVGPPKGNDWFEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVCYERTLAFDAISKFFVSYQHWTFYPVMGFARINLLVQSIVFLITQKKVRQRWLEIAGV
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                                                                            446
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                                                                            51418 MW;
59.5%;
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Score 1500.5; DB 10; Pred. No. 9.3e-121;
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                                                                         A1954FDB2DDB600F CRC64;
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                      Length
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Matches 256
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                                                                         InterPro; IPR001199; Cyt B5.
InterPro; IPR005804; FA_desat_fam.
Pfam; PF00487; FA_desaturase; 1.
Pfam; PF00173; heme_1; 1.
ProDom; PD0010812; Cyt B5; 1.
ProDom; PD001081; FA_desat_fam; 1.
PROSITE; PS50255; CYTOCHROME_B5_2; 1.
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SEQUENCE
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MAROTO F.G., Alonso D.L., Garrido J.-A.S., Ferron M.V., Ruiz
Maroto F.G., Alonso D.L., Garrido J.-A.S., Ferron M.V., Ruiz
"Cloning and Molecular Characterization of the D6-Desaturase
Echium: Functional Expression in Yeast and Tobacco.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
-i-SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
EMBL, AY055117; AAL23580.1; -.
                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; lamiids; Boraginaceae; Echium.
                                                                                                                                                                                                                                                                                 NCBI_TaxID=173991;
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               Similarity
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tive 76;
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Score 1457; DR
Pred. No. 5.2e-
76; Mismatches
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Last annotation updat
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5.2e-117;
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RMISSKELRAHASADDLWISISGDVYDVTPWLPHHPGGDLPLLTLAGQDATDAFAAYHPP

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"Cloning and Molecular Characterization of the D6-Desaturase fro

T Echium: Functional Expression in Yeast and Tobacco.";

Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

-i- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.

REMBL; AY055118; AAL23581.1; -.

R InterPro; IPR001199; Cyt B5.

R InterPro; IPR001199; Cyt B5.

R InterPro; IPR005804; FA desat fam.

Pfam; PF00487; FA desaturase; 1.

R Pfam; PF00173; heme 1; 1.

R ProDom; PD001081; FA desat fam; 1.

R ProDom; PD001081; FA desat fam; 1.

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Q8VZZ1;
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01-MAR-2002 (TrEMBLrel. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnoliophyta; eudicotyledons;
Asteridae; lamiids; Boraginaceae; Echium.
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SARPLLRRFFVG-RLSDYAVSPASADYRRLLAQLSSAGLFERVGPTPKVQLVLMAVLFYA 139
                                                                 RMISSKELRAHASADDLWISISGDVYDVTPWLPHHPGGDLPLLTLAGQDATDAFAAYHPP
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57.3%; Pred. No. 8.
cive 76; Mismatche
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Best Local S
Matches 254
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InterPro; IPR005804; FA_desat_fam.
Pfam; PF00487; FA_desaturase; 1.
Pfam; PF00173; heme 1; 1.
ProDom; PD001612; Cyt B5; 1.
ProDom; PD001081; FA_desat_fam; 1.
PROSITE; PS50255; CYTOCHROME_B5_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CV. Drakkar; TISSUE=Ripening embryos;
MEDLINE=99003197; PubMed=9786850;
Sperling P., Zaehringer U., Heinz E.;
Sporlogipid Desaturase from Higher Plants Identi
Cytochrome b5 Fusion Protein.";
U. Biol. Chem. 273:28590-28596(1998).
1. SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
EMBL; AJZ24160; CAA11857.1;
HSSP; P82291; 1CXY.
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                                                                                                                                                                                                                                                                                                           SEQUENCE
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                       SARPLIRRFFVG-RISDYAVSPASADYRRILAQUSSAGLFERVGPTPKVQLVLMAVLFYA
                                                                                                                                    RMISSKELRAHASADDLWISISGDVYDVTPWLPHHPGGDLPLLTLAGQDATDAFAAYHPP
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  TAWRHLENLHNGYHVKDHHVSDVSRDYRRLAAEFSKRGLFDKKGHVTLYTLTCVAAMLAA
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                                                                                                                                                                                                                                                                                                         449 AA;
                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                         51490 MW;
                                                                                                                                                                                                                            56.7%; Score 1429; DB 10; 57.3%; Pred. No. 1.3e-114;
                                                                                                                                                                                                       66; Mismatches 121;
                                                                                                                                                                                                                                                                                                      FEFE37AFF9D390C1 CRC64;
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STRAIN-CV. inbred line HA89;
TISSUB=Cockyledons of developing sunflower
MEDLINE=96028121; PubMed=7588718;
Sperling P., Schmidt H., Heinz E.;
                                     ProDom; PD00061; Cyt B5; 1.
ProDom; PD001081; FA desat fam;
PROSITE; PS50255; CYTOCHROME_B5
                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=cv. inbred line HA89;
TISSUE=Cotyledons of developing sunflower fruits;
MEDLINE=21116801; PubMed=11171153;
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; campanulids; Asterales; Asteraceae; Asteroideae;

Heliantheae; Helianthus.
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HSSP; P00171; 1F03.
InterPro; IPR001199; Cyt B5.
InterPro; IPR005804; FA desat fam.
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Pfam; PF00173; heme 1; 1.
PRINTS; PR00363; CYTOCHROMEB5.
PRODOm; PD000612; Cyt B5; 1.
PRODOm; PD001081; FA Gesat fam; 1.
PROSITE; PS50255; CYTOCHROME B5 2; 1.
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Bukaryota; Viridiplantae; Streptophyta;
                                                                                                                                                                                                                                                                                                                                              Longman A.J., Michaelson L.V., Napier J.A.; "Isolation and characterization of a cDNA encoding a del sphingolipid desaturase from Aquilegia vulgaris."; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.-i- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY. EMBL; AF406816; AAN03619.1; -.
                                                                                                   SEQUENCE
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se delta 8 desaturase.
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Pred. No. 3.2
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eudicotyledons; Ranunculales;
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                                                                                                                                                             Query Match
Best Local Similarity
Matches 247; Conserv
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OSSAUS;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                    Heme.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases -:- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY. EMBL; AF007561; AAD01410.1; -- InterPro; IPR001199; Cyt B5. InterPro; IPR001199; Cyt B5. InterPro; IPR005804; F4 desat fam. Pfam; PF00487; FA desaturase; 1. Pfam; PF00173; heme_1; 1.
                                                                                                                                                                                                                                                                                                              ProDom; PD000612; Cyt B5; 1.
ProDom; PD001081; FA desat fam; 1.
PROSITE; PS50255; CYTOCHROME_B5_2; 1.
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Spermatophyta; Magnollophyta; eudicotyledons;
Asteridae; lamiids; Boraginaceae; Borago.
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Borago officinalis (Bourrache) (Borage).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=13363;
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                                                                                                                                                                                                                                                                       448 AA;
                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                    51626 MW; EAC3F0BF22E0DE00 CRC64;
                                                                                                                                                          55.3%; Score 1393; DB 10; 55.8%; Pred. No. 1.7e-111; tive 73; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gamma Linolenic Acid
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Best Local S
Matches 247
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01-JUL-1997 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
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ProDom; PD000612; Cyt B5; 1.
ProDom; PD001081; FA desat fam; 1.
PROSITE; PS50255; CYTOCHROME B5_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001199; Cyt B5.
InterPro; IPR005804; FA_desat_fam.
Pfam; PF00487; FA_desaturase; 1.
Pfam; PF00173; heme_1; 1.
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MEDLINE=97268723; PubMed=9108131;
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STWKNLDKFFTGYYLKDYSVSEVSKDYRKLVFEFSKMGLYDKKGHIMFATLCFIAMLFAM 126
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Della 6 desaturase.

Della 6 desaturase.

Borago officinalis (Bourrache) (Borage).

Borago officinalis (Bourrache)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheoj

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Gore eudicotyledons; core eudicots;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; lamiids; Boraginaceae; Borago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sayanova O., Smith M.A., Lapinskas P., Stobart A.K., Dobs Christie W.W., Shewry P.R., Napier J.A.; "Expression of a borage desaturase cDNA containing an N-t cytochrome b5 domain results in the accumulation of high delta6-desaturated fatty acids in transgenic tobacco."; Proc. Natl. Acad. Sci. U.S.A. 94:4211-4216(1997).
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                                                                                                                                21 RMISSKELRAHASADDIWISISGDVYDVTPWLPHHPGGDLPLLTLAGQDATDAFAAYHPP
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SARPLLRRFFVG-RLSDYAVSPASADYRRLLAQLSSAGLFERVGPTPKVQLVLMAVLFYA 139
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                                                                        KYITSDELKNHDKPGDLWISIQGKAYDVSDWVKDHPGGSFPLKSLAGQEVTDAFVAFHPA
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                                                                                                                                                                                                                               55.2%; Score 1392; DB 10; 55.8%; Pred. No. 2e-111;
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Last annotation updat
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O92RP7;
O1-MAY-1999 (TrEMBLrel. 10, Created)
O1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
O1-MAY-1999 (TrEMBLrel. 23, Last annotation update)
O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Delta-8 sphingolipid desaturase (AT3G61580/F2A19_180).
SLD1 OR F2A19.180 OR AT3G61580.
Arabidopsis thaliana (Mouse-ear cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledone; core eudicots; Roside
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
SEQUENCE FROM N.A.
Southwick A., Nguyen |
Carninci P., Chen H.,
                                                                                                                                                                                       Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y., Bowser L., Ciannoci P., Kamiya A., Karlin-Neumann G., Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka Kawai J., Lam B., Lee J.M., Lin J., Pham P.K., Quach H.L., Sakurai Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K., Yamanura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                De Haan M., Maarse A.C., Grivell L.A., Mayer K.F.X., Quetier F., Salanoubat M. Submitted (NOV-1999) to the EMBL/GenBar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-CV. Columbia; TISSUE-Flower, MAINLY MEDLINE-99003197; PubMed-9786850; Sperling P., Zaehringer U., Heinz E.; "A sphingolipid desaturase from higher plan
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                              is cDNA clones.";
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M., Palm C.J., Jones T., Chan M.M., Chang C.H.,
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01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
10-Lta-8 sphingolipid desaturase.
11 Arabidopsis thaliana (Mouse-ear cress).
12 Bukaryota; Viridiplantae; Streptophyta; Embryophyta; The Eukaryota; Viridiplantae; Streptophyta; Embryophyta; The Spermatophyta; Magnoliophyta; eudicotyledons; core eudicerosids II; Brassicales; Brassicaceae; Arabidopsis.
11 CRBI TaxID-3702;
12 [1]
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Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
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L132962; CAB71088.1; -.
L; AF428420; AAL16189.1; -.
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Napier J.A.; desaturases.";

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Pfam; PF00173; heme 1; 1.
ProDom; PD0006412; Cyt B5; 1.
ProDom; PD001081; FA_desat_fam;
PROSITE; PS50255; CYTOCHROME_B5
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[2]
Borago officinalis (Bourrache) (Borage).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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Hass B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov Feldmann K.A., Flavell R.B., White O., Salzberg S.L.; "Full-length messenger RNA sequences greatly improve genome
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Delta-6-desaturase.
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MEDLINE=21092516; PubMed=11162428;

Libisch B., Michaelson L.V., Lewis M.J., Shewry P.R., 1

"Chineras of Delta6-fatty acid and Delta8-sphingolipid

Biochem. Biophys. Res. Commun. 279:779-785(2000).
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Sperling P., Libisch B., Zaehringer U., Napier J.A.,
"Functional identification of a delta 8-sphingolipid
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Best Local S
Matches 240
Eukaryota; Fungi; Z
Mucor.
NCBI_TaxID=29923;
[1]
                                                                      Q9HDG8
Q9HDG8;
01-MAR-2001
01-MAR-2001
01-MAR-2003
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El Filali A., Anderson M., Abbas K.;

El Filali A., Anderson M., Abbas K.;
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InterPro; IPR0021904; FA desat_fam.
Pfam; PF00487; FA desaturase; 1.
Pfam; PF00173; heme_1; 1.
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-i- SIMILARITY: BELONGS TO THE
EMBL; AY131238; AAM94245.1; -.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eu
Asteridae; Ericales; Sapotaceae; Argania.
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ProDom; PD001081; FA desat fam;
PROSITE; PS50255; CYTOCHROME B5
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Eukaryota, Viric
                                               Delta-6 desaturase.
Mucor rouxii.
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                                     Zygomycota;
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54.2%; Pred. No. 6.16
tive 72; Mismatches
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annotation
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                                     Mucorales;
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eudicots;
                                     Mucoraceae;
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RESULT Q8NKG9 ID Q8 AC Q8 DT 01 DT 01

Q8NKG9

PRELIMINARY;

568 AA

Q8NKG9; 01-OCT-2002 01-OCT-2002 01-MAR-2003

(TrEMBLrel. (TrEMBLrel. (TrEMBLrel.

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ProDom; PD001081; FA Gesat fam; 1.

PROSITE; PS00095; C5 MTASE 2; 1.

PROSITE; PS00191; CYTOCHROME B5_1;

PROSITE; PS50255; CYTOCHROME B5_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001525; C5_DNA_meth.
InterPro; IPR001199; Cyt_B5.
InterPro; IPR005804; FA_desat_fam.
Pfam; PF00487; FA_desaturase; 1.
Pfam; PF00173; heme_1; 1.
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- SIMILARITY: BELONGS TO THE
EMBL; AF296076; AAG36960.1; -
EMBL; AF290983; AAG36959.1; -
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STRAIN=ATCC 24905;
MEDLINE=20563795; PubMed=11112411;
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HNLRQCVPLVKKFCDEVGLHYYMYNFSTGNGVVLGTLKSVADQ.500
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                                                       CHLRKVAPAVRDLCKKHGLTYSAATFWGANVLTWKTLRAAALQ 440
                                                                                                               ITLSHFGMST---EDRGPDEPFPAKMLRTTMDVDCPEWLDWFHGGLQYQAVHHLFPRLPR
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31.4%; Pred. No. 4.7e-55;
Live 78; Mismatches 175;
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Best Local Similarity
Matches 151; Conserv
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-!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
EMBL; AB085689; BAB93117.1; -.
InterPro; IPR001199; Cyt B5.
InterPro; IPR005804; FA desat_fam.
Pfam; PF00407; FA desaturase; 1.
Pfam; PF00173; heme 1; 1.
ProDom; PD001081; FA desat_fam; 1.
PROSITE; PS50255; CYTOCHROME_B5_2; 1.
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Saccharomyces kluyveri (Yeast)
Eukaryota; Fung; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Takakuwa N., Kinoshita M., Oda Y., Ohnishi M.;
"Isolation and characterization of the genes encoding delta
sphingolipid desaturase from Saccharomyces kluyveri and Kluy
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                                KTLRAAALQART 443
                                                                      CPRWLDFLHGGLQFQVVHHLFPRLPRHNLRAAQPYVIEFCEKVGIKYSIYGFSKGNGVVL 525
                                                                                                        CSPWMDWFHGGLQFQIEHHLFPRLPRCHLRKVAPAVRDLCKKHGLTYSAATFWGANVLTW 431
                                                                                                                                            KLQTGWDRFQYIMVSHITTMLVHVQITLSHFAMSTSDLGV----GEGFPMRQLRTSMDVD 465
                                                                                                                                                                               SLPNWWERVAFVLESFTICGIQHVQFCLNHF---SSDVYVGPPKGNDWFEKQTAGTLDIL 371
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27.4%; Pred. No. 7.4e-45;
tive 87; Mismatches 166; Indels 148;
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Search completed: January 1, Job time: 43.665 secs

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Match
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/FCTUS_COMB.pep:*

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 US-08-366-779-5
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US-08-934-254-27
US-08-833-610-5
US-08-834-033A-15
US-08-834-033A-15
US-08-834-055-7
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Query Match 55.0%; Score 1387; DB 1; Length 448; Best Local Similarity 55.5%; Pred. No. 1.1e-134; Matches 246; Conservative 73; Mismatches 122; Indels 2	US-08-366-779-5  US-08-366-779-5  Sequence 5, Application US/08366779  Patent No. 5614393  GENERAL INFORMATION: APPLICANT: Thomas, Terry L. APPLICANT: Nuccio, Michael APPLICANT: Nuccio, Michael APPLICANT: Numberg, Andrew N. TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A TITLE OF INVENTION: DELTA 6-DESATURASE NUMBER OF SEQUENCES: 25 CORRESPONDENCE ADDRESS: ADDRESSEE: Scully, Scott, Murphy & Presser STREET: 400 Garden City Plaza CITY: Garden City STATE: New York COUNTRY: United States CITY: Garden City Plaza CITY: Garden City Plaza COMPUTER READABLE FORM: ENDIUM TYEE: Ploppy disk COMPUTER READABLE FORM: COMPUTER READABLE FORM: COMPUTER READABLE FORM: COMPUTER READABLE FORM: COMPUTER SEAUCHT NEVERSHER #1.0, Version #1.25 CURRENT APPLICATION NUMBER: US/08/366,779 FILING DATE: 30-DEC-1994 CLASSIFICATION NUMBER: US/08/366,779 FILING DATE: 30-DEC-1994 CLASSIFICATION NUMBER: B383ZXW TELEPHONE: (516) 742-443 TELEPHONE: (516) 742-443 TELEPHONE: (516) 742-436 TELEPHONE: (516) 742-436 TELEPHONE: (516) 742-436 TELEPHONE: (516) 742-436 TELEPHONE: (516) 742-436 TELEPHONE: (516) 742-436 TELEPHONE: (516) 742-436 TELEPHONE: (516) 742-436 TELEPHONE: (516) 742-436 TELEPHONE: (516) 742-436 TELEPHONE: (516) 742-436 TELEPHONE: (516) 742-436 TELEPHONE: (516) 742-436 TELEPHONE: (516) 742-436 TELEPHONE: (516) 742-436 TELEPHONE: (516) 742-436 TELEPHONE: (516) 742-436 TELEPHONE: (516) 742-436 TELEPHONE: (516) 742-436 TELEPHONE: (516) 742-436 TELEPHONE: (516) 742-436 TELEPHONE: (516) 742-436 TELEPHONE: (516) 742-436 TELEPHONE: (516) 742-436 TELEPHONE: (516) 742-436 TELEPHONE: (516) 742-436 TELEPHONE: (516) 742-436 TELEPHONE: (516) 742-436 TELEPHONE: (516) 742-436 TELEPHONE: (516) 742-436 TELEPHONE: (516) 742-436 TELEPHONE: (516) 742-436 TELEPHONE: (516) 742-436	28 408.5 16.2 323 4 US-09-227-613-17 Sequer 29 408.5 16.2 355 2 US-08-834-655-5 Sequer 30 408.5 16.2 355 3 US-08-834-033A-6 31 408.5 16.2 355 3 US-08-834-033A-6 31 408.5 16.2 355 3 US-09-363-574-5 Sequer 32 408.5 16.2 355 3 US-09-363-526-5 Sequer 33 406.5 16.1 444 4 US-09-227-613-42 Sequer 34 406.5 16.1 444 4 US-09-227-613-12 Sequer 36 406 16.1 444 4 US-09-227-613-12 Sequer 37 406 16.0 444 4 US-09-227-613-12 Sequer 38 406 16.0 444 4 US-09-227-613-12 Sequer 39 404 16.0 445 4 US-09-227-613-12 Sequer 40 390 15.5 432 4 US-09-227-613-9 Sequer 41 390 15.5 465 4 US-09-227-613-8 Sequer 42 390 15.5 465 4 US-09-227-613-8 Sequer 43 390 15.5 465 4 US-09-327-613-8 Sequer 44 320 12.7 446 2 US-09-33-610-2 Sequer 54 320 12.7 446 3 US-08-833-610-2 Sequer 55 320 12.7 446 3 US-08-833-610-2 Sequer 56 320 Sequer 57 320 Sequer 58 41 Sequer 58 42 Sequer 58 43 Sequer 58 44 Sequer 59 59 59 59 59 59 59 59 59 59 59 59 59 5
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US-08-789-936-5
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                                                                                                                                                   APPLICATION NUMBER: US/08/789,936
FILING DATE: 28-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/366,779
FILING DATE: 30-DEC-1994
ATTORNEY/AGENT INFORMATION:
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       TELEX: 230 901 SANS UR INFORMATION FOR SEQ ID NO:
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APPLICANT:
APPLICANT:
                                                                           NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 81
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                         TELEFAX:
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                                         (516) 742-4366
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Nunberg, Andrew N.
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                                                                                                                                                                                                                                                                                                                                                                                                               United States
                                                                (516) 742-4343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-934-254-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/08934254
Patent No. 6355861
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino TOPOLOGY: li
                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Scully, S
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Thomas, TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                  CITY: Garden City
STATE: New York
REFERENCE/DOCKET NUMBER: 83
                                                                             FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                ZIP: 11530
                          NAME: Presser, Leopold REGISTRATION NUMBER: 1
                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                      STREET:
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                                                                                                                                                                                                                                                                 United States
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                                                                                                                 US/08/934,254
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                                                                                                                                                       Version
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                                                                                                                                                                                                                                                                                                                                               Sequence 27, Application US/08934254
Patent No. 6355861
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Best Local Similarity
Matches 246; Conserv
                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC
TITLE OF INVENTION: DELTA 6-DESATURASE
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (516) 742-434
TELEPAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 5
                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,254
                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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LENGTH: 448 amino acid
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                                                                                                                                                                          STREET: 400 Garden
CITY: Garden City
STATE: New York
                                                                                                                                      ZIP: 11530
                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         427
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400 Garden City Plaza
                                                                                                                                                        United States
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                                                                                                      Floppy disk
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Pred. No. 1.1e-134;
/3; Mismatches · 122; Indels
                                                                                                                                                                                                                        Murphy & Presser
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US-08-833-610-5
US-08-833-610-5
; Sequence 5, Application US/08833610
; Patent No. 5972664
; Patent No. 5972664
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                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: KNUTZON, DEBORAH
APPLICANT: MURKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
                                            TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY AC NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
STREET: 260 SHERIDAN AVE, P.O. BOX 60039
STATE: C
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Matches 253; Conservative
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Best Local Similarity
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NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 8383
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEPHONE: (516) 742-4346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 230 901 SANS UR INFORMATION FOR SEQ ID NO: 27:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 SARPLLRRFFVG--RLSDYAVSPASADYRRLLAQLSSAGLFERVGPTPKVQLVLMAVLFY 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 KYITAEDLRRHNKSGDLWISIQGKVYDCSRWAAEHPGGEVPLLSLAGQDVTDAFIAYHPG
                                                                                                                                                                                                                                           WWERVAFVLFSFTICGIQHVQFCLNHFSSDVYVGPPKGNDWFEKQTAGTLDILCSPWMDW 378
                                                                                                                                                                                                                                                                                                             LVSYQHWTYYPVMIFGRVNLFIQTFLLLLTRRDVPDRALNLMGIAVFWTWFPLFVSCLPN
                                                                                                                                                                                                                                                                                                                                                                    FISYQHWTFYPVMCIARINLLAQSALFVLTEKRVPQRLLEIAGVATFWAWYPLLVASLPN 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLSIAWWKCNHNTHHIACNSLDHDPDLQHMPLFAVSPKLFGNIWSYFYQRTLAFDAASKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AIVYGVLASESVGVHMLCGALLGLLWIQAAYVGHDSGHYQVMPTRGYNRITQLIAGNILT 186
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AVQARDLNSAPCPKKLGYGEAYNTHG
                                                 ALQARTATSGGAPKNLVW-EAVNTHG 462
                                                                                                                                                    FHGGLOFOIEHHLFPRLPRCHLRKVAPAVRDLCKKHGLTYSAATFW-GANVLTWKTLRAA 437
                                                                                                                                                                                                          WPERFGFVLISFAVTAIQHVQFTLNHFSGDTYVGPPKGDNWFEKQTKGTIDITCPPWMDW
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; Sequence 15, Application US/08834033A; Patent No. 6075183; GENERAL INFORMATION; APPLICANT: KUUTZON, DEBORAH; APPLICANT: MUKERAI, PRADIPAPPLICANT: HUANG, YUNG-SHENG; APPLICANT: THURMOND, JENNIFER
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
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NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: .CGNE.123.00US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)328-4400
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC compatible
COMPUTER: PC compatible
COMPUTER: PC compatible
COMPUTER: PC compatible
COMPUTER: PC compatible
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/833,610
FILING DATE: 11-APR-1997
CLASSIFICATION: 435
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TYPE: amino acid
STRANDEDNESS: not releva
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nilarity 55.3%; Pred. No. 6.4e-133;
Conservative 73; Mismatches 122; Indels
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Best Local (
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INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: US/08/834
FILING DATE: 11-APR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAE
TELECOMMUNICATION INFORMATION:
TELECHNNE: (415) 433-4150
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TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS
NUMBER OF SEQUENCE: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
STREET: 2001 FERRY BUILDING
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LENGTH: 446 amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STRANDEDNESS: not
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 QARTATSGGAPKNLVWEAVNT 460
                                                                                                  GERIMFVIASLSVTGMQQVQFSLNHFSSSVYVGKPKGNNWFEKQTDGTLDISCPPWMDWF
                                                                                                                               WERVAFVLFSFTICGIOHVOFCLNHFSSDVYVGPPKGNDWFEKQTAGTLDILCSPWMDWF
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                                                                 HGGLQFQIEHHLFPRLPRCHLRKVAPAVRDLCKKHGLTYSAATFWGANVLTWKTLRAAAL 439
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US-08-834-655-7
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Patent No.
                                                                                                                                                                                                                                                                                                                                                           Matches 149; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/834,655
FILING DATE: 11-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                        V Match 34.9%; Score 881; DB 2; Local Similarity 59.6%; Pred. No. 8.8e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (650) 328-4477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: not
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.124.00US
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243
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                    GGLQFQIEHH 390
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GGLOFQLEHH 252
                                                                     ERFFFVFTSFTVTALQHIQFTLNHFAADVYVGPPTGSDWFEKQAAGTIDISCRSYMDWFF
                                                                                                    ERVAFVLFSFTICGIQHVQFCLNHFSSDVYVGFPKGNDWFEKQTAGTLDILCSPWMDWFH 380
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HUANG, YUNG-SHENG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide
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RESULT 8

RESULT 9 US-09-363-574-7 ; Sequence 7, Ap

Application US/09363574

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Best Local Similarity
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APPLICATION NUMBER: US/08/834
FILING DATE: 11.APR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEPHONE: (415) 433-8716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: N/A
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: not
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOPTWARE: WORDPERFECT 5.1
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                               GGLQFQIEHH 390
                                                                     ERFFFVFTSFTVTALQHIQFTLNHFAADVYVGPPTGSDWFEKQAAGTIDISCRSYMDWFF 242
                                                                                                                                          SYCHFTYYPVNCFGRINLFIOTFLLLFSKREVPDRALNFAGILVFWTWFPLLVSCLPNWP 182
                                                                                                                                                                 SYQHWTFYPVMCIARINLLAQSALFVLTEKRVPQRLLBIAGVATFWAWYPLLVASLPNWW 320
                                                                                                                                                                                                                SIAWWKWTHNAHHLACNSLDYDPDLQHIPVFAVSTKFFSSLTSRFYDRKLTFGPVARFLV
                                                                                                                                                                                                                                                                                   LYGVLACTSVFAHQIAAALLGLLWIQSAYIGHDSGHYVIMSNKSYNRFAQLLSGNCLTGI
GGLQFQLEHH 252
                                                                                                       ERVAFYLFSFTICGIQHVQFCLNHFSSDYYVGPPKGNDWFEKQTAGTLDILCSPWMDWFH 380
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HUANG, YUNG-SHENG
THURMOND, JENNIFER
CHAUDHARY, SUNITA
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RESULT 10
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Sequence 7, Application US/09363526 Patent No. 6410288 GENERAL INFORMATION:
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Matches
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH L.L.P.
STREET: 2001 FERRY BUILDING
CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 433-8716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/363,574 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: not relevant TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: WARD, MICHAEL R. REGISTRATION NUMBER: 38,651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
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59.6%; Pred. No. 8.8e-83;
tive 39; Mismatches 62; Indels
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US-08-834-655-2

Sequence 2, Application Patent No. 5968809
GENERAL INFORMATION:

Application US/08834655

APPLICANT:

KNUTZON, DEBORAH MURKERJI, PRADIP

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: N/A
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,526
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APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS
NUMBER OF SEQUENCES: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: no
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STREET: 20
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                   381 GGLQFQIEHH 390
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                                                                                                                                                                                                            63 SIAWWKWTHNAHHLACNSLDYDPDLQHIPVFAVSTKFFSSLTSRPYDRKLTFGPVARFLV
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                                                                                      ERVAFVLFSFTICGIQHVQFCLNHFSSDVYVGPPKGNDWFEKQTAGTLDILCSPWMDWFH
GGLQFQLEHH 252
                                                                                                                                         SYQHFTYYPVNCFGRINLFIQTFLLLFSKREVPDRALNFAGILVFWTWFPLLVSCLPNWP
                                                                    ERFFFVFTSFTVTALQHIQFTLNHFAADVYVGPPTGSDWFEKQAAGTIDISCRSYMDWFF
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2001 FERRY BUILDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         not relevant
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Matches 138;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
TYPE: amino acid
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: RAE-VENTER, BARBARA
REGISTRATION INVMBER: 32,750
REGERENCE/DOCKET NUMBER: CGI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 328-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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CITY: PALO ALTO
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                                                                   335 VSQAVCGNLLAIVFSLNHNGMPVISKEEAV----DMDFFTKQIITGRDVHPGLFANWFTG
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GLQFQIEHHLFPRLPRCHLRKVAPAVRDLCKKHGLTY 418
                                                                                                                                                                                                            NLLAQSALFVL-----TEKRVPQRLLEIAGVATFWAWY-PLLVASLPNWWERVAFVL
                                                                                                                                                                                                                                                                                                                                                                                               GWMGHDSGHHRITGHPVLDRVVQVLSGNCLTGLSIAWWKCNHNTHHIACNSLDHDPDLQH 227
                                                                                                                 FSFTICG-IQHVQFCLNH-----FSSDVYVGPPKGNDWFEKQTAGTLDILCSPWMDWFHG 381
                                                                                                                                                                                                                                                                                                                                                      GWLAHDFLHHQVFQDRFWGDLFGAFLGGVCQGFSSSWWKDKHNTHHAAPNVHGEDPDIDT
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                                                                                                                                                               SWCLQSILFVLPNGQAHKPSGARVPISLVEQLSLAMHWTWYLATMFLFIKDPVNMLVYFL
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Pred. No. 2e-45;
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Best Local Similarity
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FILING DATE: 11-APR-1997
CLASSIFICATION: 800
ATTORNEY_AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: WORDPERFECT 5.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: no
TOPOLOGY: linear
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                                 MPLFAVSP---KLFGNI-----WSYFYQRTLAFDAASKFFISYQHWTFYPVMCIARI 276
                                                                                            GWMGHDSGHHRITGHPVLDRVVQVLSGNCLTGLSIAWWKCNHNTHHIACNSLDHDPDLQH 227
                                                                                                                                             ------SSKAYYAFKVSFNLCIWGLSTVIVAKWGQTSTLANVLSAALLGLFWQQC 167
                                                                                                                                                                               VGPTPKVQLVLMAVLFYA-----ALYLVLAC----ASAWAHLLAGGLIGFVWIQS 167
                                                                                                                                                                                                                                                    AGQDATDAFAAYHPPSARPLLRRFFVGRLS----DYAVSPASADYRRLLAQLSSAGLFER 121
                                                                                                                                                                                                                                                                                          AAAPSVRTFTRAEVLNAEALNEGKKDAEAPFLMI-IDNKVYDVREFVPDHPGGSV-ILTH 59
                                                                                                                                                                                                                                                                                                                            AGAGDVRMISSKEL-----RAHASADDLWISISGDVYDVTPWLPHHPGGDLPLLTL
                                                                     GWLAHDFLHHQVFQDRFWGDLFGAFLGGVCQGFSSSWWKDKHNTHHAAPNVHGEDPDIDT
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HUANG, YUNG-SHENG
THURMOND, JENNIFER
CHAUDHARY, SUNITA
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2001 FERRY BUILDING
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Pred. No. 2e-45;
54; Mismatches !
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US-09-363-574-2
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Patent No. 6136574
GENERAL INFORMATION:
                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAE
TELECOMPUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: not rel
TOPOLOGY: linear
MOLECULE TYPE: peptide
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
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122 VGPTPKVQLVLMAVLFYA------ALYLVLAC----ASAWAHLLAGGLIGFVWIQS 167
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                                                           60 VGKDGTDVFDTFHPEAAWETLANFYVGDIDESDRDIKNDDFAAEVRKLRTLFQSLGYYD-
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                                                                                                                                                                                                                                                                                                                                                             not relevant
                                                                                                                                                                                                                  20.7%; Score 523; DB 3 30.2%; Pred. No. 2e-45; tive 64; Mismatches 1
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Patent No. 64102
                Query Match
Best Local Similarity
   Matches 138;
                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09,
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,6
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PATENTIA RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
ZIP: 941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: LIMBACH AND LIMBACH L.L.P. STREET: 2001 FERRY BUILDING CITY: SAN FRANCISCO
                                                                                                           STRANDEDNESS: not relevant TOPOLOGY: linear
                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                       TELEFAX:
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                                                                                                                                                                                                                      N/A
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CHAUDHARY, SUNITA
CHAUDHARY, SUNITA
VENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
VENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN
EQUENCES: 18
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MURKERJI, PRADIP
HUANG, YUNG-SHENG
                                                                                                                                                                                                                                       (415) 433-8716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
                                                                                            peptide
20.7%; Score 523; DB 4
30.2%; Pred. No. 2e-45;
ative 64; Mismatches 1
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                                                                                                                                                                                                                                                                                                            38,651
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                                   DB 4; Length 457;
   Indels
   84;
   Gaps
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Sequence 18, Application US/09330235

| Sequence 18, Application US/09330235
| Patent NO. 6459018
| GENERAL INFORMATION:
| APPLICANT: Knutzon, Debbie
| TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN PLANTS
| FILE REFERENCE: MOCO.156.00US
| CURRENT APPLICATION NUMBER: US/09/330,235
| CURRENT FILLING DATE: 1999-06-10
| PRIOR APPLICATION NUMBER: 60/089,043
| PRIOR APPLICATION NUMBER: 60/089,043
| PRIOR FILING DATE: 1998-06-12
| SOPTWARE: PatentIn version 3.0
| SEQ ID NO 18
| SERVING NO 18
| LENGTH: 457
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US-09-330-235-18
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; ORGANISM: Mortierella alpina
US-09-330-235-18
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Best Local Similarity
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                                         168 GWMGHDSGHHRITGHPVLDRVVQVLSGNCLTGLSIAWWKCNHNTHHIACNSLDHDPDLQH 227
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                                                                                                                                               122 VGPTPKVQLVLMAVLFYA------ALYLVLAC----ASAWAHLLAGGLIGFVWIQS 167
                                                                                                                                                                                                                                                                                                                                        15 AGAGDVRMISSKEL-----RAHASADDLWISISGDVYDVTPWLPHHPGGDLPLLTL
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                                                                                                                                                                                                                                                                                             2 AAAPSVRTFTRAEVLNAEALNEGKKDAEAPFLMI-IDNKVYDVREFVPDHPGGSV-ILTH 59
GWLAHDFLHHQVFQDRFWGDLFGAFLGGVCQGFSSSWWKDKHNTHHAAPNVHGEDPDIDT
                                                                                                 -----SSKAYYAFKVSFNLCIWGLSTVIVAKWGQTSTLANVLSAALLGLFWQQC 167
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Search completed: January 1, 2004, 06:38:13
Job time: 17.251 secs

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Maximum Match 100%
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*

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17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US10E_PUB.pep:*
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US-10-029-756-5
US-10-029-756-27
US-09-967-477B-8
US-09-769-863-14
US-10-054-534B-14
US-10-349-34137
US-10-369-493-4137
US-10-278-391-4
US-10-191-513A-41
US-10-191-513A-41
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Sequence 27, Appli
Sequence 14, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
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Sequence 4, Appli
Sequence 7, Appli
Sequence 11, Appl
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Sequence 20, Appli
Sequence 20, Appli
Sequence 20, Appli
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                         Sequence
Sequence
                         20, Appl
6108, Ap
1, Appli
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e 3,	e 10,	e 27,	e u	e 2,	e 30,	е 37,	e 46,	equence	e 31, App	9835, A	55,	69,	e 913	w	e 20,	equence 20,	Sequence 4, Appli	Sequence 6107, Ap	4.	Sequence 35, Appl	38,	9,	e 12,	e u	e 42,		equence 29,	e 29,	equence 29,

## ALIGNMENTS

RESULT 1 US-10-340-779A-11

Sequence 11, Application US/10340779A Publication No. US20030152983A1 GENERAL INFORMATION:

APPLICANT: Mapler, Johnathan A.
APPLICANT: Mapler, Johnathan A.
APPLICANT: Mapler, Johnathan A.
APPLICANT: Michaelson, Louise
APPLICANT: Michaelson, Louise
FILE REFERENCE: 005407.00004
FILE REFERENCE: 005407.00004
CURRENT FILING DATE: 2003-03-24
FRIOR APPLICATION NUMBER: US/9/582,034
PRIOR FILING DATE: 1998-12-19
PRIOR APPLICATION NUMBER: PCT/GB98/03895
PRIOR APPLICATION NUMBER: UK 9814034.6
PRIOR APPLICATION NUMBER: UK 9814034.6
PRIOR APPLICATION NUMBER: UK 9814034.6
PRIOR APPLICATION NUMBER: UK 9727256.1
PRIOR APPLICATION NUMBER: UK 9727256.1
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CURRENT FILING DATE: 2003-03-24
PRIOR APPLICATION NUMBER: US 09/582,034
PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: PCT/GB98/03895
PRIOR APPLICATION NUMBER: UK 9814034.6
PRIOR APPLICATION NUMBER: UK 9814034.6
PRIOR APPLICATION NUMBER: UK 9727256.1
PRIOR APPLICATION NUMBER: UK 9727256.1
PRIOR APPLICATION NUMBER: UK 9727256.1
PRIOR APPLICATION NUMBER: UK 9727256.1
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LENGTH: 448
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                    Query Match 55.2%; Score 1392; DB 12; Best Local Similarity 55.8%; Pred. No. 1.4e-127; Matches 247; Conservative 73; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Napier, Johnathan A. APPLICANT: Michaelson, Louise APPLICANT: Stobart, Keith TITLE OF INVENTION: Desaturase FILE REFERENCE: 005407.00004
                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Borago officinalis
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                            140 ALYLVLACASAWAHLLAGGLIGFVWIQSGWMGHDSGHHRITGHPVLDRVVQVLSGNCLTG
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                                                                                                                                                            STWKNLDKFFTGYYLKDYSVSEVSKDYRKLVFEFSKMGLYDKKGHIMFATLCFIAMLFAM
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TOPOLOGY: linear

MOLECULE TYPE: Protein

SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-029-756-5
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                                                                                                                         Query Match
Best Local Similarity
Matches 246; Conserv
                                                                                                                                                                                                                                                                                                                                                    TELEX: 230 901 SANS INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/029,756
FILING DATE: 21-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION NUMBER: 08/934,254
APPLICATION NUMBER: 08/934,254
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/934,254
FILING DATE: <Unknown>
APPLICATION NUMBER: DECOMPATION:
NUMBE: DECOMPATION:
                                                                                                                                                                                                                                                                                                                                                                                    NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 8383
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4346
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
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                                                                                21 RMISSKELRAHASADDLWISISGDVYDVTPWLPHHPGGDLPLLTLAGQDATDAFAAYHPP
    81 SARPLLRRFFVG-RLSDYAVSPASADYRRLLAQLSSAGLFERVGPTPKVQLVLMAVLFYA 139
                                          7 KYITSDELKNHDKPGDLWISIQGKAYDVSDWVKDHPGGSFPLKSLAGQEVTDAFVAFHPA
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                                                                                                                                                                                                                                                                                                            LENGTH: 448 amino acids
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                                                                                                                           Conservative
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NVENTION: PRODUCTION OF GAMMA LINGLENIC
                                                                                                                                                                                                                                                                                                                                                                          230 901 SANS UR
                                                                                                                         55.0%; Score 1387; DB 14; 55.5%; Pred. No. 4.2e-127; tive 73; Mismatches 122;
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US-10-029-756-27
; Sequence 27, Application US/10029756
; Publication No. US20020108147A1
; GENERAL INFORMATION:
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US-10-029-756-27
                                                                                                             TELEFAX: (516) 742-4:
TELEX: 230 901 SANS (
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                NAME: Presser, Leopold
REGISTRATION NUMBER: 19 827
REFERENCE/DOCKET NUMBER: 8383ZYXWVU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/10/029,756
FILING DATE: 21-Dec-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/934,254
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
                              LENGTH: 452 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Garden Ci
STATE: New York
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                  27:
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Best Local S
Matches 253
                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 8
                                                                                                                                       Query Match
Best Local Similarity
Matches 154; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/09967477B Patent No. US20020156254A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/236,303
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 60/297,562
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Haiping Hong
TITLE OF INVENTION: FAD4, FAD5, FAD5-2, AND FAD6, NOVEL
TITLE OF INVENTION: FATTY ACID DESATURASE FAMILY MEMBERS AND USES THEREOF
FILE REFERENCE: BNZ-001
                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/967,477B CURRENT FILING DATE: 2002-04-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Xiao Qiu
APPLICANT: Haiping
                                                                                                                                                                                                                                                                  LENGTH: 459
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52
                                 65 LAGQDATDAFAAYHPPSARPLLRRFFVGRLSDYAVS-----PAS-----
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QAGEDATDAFAVFHPSSALKLLEQFYVGDVDETSKAEIEGEPASDEERARRERINEFIAS
                                                                                       VDAMPAPGDAAGAGDVRMISSKELRAHASADDLWISISGDVYDVTPWLPHHPGGDLPLLT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LVSYQHWTYYPVMIFGRVNLFIQTFLLLLTRRDVPDRALNLMGIAVFWTWFPLFVSCLPN 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FISYQHWTFYPVMCIARINLLAQSALFVLTEKRVPQRLLEIAGVATFWAWYPLLVASLPN 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AIVYGVLASESVGVHMLCGALLGLLWIQAAYVGHDSGHYQVMPTRGYNRITQLIAGNILT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KYITAEDLRRHNKSGDLWISIQGKVYDCSRWAAEHPGGEVPLLSLAGQDVTDAFIAYHPG
                                                                    VDLKP------GVKRLVSWKEIREHATPATAWIVIHHKVYDISKW-DSHPGGSV-MLT 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AVQARDLNSAPCPKKLGYGEAYNTHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALQARTATSGGAPKNLVW-EAVNTHG 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FHGGLQFQIEHHLFPRLPRCHLRKVAPAVRDLCKKHGLTYSAATFW-GANVLTWKTLRAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPERFGFVLISFAVTAIOHVOFTLNHFSGDTYVGPPKGDNWFEKOTKGTIDITCPPWMDW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FFGGLQFQLEHHLFPRLPRGQLRKIAPLARDLCKKHGMPYRSFGFWDDANVRTIRTLRDA
                                                                                                                                         Conservative
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                                                                                                                                                        24.3%; Score 612; DB 10; 32.8%; Pred. No. 3.5e-51;
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                                                                                                                                         Mismatches 157;
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                                                                                                                                         Indels
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                                 ----AD 105
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US-09-769-863-14
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CURRENT FILING DATE: 2001-01-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 453
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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-09-769-863-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Das, Tapas
APPLICANT: Thurmond, Jennifer
APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: DESATURASE GENES AND USES
FILE REFERENCE: 6763.US.O1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Huang, Yung-Sheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 22.6%; Score 571; DB 12; Length 453;
Local Similarity 31.2%; Pred. No. 3.6e-47;
hes 138; Conservative 77; Mismatches 163; Indels 6
                                                                                                                                                                                                                                                                                                                                     68 LKLLEQYYVGDVDQSTAAVDTSISDEVKKSQSDFIASYRKLRLEVKRLGLYDSSKLYYLY 127
                                                                                                                                                                                                                                                                                                                                                                                                                                     10
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                                                                                       FAVSPKLFGNIWSYFYQRTLAFDAASKFFISYQHWTFYPVMCIARINLLAQSALFVL---
                                                                                                                                                                             RITGHPVLDRVVQVLSGNCLTGLSIAWWKCNHNTHHIACN-----SLDHDPDLQHMPL
                                                                                                                                                                                                                                         KCASTLSIALVSAAICLHFDSTAMYMVAAV---
                                                                                                                                                                                                                                                                  RPLLRRFFYG-----RLSDYAVSPAS---ADYRRLLAQLSSAGLFE-----
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----TEKRVPQRLLEIAGVATFWAW-YPLLVASLPNWWERVAFVLFSFTICGI-QHVQFC 341
                                          LA-----WSLKMAQHAVDSPVGLFFMRYQAYLYFPILLFARISWVIQSAMYAFYNV
                                                                                                                                         QVFENHLFGDLVGVMVGNLWQGFSVQWWKNKHNTHHAIPNLHATPEIAFHGDPDIDTMPI
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CURRENT APPLICATION NUMBER: US/10/054,534B
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: US 09/769,863
PRIOR FILING DATE: 2001-01-25
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 453
TYPE: PRI
ORGANISM: Saprolegnia diclina
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Best Local Similarity
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APPLICANT: Mukerji, Pradip
APPLICANT: Huang, Yung-Sheng
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APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 LKLLEQYYVGDVDQSTAAVDTSISDEVKKSQSDFIASYRKLRLEVKRLGLYDSSKLYYLY 127
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                                                                 KVAPAVRDLCKKHGLTYSAATF
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                      ALNVLVKSLCKQYDIPYHETGF
                                                                                                                                                             LNHFSSDVYVGPPKGNDWFEKQTAGTLDILCSPWMDWFHGGLQFQIEHHLFPRLPRCHLR 401
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                                                                                                                                                                                                                                                               ----TEKRVPQRLLEIAGVATFWAW-YPLLVASLPNWWERVAFVLFSFTICGI-QHVQFC
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                                                                                                                   VGHNGMEVFDKDSKPDFW-KLQVLSTRNVTSSLWIDWFMGGLNYQIDHHLFPMVPRHNLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163;
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                         Sequence 4137, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
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SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 453
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PRIOR APPLICATION NUMBER: US/09/769,863
PRIOR FILING DATE: 2001-01-25
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APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
FILE REFERENCE: 6763 US /01
CURRENT APPLICATION NUMBER: US/10/431,952
CURRENT FILING DATE: 2003-05-08
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APPLICANT: Muker
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wes 138; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/1027
Publication No. US20030159164A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 123;
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Best Local Similarity
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,391
FILING DATE: 23-Oct-2002
CLASSIFICATION: 800
                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LI
STREET: 220 MONTGOMERY STREET,
CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                  TITLE OF
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                                                                                                                                                                                            COUNTRY: UNITED STATES
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                                                                                                                                                                                                                                                                                                                              NUKERJI, PRALL.
INVENTION: COMPOSITIONS
SYNTHESIS OF
                                                                                                                                                                                                                                                                                                                                                                                        KELDER, BRUCE
HUANG, YUNG-SHENG
KIRCHNER, STEPHEN C
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Pred. No. 4.7e-47;
3; Mismatches 139;
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                                                                                                                                                                                            AMERICA
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US-10-191-513A-11
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                                                                                                                                                                            Sequence 11, Application US/10191513A
Publication No. US20030104596A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pardip
APPLICANT: Leonard, Amanda E.
APPLICANT: Huang, Yung-Sheng
APPLICANT: Tapas, Das
TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES
TITLE REFERENCE: 6295 US.D3
CURRENT APPLICATION NUMBER: US/10/191,513A
CURRENT FILING DATE: 2002-09-25
PRIOR APPLICATION NUMBER: US 09/227,613
PRIOR FILING DATE: 1999-01-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local Similarity
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TELEFAX: (415) 397-8:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OHT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 29-MAY-1998
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            228 MPLFAVSP---KLFGNI-----WSYFYQRTLAFDAASKFFISYQHWTFYPVMCIARI 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           138;
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                                                                                                                                                      Mukerji, Pardip
Leonard, Amanda E.
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                                                                                                                                                                                                                                                                                                                                                                                            GLQFQIEHHLFPRLPRCHLRKVAPAVRDLCKKHGLTY 418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FSFTICG-IQHVQFCLNH-----FSSDVYVGPPKGNDWFEKQTAGTLDILCSPWMDWFHG 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NLLAQSALFVL-----TEKRVPQRLLEIAGVATFWAWY-PLLVASLPWWWERVAFVL
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APPLICANT: Huang, Yung-Sheng
APPLICANT: Tapas, Das
TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
FILE REFERENCE: 6295.US.D3
CURRENT APPLICATION NUMBER: US/10/191,513A
CURRENT FILING DATE: 2002-09-25
PRIOR APPLICATION NUMBER: US 09/227,613
PRIOR APPLICATION NUMBER: US 09/227,613
PRIOR APPLICATION NUMBER: PCT/US98/07422
PRIOR APPLICATION NUMBER: US 08/833,610
PRIOR APPLICATION NUMBER: US 08/833,610
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PRIOR APPLICATION NUMBER: US 08/833,610
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APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pardip
APPLICANT: Leonard, Amanda E.
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PRIOR FILING DATE: 1998-04-10
PRIOR APPLICATION NUMBER: US 08/833,610
PRIOR FILING DATE: 1997-04-11
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                           Sequence 41, Application US/10191513A Publication No. US20030104596A1
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Best Local (
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OTHER INFORMATION: Xaa = Unknown or other at position
-10-191-513A-11
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TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWCLQSILFVLPNGQAHKPSGARVPISLVEQLSLAMHWTWYLATMFLFIKDPVNMLVYFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLNYQIEHHLFPSMPRHNFSKIQPAVETLCKKYNVRY 427
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Pred. No. 1.8e-42;
4; Mismatches 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -DMDFFTKQIITGRDVHPGLFANWFTG
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APPLICANT: Najber, Johnathan A.
APPLICANT: Michaelson, Louise
APPLICANT: Stobart, Keith
TITLE OF INVENTION: Desaturase
FILE REFERENCE: 005407.00004
CURRENT APPLICATION NUMBER: US/10/340,779A
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: PCT/GB98/03895
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: WK 9814034.6
PRIOR APPLICATION NUMBER: WK 9814034.6
PRIOR APPLICATION NUMBER: WK 9814034.6
PRIOR APPLICATION NUMBER: WK 9817256.1
PRIOR FILING DATE: 1998-06-29
PRIOR FILING DATE: 1998-06-29
PRIOR FILING DATE: 1998-06-29
PRIOR FILING DATE: 1998-06-29
PRIOR APPLICATION NUMBER: WK 9727256.1
PRIOR APPLICATION NUMBER: WR 9727256.1
PRIOR FILING DATE: 1997-12-23
NUMBER OF SEQ ID NOS: 23
NUMBER OF SEQ ID NOS: 23
NUMBER OF SEQ ID NOS: 23
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US-10-340-779A-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (458)...(458)
; OTHER INFORMATION: Xaa = Unknown or other at position 458
US-10-191-513A-41
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20, Application US/10340779A Publication No. US20030152983A1 GENERAL INFORMATION:
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MPLFAVSP---KLFGNI------WSYFYQRTLAFDAASKFFISYQHWTFYPVMCIARI 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GWMGHDSGHHRITGHPVLDRVVQVLSGNCLTGLSIAWWKCNHNTHHIACNSLDHDPDLQH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FSFTICG-IQHVQFCLNH-----FSSDVYVGPPKGNDWFEKQTAGTLDILCSPWMDWFHG
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30.2%;
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Pred. No. 1.8e-42;
4; Mismatches 171
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                                                                                                                                                                         ; TYPE: PRT ; ORGANISM: Caenorhabditis elegans US-10-369-493-6108
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US-10-369-493-6108
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                                                                                      Best Local
Matches 13
                                                                                                                                                                                                                                                             SEQ ID NO 6108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
ERIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
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                                                                                                                                                                                                                                         ENGTH: 473
                                                                                      138;
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                                           35 DDLWISISGDVYDVTPWLPHHPGG-----DLP------LLTLAG------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90 ----FVGR-----LSDYAVSPAS----ADYRRLLAQLSSAG-----L 118
                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HHRITGHPVLDRVVQVLSGNCLTGLSIAWWKCNHNTHHIACNSLDHDPDLQHMPLFAVSP 235
  DGKWLYLSEEL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KYVKEWCKENNLPYLVDDYFDGYAMNLQQLKNMAEHIQAKAA 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DKY--PANSRILNNFAALQILTTRNMTPSPFIDWLWGGLNYQIEHHLFPTMPRCNLNACV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DVYVGPPKG----NDWFEKQTAGTLDILCSPWMDWFHGGLQFQIEHHLFPRLPRCHLRKVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VYQRNAFWEQATIVGHWAWVFYQLFLLPTWPLRVAYFIISQMGGGLLIAHV-VTFNHNSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LL-----EIAGVATEWAWYPLLVASLPNWWERVAFVLFSFTICG--IQHVQFCLNHFSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---GDLCKY----KASFEKAILKIVPYQHLYFTAMLPMLRFSWTGQSVQWVFKENQMEYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLFGNIWSYFYORTLAFDAASKFFISYOHWTFYPVMCIARINLLAOSALFVLTEKRVPOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GEHDEFLEKQLEKRLDKVDINVSAYDVSVAQEKKMVESFEKLRQKLHDDGLMKANETYFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DGKWLYLSEEL-----VKKHPGGAV-IEQYKNSDATHIFHAFHEGSSQAYKQLDLLKKH 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HQQPFKNRPLNDTISLFFGNFLQGFSRDWWKDKHNTHHAATNVIDHDGDIDLAPLFAFIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FKAIS-----TLSIMAFAFYLQYLGWYITSAC-------LLALAWQQFGWLTHEFC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FERVGPTPKVQLVLMAVLF---YAALYLVLACASAWAHLLAGGLIGFVWIQSGWMGHDSG 175
                                                                                      Conservative
                                                                                  18.0%; Score 454.5; DB 12; 28.1%; Pred. No. 9.8e-36; tive 71; Mismatches 169;
-VKKHPGGAVIEQYSIPPLNKNIETRGIITTRGSSNALDILYFY
                                                                                      Indels 113;
                                                                                                                             Length 473;
                                                                                      Gaps
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Sequence 1, Application US/10262617
Publication No. US20030077747A1
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl J.
APPLICANT: Gorley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: DELTA-6 DESATURASE HOMOLOGS
FILLE REFERENCE: PF-0494-1 DIV
CURRENT APPLICATION NUMBER: US/10/262,617
CURRENT FILING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: 09/048,888
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                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030077747A1 2451043CD1
US-10-262-617-1
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US-10-262-617-1
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Best Local Similarity
Matches 129; Conserv
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NUMBER OF SEQ ID NOS: 4
SOFTWARE: PERL Program
SEQ ID NO 1
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120 ERVGPTPKV----QLVLMAVLFYAALYLVLACASAWA-HLLAGGLIGFVWIQSGWMGHDS 174
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                                                                   69 DATDAFRAFHODLNFVRKFLOPLLIGELAPEEPSODGPLNAOLVEDFRALHQAAEDMKLF 128
                                                                                                                 69 DATDAFAAYHPP--SARPLLRRFFVGRLSDYAVS---PASA----DYRRLLAQLSSAGLF
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                                                                                                                                                                                                                                                         17.1%; Score 431.5; DB 15; Length 445; 28.6%; Pred. No. 1.6e-33; ative 72; Mismatches 199; Indels 51;
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                   PAVRDLCKKHGLTYSAATFWGANVLTWKTLR 435
                                                          IPKE--IGHEKHRDWVSSQLAATCNVEPSLFTNWFSGHLNFQIEHHLFPRMPRHNYSRVA
                                                                             FSSDVYVGPPKGNDWFEKQTAGTLDILCSPWMDWFHGGLQFQIEHHLFPRLPRCHLRKVA 404
                                                                                                                                                                                                                                              GHASIFKKSWWNHVAQKFVMGQLKGFSAHWWNFRHFQHHAKPNIFHKDPDVTVAPVF---
                                                                                                                       --- VCMQWADLLWAASFYARF--FLSYLP-FYGVPGVLLFFVAVRVLESHWFVWITQMNH 343
                                                                                                                                                   EKRYPORLLEIAGVATFWAWYPLLVASLPNWWERVAFVLFSFTICGIQHVQFC----LNH 344
                                                                                                                                                                                                                                                                            GHHRITGHPVLDRVVQVLSGNCLTGLSIAWWKCNHNTHHIACNSLDHDPDLQHMPLFAVS
PLVKSLCAKHGLSYEVKPFLTALVDIVRSLK 432
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Search completed: January 1, 2004, 06:58:35 Job time : 89.0127 secs

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ALIGNMENTS

RESULT 1
AY234126
LOCUS
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DEFINITION
Primula vialii sphingolipid delta-8 desaturase mRNA, complete cds.
ACCESSION
AY234126.

REYMORDS
SOURCE
ORGANISM
Primula vialii
DORGANISM
Primula vialii
ENtaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; Ericales; Primulaceae; Primula.

REFERENCE
1 (bases 1 to 1385)
Sayanova,O.V., Beaudoin,F., Michaelson,L.V., Shewry,P.R. and
Napier,J.A.

Pred. No.

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Direct Submission

Direct Submission

Submitted (10-FEB-2003) Crop Performance & Improvement, Long Submitted (10-FEB-2003) Crop Performance & Improvement, Long Submitted (10-FEB-2003) Crop Performance & Improvement, Long Submitted (10-FEB-2003) Crop Performance & Improvement, Long Submitted (10-FEB-2003) Crop Performance & Improvement, Long Submitted (10-FEB-2003) Crop Performance & Improvement, Long Submitted (10-FEB-2003) Crop Performance & Improvement, Long Submitted (10-FEB-2003) Crop Performance & Improvement, Long Submitted (10-FEB-2003) Crop Performance & Improvement, Long Submitted (10-FEB-2003) Crop Performance & Improvement, Long Submitted (10-FEB-2003) Crop Performance & Improvement, Long Submitted (10-FEB-2003) Crop Performance & Improvement, Long Submitted (10-FEB-2003) Crop Performance & Improvement, Long Submitted (10-FEB-2003) Crop Performance & Improvement, Long Submitted (10-FEB-2003) Crop Performance & Improvement, Long Submitted (10-FEB-2003) Crop Performance & Improvement, Long Submitted (10-FEB-2003) Crop Performance & Improvement, Long Submitted (10-FEB-2003) Crop Performance & Improvement, Long Submitted (10-FEB-2003) Crop Performance & Improvement, Long Submitted (10-FEB-2003) Crop Performance & Improvement, Long Submitted (10-FEB-2003) Crop Performance & Improvement, Long Submitted (10-FEB-2003) Crop Performance & Improvement, Long Submitted (10-FEB-2003) Crop Performance & Improvement, Long Submitted (10-FEB-2003) Crop Performance & Improvement, Long Submitted (10-FEB-2003) Crop Performance & Improvement, Long Submitted (10-FEB-2003) Crop Performance & Improvement, Long Submitted (10-FEB-2003) Crop Performance & Improvement, Long Submitted (10-FEB-2003) Crop Performance & Improvement, Long Submitted (10-FEB-2003) Crop Performance & Improvement, Long Submitted (10-FEB-2003) Crop Performance & Improvement, Long Submitted (10-FEB-2003) Crop Performance & Improvement, Long Submitted (10-FEB-2003) Crop Performance & Improvement, Long Submitted (10-FEB-2003) Crop Performance &
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1 (Dases 1 to 1681)
Sayanova, O.V., Beaudoin, F., Michaelson, L.V., Shewry, P.R. and
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Napier, J.A.
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FEBS Lett. 542 (1-3), 100-104
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                                                                         /translation="MADPPNPKTGYITSSDLKAHNKAGDLMISIGQVYDUSSWAAL HPGGTAPLMALAGHDVTDAFAKHHHPGGTAPLARISUSSWAAL HPGGTAPLMALAGHDVTDAFAKHTPGFTSARLLPELSARLLLEHSVSSVEPTSSDYRKLLH HPGGTAPLARISUSSTWAHLAGGVWAWIOSGW LGHDSGHYQIMSSRKTINRFAQVLSGNCLAGISIAWKWNHNAHHLACNSLDYDPDLQH MDFFVVSSKFTNSLTSSFYDRKLNFDGVSRFLVSYDHWSFYPWNGLARLNLFAQSFMLLFSSRKVDRAVQEIGGIGVFWYWYBLLVSCLPWGEBRINGVASFSVTGIOHVOFCLW HFSAGFYDWASFSVTGIOHVOFCLW HFSAGFYDWASFSYTGIOHVOFCLW HFSAGFYDWASFSWAGIARUS HAND HPSAEVYLGPPEGNDWFEKQTAGTLNISCHSWMDWFHGGLQFQIEHHLFPRLPRSQLR
                                                         KVSPFVRDLCKKHNLPYNVTSFTMANVLTLKTLRNAAIQARDLSNPTPKNLVWEAVNT
                                                                                                                                                                                                                /product="sphingolipid delta-8 desaturase"
/protein_id="AAP23033.1"
/db_xref="GI:30350275"
                                                                                                                                                                                                                                                                                                                            /organism="Primula farinosa"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                         /note="cytochrome b5 fusion desaturase"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                 ocation/Qualifiers
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Query Match

37

. 18;

Score 326.8;

B

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Length 1681;

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ACCESSION
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Triticum aes
AF031194
AF031194.1
Triticum aestivum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.

1 (bases 1 to 1788)
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                                                                 Triticum aestivum (bread
                                                                                                                                                                                                                                                                    CCTGATAGGGGNATGTTTGNGCTTGCTAGCTTTTGCTGTTTTGTNCCNATCCAGCACATTCA
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0; Mismatches 283
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(S276) mRNA,
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Matches 543
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TITLE
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Delhaize,E., Hebb,D.M., Gardno
Direct Submission
Submitted (23-OCT-1997) Plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Australia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Delhaize, E., Hebb, D.M., Gardner, R.C. and Richards, K.D. Aluminum tolerance in yeast conferred by over-expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                            ACTATGACCCTGATCTGCAGCACATGCCGGTCTTTGCAGTTTCGTCGCGGTTCTTCAATT
                                                                                CTGTCTGCGGGGTCTTCTCCGACAGCACTTTCGTGCACGTGCTTTCCGCTGCATTGA
                                                                                                                                                                                                                                                                                                                                 CCCCCGCCTCCGCCGACTTCCGCCGCCGCCAGCTCTCCTCCGCGGGCCTCTTCG
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             ACCATGACCCTGACCTCCAGCACTTGCCGCTCTTCGCGGTTTCCACCAAGCTCTTCAACA
                                                                                                                     CCAGGCACCCTGCAACCGCCTCCTGCAGGTGGTCTCCGGGAACTGCCTCACCGGCC
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                                                                                                                                                                      TTGGCTTCATCTGGATCCAGTCGGGCTGGATTGGCCATGACTCCGGCCACCACCAAATCA
                                                                                                                                                                                              TAGGCTTTCTCTGGATTCAGAGCGGCTGGATAGGCCACGACTCCGGCCATTACAACGTGA
                                                                                                                                                                                                                                                                              AGCGCGTCGGCCACACCCCCAAGTTCCTGCTCGCAATGTCGGTGCTCTTCTGCATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                      36.1%;
nilarity 61.6%;
Conservative
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ATTGAAPKNLVWEALNTHG"
1 588 c 450 g 429 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="S276"
/note="similar to Borago officinalis delta
from GenBank Accession Number U79010"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'product="S276"
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|21. .1530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mol_type="mRNA"
cultivar="ET3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Triticum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 317.6; DB 8;
Pred. No. 2.8e-64;
0; Mismatches 335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gardner, R.C.
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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AY234125
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Submitted (10-FEB-2003) Crop Performance & Improve
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1 (bases 1 to 1410)
Sayanova, O.V., Beaudoin, F., Michaelson, L.V., Shewry, P.R. and
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Primula farinosa fatty acid c
AY234125
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                /translation="MANKSPENPKTGYITSSDLKSHNKAGDLMISIHQQYDVSSWAA LHPGGTAPLMALAGHDYDDAFLAYHPSTARLLPPLSTWLLCOMHSVSFFSSDYRKLL DNFHKHGLFFAARGHTAYAATFVPM AMFLMSVTGVLCSDSAWVHLASGGAMGFAMIQOG WIGHDSGHYRIMSDRKWNWFAQILSTNCLQGISIGWMKNNHNAHHIACNSLDYDDDLQ YIPLLVVSPKFFNSLTSRFYDKKLNFDGVSRFLVCYQDWTFYPVMCVARLNMLAQSFI
                                                                                                                                                    /codon_start=1
/product="fatty acid delta-6
/protein_id="AAP23034.1"
/db_xref="GI:30350277"
                                                                                                                                                                                                                                                                                                                                       /organism="Primula farinosa"
/mol_type="mRNA"
/db_xref="taxon:133892"
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or n-3 fatty acid su
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Beaudoin, F.,
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ACCESSION
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cds. AF005096 AF005096

communis

desaturase/cytochrome b5

protein

mRNA,

complete

linear

PLN 05-JAN-1999

1856 bp

mRNA

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BASE COUNT
ORIGIN
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Best Local Similarity
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                                  TTCTGGTTGAATCACCTTGCTGAAAATTTATATGNCGGGC
                                                                    GCGAGAGGATT
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TTCAGCTTGAACCATTTTTCTTCGGACGTCTATGTGGGCC
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Submitted (22-MAY-1997) Cell Biology, IACR-Long Ashton Research Station, Long Ashton, Bristol BS18 9AF, UK
Location/Qualifiers
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Sayanova,O., Smith,M.A., Lapinskas,P., Stobart,A.K., Dobson,G., Christie,W.W., Shewry,P.R. and Napier,J.A.
Expression of a borage desaturase cDNA containing an N-terminal cytochrome b5 domain results in the accumulation of high levels delta6-desaturated fatty acids in transgenic tobacco proc. Natl. Acad. Sci. U.S.A. 94 (8), 4211-4216 (1997)
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                                                                                                                                                                                                                                                                                                                               TATGGAGTTCTTTGCTCTAATAGTACATGGGTGCATCTTATTTCTGGTGGCTTAATGGGG
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GATCCAGATCTGCAGCATATGCCTTTCTTTGCGGTATCCTCAAAATTTTTCAGTTCAATT
                                    GACCCTGATCTGCAGCACATGCCGGTCTTTGCAGTTTCGTCGCGGTTCTTCAATTCCATA 485
                                                                                                                      AGCCGTCGATTCAATCGTTTGGCGCAGATCTTATCTGGAAATTGTCTTGCAGGAATCAGT
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SPLIHLAGQDVTDAFVAYHEGTAWQYLLKEFTGYHLKDYSVSETSKDYRRLVAEFSKL
GPEKKGHIAFITLVSMYMLLALSVYGVLCSNSTWVHLISGGLWGFMWIOSGWIGHDSG
HYQVMMSRRFNRLAQILSGNCLAGISIAWKWNHNTHHIACNSLDFDPDLQHMPFFAV
SSKFFSSITSYPYERKOMFDCAARFLVSYQHLTFYPVMCFARIDHOSGYSLLLISKRR
VANRGOBILGULVFWIMYPFLINSCLPHWGERVMFVAASFSVTRIQHUDGTCNIHFSSGY
VANRGOBILGULVFWIMYPFLINSCLPHWGERVMFVAASFSVTRIQHUDGTKGTLDITGSSW
VALGLLIANDWFENQTKGTLDITCSSWMDWFHGGLQFQMEHHLFPRLFRVKLRKVSPFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="desaturase/hydroxylase; Member of the mono-oxygenase superfamily. Contains an N-terminal extension which is related to cytochrome b5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RELCKKHNLPYDSASFWNANELTFKTLRAAALQARDLSNPIPKNLVWEAVNTHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
/product="desaturase/cytochrome b5
/protein_id="AAD01240.1"
/db_xref="GI:4101626"
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_xref="taxon:3988"
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sphingolipid-desaturase
patent: wO 0000593-A 1 06-JAN-2000;
ZAEHRINGER ULRICH (DE); HEINZ ERNST (DE);
SPERLING PETRA (DE); GVS GES FUER ERWERB (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brassica napus (rape)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1 from AX007239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zaehringer, U., Heinz, E., Schmidt, H.
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                                                                                          Similarity
   CCGCATGGCGCCACCTCGAAAACCTCCACAACGGCTACCACGTGAAAGACCACCACGTGT
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                                   CCGCCTCCTCCTCCCCCCCCTTCTCCACCTCCCACCGTCTTTCCGACCACACCGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTACTTGTGTTCTGGATTTGGTATCCTTTCCTTGTTTCTTGCTTACCCAATTGGGGAGAG
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                                                                                                                                                            RRYVPDRALNIAGILVFWTWFPLLVSFLPNWQBRIIFVFLSWAVTAIGHVQFCLNHFA
ADVYTGPPNGNDWFEKQTAGTLDISCRSYMDWFFGGLQFQLEHHLFPRLFRCHLRGVS
PVVQBLCKKHNLPYRSLSWWEANVWTLRTLRKAAVQARDVTNFVLENLLWEALNTHG"
369 c 375 g 468 t
                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Brassica napus"
/mol_type="genomic DNA"
/db_xref="taxon:3708"
                                                                                                                                                                                                                                                                                                                             protein_id="CAC07389.1"
/db_xref="GI:9995106"
                                                                                                                                                                                                                                                                                                                                                                 codon_start=1
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                                                                     Score 279; DB 6;
Pred. No. 3.6e-55;
D; Mismatches 319
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Sperling,P., Zahringer,U. and Heinz,E. A sphingolipid desaturase from higher new cytochrome b5 fusion protein
                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                           delta-8 sphingolipid desaturase;
Brassica napus (rape)
Brassica napus
Eukaryota; Viridiplantae; Strepto
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Brassica napus mRNA fo
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99003197
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Allgemeine Botanik der
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Direct Submission
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   CTGTCTGCGGCGTCCTCTTCTCCGACAGCACTTTCGTGCACGTGCTTTCCGCTGCATTGA
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                                TGCTCAGCCGCCCCCCCAACCGCGCAATTCAGATTCTCTCCGGCAACATTCTCGCCGGAA
                                                                                              TGGGCCTTCTCTGGATACAGAGCGCTTACGTGGGACATGACTCTGGTCATTACAACGTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="Sptrembl:Q9ZRP8"
//translation="MSEQTKKRFITSDDLKKHNQPGDLWISJOGKVYDVSHWVKSHPG
GEARILLLAGQDVTDAFIAYHPGTAMTHENLLHNGYHVKDHHVSDVSRDYRRLAAEFS
KRGLFDKKGHVTLYTLTCVAAMLAAVYYGVVACTSIWAHLISAVLLGLLWIGSAYVGH
DSGHYNVTSTKPCNKLVQLLSGNCITGISIAWWKWTHNAHHISCNSLDHDPDLQHIPV
LAVSNKFFKSWTSRFYGRKLTFDPLAKFINSCPFINGCFRINLFIQTLLLLFS
RRYVDDRALMIAGILVFWTWFPELUSSLPNWOFFGGLQPQLEHHLFPRLPRCHLRGVS
RRYVDBRALMIAGILVFWTWFPELUSSLPNWDWFFGGLQPQLEHHLFPRLPRCHLRGVS
ADVYTGPPNGNDWFEKQTAGTLDISCRSYMDWFFGGLQPQLEHHLFPRLPRCHLRGVS
ADVYTGPPNGNDWFRSSWWEANVWTLRTLRKAAVQARDVTNPVLENLLWEALLHTHG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /prounce="delta-8 sphingolipid desaturase"
/protein_id="CAA11857.1"
/db_xref="G1:3819708"
/db_xref="GOA:Q9ZRP8"
/db_xref="GOA:Q9ZRP8"
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/product="delta-8 sphi
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/tissue type="ripening emi
/dev_stage="18 to 35 DAF"
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420 612 360 372

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BOUTCE 110149 /reganism="Arabidopsis thaliana" /rol_type="genomic DNA" /cultivat="Columbia" /cultivat="Columbia" /b xref="taxon:3702" /chromosome="2" /map="CIC02E07" /clone="T3F17"	AUTHORS  TITLE  Submitted (V9-FMAR-2000) THE INSTITUTE OF SENOR REFERENCE, 9/12  Medical Center Dr., Rockville, MD 20850, USA  REFERENCE  3 (bases 1 to 110149)  AUTHORS  TOWN,C.D. and Kaul,S.  TITLE  Direct Submission  JOURNAL  Submitted (27-FEB-2002) The Institute for Genomic Research, 9712  Medical Center Dr., Rockville, MD 20850, USA, cdcown@rigr.org  COMMENT  On Apr 18, 2002 this sequence version replaced gi:6598465.  FEATURES  Location/Qualifiers	( ) (bases 1 to 110149)  1 (bases 1 to 110149)  Rounsley,S.D., Lin,X., Kaul,S., Shea,T.P., Fujii,C.Y., Mason, Shen,M., Ronning,C.M., Fraser,C.M., Somerville,C.R. and Vente Unpublished  2 (bases 1 to 110149)  Lin,X.  Direct Submission	AC005397.3 GI:20197: HTG. Arabidopsis thaliana Arabidopsis thaliana Eukaryota; Viridipla; Spermatophyta; Magno	Qy 837 GNT 839  Db 1091 GTT 1093  RESULT 8 AC005397/c AC005397 110149 bp DNA linear PLN 11-MAR-2002 DEFINITION Arabidopsis thaliana chromosome 2 clone T3F17 map CIC02E07, ACCESSION AC005397	719 CCTC 972 CAAC 779 GTTC 1031 GTTC	793 601 853 660 913	Db 613 TATCGATCGCTGGAAATGGACCGCATAACGTCACCATATCTCTTGTAATAGTCTTG 672  Qy 421 ACTATGACCCTGATCTGCAGCACATGCCGGTCTTTGCAGTTTCGTCGCGGTTCTTCAATT 480
CDS	gene mRNA	CDS	repeat_region gene mRNA		mRNA CDS	repeat_region gene	misc_feature repeat_region gene mRNA CDS
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mRNA
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GRNSSETDGSTDGSDGNTTGADEPKLKRSREGTPTKDGKQLVQASSFHSVSPSSGDTG
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22157...22240,22334...22429,22512...22556,22644...22709))
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QTIVSGGEDKVIRIWDAETGKLLKQSDEEVGHKKDITSLCKAADDSHFLTGSLDKTAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="synonym: T3F17.7; supported by cDNA:
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19279. .19368,19462. .19548,19649. .19728,19837. .20058)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VGDHLAVITTDHFVGTSSAIHVKRIAEDPEDQVGDSVLVLQSEDGKKKINRAVAGPLN
QTIVSGGEDAAIRIMDAETGKLLKQSDEEVGHKEAITSLCKAADDSHFLTGSHDKTAK
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TILQEEIGGVKGHFGPINALAFSPDGKSFSSGGEDGYVRLHHFDSNYFNIKI"
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KLADDPDGASLSATAVARVENKRIPNSLUFYYCENTAVDLSVGSCENDETCNGETTNNGF
RQEPKNSTSVKVETTYVKNQLVERGLAKRLAAKFQSKDLVINVVAKTKVGLGVGGIKIG
MLAVNLRCGGVSLNKLDTDSPKCILNTLKWYKIISN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KILQEEIGGVKGHFGPINALAFNPDGKSFSSGGEDGYVRLHHFDSDYFNIKI"
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19279. .19368,19462. .19548,19649. .1972
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.19728,19837. .1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGGTTCTTCAATTCCATAACCTCTCATTNCTATGGGAGGAAGTTNGAGTTTGATTNCATT
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                                                                                                                                                                                                                                                                                                                                                              GCTCGATTCTTAATCAGCTACCAACACTGGACATTTTACCCAGTAATGTGCGTCGGAAGA 4523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGCAACAGCCTCGACTATGACCCTGATCTGCAGCACATGCCGGTCTTTGCAGTTTTCGTCG
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LRIEILGGPSDSRSDAEGCTSIADWARHRKRRREDNKKDNGVAISDIVACAEEQILTD
NNQPDMDDAPGGDNLDDEGEAMVEEALSGDDDASSEPNWGIDCSTVVRVKELHISSPI
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complement(24966..27557)
/gene="At2g46260"
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/protein_id="AAC62880.2"
/db_xref="GI:20197378"
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Matches 508; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@nias.affrc.go.jp, URI:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)

The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data.

NOTE: It currently consists of 1 contigs Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and coession number will be preserved.
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AP005554 96312 bp DNA Oryza sativa (japonica cultivar-group) chro O11118 A10, *** SEQUENCING IN PROGRESS ***.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (23-JUL-2002) Takuji Sasaki, National Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sasaki,T., Matsumoto,T., Hattori,M., Sakaki,Y. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Published Only in Database (2002)
2 (bases 1 to 96312)
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                              GCGGCGTCCTCTCCCGACAGCACTTTCGTGCACGTGCTTTCCGCTGCATTGATAGGCT 246
                                                                                          AGGGCCACACAACCTCCATCCTCTCTCCCTTATTCTCACCCTTTTTCCTCTCTCTGTCT
                                                                                                                            CGTCCGCCGACTTCCGCGCCTCCTCGCGCAGCTCTCCTCCGCGGGGGCTGTTCGAGCGGG 88495
                                                                                                                                                CCTCCTCCGACTACCGCAAGCTCTTCTCCGACCTCTCCGCGCTCAACCTCTTCAACCGCA
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                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                    /mol type="genomic DNA"
/cultivar="Mipponbare"
/db xref="taxon:39947"
/chromosome="9"
/clone="OJ1118 A10"
a 21050 c 21350 g 27305
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Location/Qualifiers
                                             TACCGCAAGCTCTTCTCCGACCTCTCCGCGCTCAACCTCTTCAACCGCAAGGGCCACACA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTGAATCACCTTGCTGAAAATTTATATGNCGGGC--ACNANTGGGAATGACTGGNT 839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGGNATGTTTGNGCTTGCTAGCTTTTGTTGTNCCNATCCAGCACATTCAGTTCTGG 785
TACCGGAGGCTTTTGAACGAGATGTCGCGGTCCGGGATCTTCGAGAAGAAGGGCCACCAC
                                                                                                  CCGCTCTTCACCGGCTACTACCTCCAAGGACTTCGAAGTGTCGGAGATCTCCAAGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCGCCGCGTTCTGGGTTTGGTACCCAATGGTGGTGTCCTGCCTTGCCCAATTGGTGGGAGA
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Pred. No. 5e-54;
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Direct Submission
Submitted (10-SEP-2001) Biochemistry, Universidad de
Campus Universitario, La Canada s.n., Almeria 04120,
                                                                                                                                                                                                                                                                                                                      Echium gentianoides delta-6-desaturase
                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; lamids; Boraginaceae; Echium.
                                                                   2 (bases 1 to 1478)
Maroto, F.G., Alonso,
                                                                                                                      Cloning and Molecular Characterization Echium: Functional Expression in Yeast
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svvvgdpkgndwfekqucgtldiscpswmdwfhggldydyhhilpfklprchlrkisp
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/db_xref="GI:17223795"
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/db_xref="taxon:173991"
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Echium pitardii var. pitardii
Echium pitardii var. pitardii
Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
Asteridae, lamids, Boraginaceae, Echium.

1 (bases 1 to 1450)
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Maroto, F.G., Alonso, D.L.,
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/db_xref="taxon:174255"
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/mol_type="genomic DNA"
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        ATTGGATATCTCTTGTGNCCCT
                                    GCTAGCTTTGCTGTTTGTNCCNATCCAGCACATTCAGTTCTGGTTGAATCACCTTGCTGA
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	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 1684)	REFE
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/transl_except= (pos:692..743, aa:Nhe-Leu)
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/transl_except= (pos:630..632, aa:Xaa)
/note= "Xaa is an unknown amino acid; the CDS
not include start and stop codons"
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ABZ12753
AAC51462
AAZ44833
AAC731846
AAZ44851
AAD01349
ABX27196
ABL93274
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AAD21684

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C. purpureus delta Aspergillus oryzae Mutational hot spo Human retinitis pi Human GDP-mannose Human prostate spe Listeria innocua D Listeria innocua D Listeria innocua C

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Matches 880;
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The present sequence is useful for producing transgenic plants having altered levels of sphingolipid desaturase which in turn would alter the fatty acid composition. The enzyme is useful for producing polyclonal or monoclonal antibodies. The polymucleotide is also useful as a primer or probe for screening cDNA libraries to isolate desired full-length cDNA clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polynucleotide encoding delta-6 desaturase enzyme useful for producing transgenic plants and for producing antibodies specific to which is useful for screening cDNA expression libraries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Page 44-45; 57pp; English.
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The present sequence is a cDNA encoding sphingolipid desaturase from clone ssl.pk0017.b4:fis isolated from soybean seedling cDNA library, ssl. The present sequence is useful for producing transgenic plants having altered levels of sphingolipid desaturase which in turn would alter the fatty acid composition. The enzyme is useful for producing polyclonal or monoclonal antibodies. The polynucleotide is also useful as primer or probe for screening cDNA libraries to

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                                                                                                             Polynucleotide encoding delta-6 desaturase enzyme useful for producing transgenic plants and for producing antibodies specific to which is useful for screening cDNA expression libraries -
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The present sequence is useful for producing

The present sequence is useful for producing

transgenic plants having altered levels of sphingolipid desaturase which
in turn would alter the fatty acid composition. The enzyme is useful
for producing polyclonal or monoclonal antibodies. The polymucleotide
is also useful as primer or probe for screening cDNA libraries to
isolate desired full-length cDNA clones.
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SXCCCCCCCXSXFFFX
                                                                                                                           Polynucleotide encoding delta-6 desaturase enzyme useful for producing transgenic plants and for producing antibodies specific to which is useful for screening cDNA expression libraries -
                                                                                                           Claim
                                                                                                                                                                  WPI; 2000-412336/35.
P-PSDB; AAY71552.
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The present sequence is a cDNA encoding sphingolipid desaturase from clone cdelc.pk001.08:fis isolated from corn developing embryo cDNA library, cdelc. The present sequence is useful for produci transgenic plants having altered levels of sphingolipid desaturase whi in turn would alter the fatty acid composition. The enzyme is useful for producing polyclonal or monoclonal antibodies. The polynucleotide is also useful as primer or probe for screening cDNA libraries to isolate desired full-length cDNA clones. 2 Page 41-42; 57pp; English. for producing saturase which

Sequence 1764 BP; 310 A; 602 C; 456 G; 396 T; 0 other;

Length 1764;

밁 S 밁 Ś В δ 밁 Ś 밁 δ 밁 Ś 맑 S 맑 δ 밁 Ş 밁 Ś 뭉 S 밁 Ś Query Match Best Local S Matches 519 541 807 361 987 660 927 601 867 481 747 421 687 627 301 567 241 507 181 447 121 387 327 720 61 519; Similarity CCGCCGCCTCCTCCGACTACCGCAAGCTCTTCTCCGACCTCTCCCGCGCTCAACCTCTTCA 120 CETEGGÉGÉGÉGÉGÉTÉCTÉCGÉCGÉTTÉTTÉGTTGGÉCÉGCÉTCTETGACTACGÉCÉTET CCGCCTCCCTCCTCCCCCCCCTCTCCACCTCCACCGTCTTTCCGACCACACCGTCT CTGATAGGGGNATGTTTGNGCTTGCTAGCTTTGCTGTTTGTNCCNATCCAGCACATTCAG TGCAGACAATTCTGCTATTGTTTTCGAGGNGAAAAGTGCAGGA-TAGAGCTTGAACATAA 659 ACATATGGTCCTACTTCTACCAACGGACCCTGGCGTTCGATGCCGCCTCGAAATTCTTCA CCATAACCTCTCATTNCTATGGGAGGAAGTTNGAGTTTGATTNCATTGCTANGTTCTTGA ACTATGACCCTGATCTGCAGCACATGCCGGTCTTTGCAGTTTCGTCGCGGTTCTTCAATT TGCTCAGCCGCCGCCTCAACCGCGCAATTCAGATTCTCTCCGGCAACATTCTCGCCGGAA 360 TAGGCTTTCTCTGGATTCAGAGCGGCTGGATAGGCCACGACTCCGGCCATTACAACGTGA CTGTCTGCGGCGTCCTCTCTCCCGACAGCACTTTCGTGCACGTGCTTTCCGCTGCATTGA CGGGGGTCGCCACATTCTGGGCTTGGTACCCGTTGCTGGTGGCTTCCCTGCCGAATTGGT receenrectrererringenerrectrerringenerrectrecenerrecenerringener CGCAGTCCGCCCTGTTCGTTCTCACGGAGAAGAGGGTGCCGCAGCGGTTGCTTGAGATCG TCAGCTACCAGCACTGGACCTTCTACCCGGTAATGTGCATCGCCAGGATAAATCTTCTCG ACCATGACCCGGACCTCCAGCACATGCCGCTCTTTGCCGTCTCCCCCAAGCTGTTCGGCA CCGGCCATCCGGTCCTCGACCGCGTCGTGCAGGTGCTCTCCGGGAACTGCCTCACCGGCC CGCTGTACCTCGTCCTCGCATGCGCCAGCGCCTGGGCGCACCTCCTCGCGGGGGGTCTCA AACGCGTCGGCCCCACCCCCAAGGTCCAGCTCGTCCTGATGGCCGTCCTCTTCTACGCCG CCCCCGCGTCCGCCGACTACCGCCCCCCCCCCCCCCGCGCCTATCCTCCGCGGGCCTCTTCG TCAGCATCGCCTGGTGGAAGTGTAACCACACACACGCACATCGCCTGCAACAGCCTGG TTGGCTTCGTCTGGATCCAGTCCGGCTGGATGGGCCACGACTCGGGCCACCACCGCATCA Conservative 34.3%; 0, Score 302; DB 21; Pred. No. 1.9e-66; Mismatches 319; Indels 4. Gaps 719 986 866 540 806 420 300 180 446 926 600 480 746 686 626 566 240 506 386

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         This invention describes a novel sphingolipid desaturase that selectively introduces a double bond into the sphingobase of the ceramide residue of sphingolipids and capnoids. A DNA sequence encoding the sphingolipid desaturase, or a vector containing the DNA sequence, can be used to produce transgenic plants, especially croop plants, with an increased or decreased delta-8-unsaturated long-chain base content or an altered delta-8-unsaturated long-chain base content or an altered compensate for a delta-8-unsaturated long-chain base deficiency, to exclude production of delta-8-unsaturated bases, to increase tolerance or resistance to soil salinity, ion stress or toxicity, drought, wet conditions, cold or frost and/or phytopathogenic microorganisms, or to alter size growth and flowering time. Cells, transgenic organisms or plants containing the DNA sequence can be used to produce sphingolipids and capnoids with unsaturated sphingobases. The sphingolipids or capnoids materials. This sequence encodes the Brassica napus sphingolipid of desaturase eldl protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sphingolipid desaturase; sld1; sphingobase; ceramide; capnoid; transgenic plant; crop plant; delta-8-unsaturated long-chain base; tolerance; resistance; soil salinity; ion stress; toxicity; drought; cold; frost; phytopathogenic microorganism; flowering time; cosmetic pharmaceutical; food; chemical raw material; ds.
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                                                                                                                                                                                                                                                                                             Claim
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Pred. No. 1.2e-60;
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99US-0139457. 99US-0139458. 99US-0139469. 99US-0139461. 99US-0139462. 99US-0139463. 99US-0139750.	99US-0118540. 99US-0118647. 99US-0119119. 99US-0119452. 99US-0119453. 99US-0119454. 99US-0119456.	99US-0134370 99US-0134768 99US-0134941 99US-0135124 99US-0135353 99US-0136021 99US-0136021 99US-0136782 99US-0137528 99US-0137528 99US-0137528 99US-0137528 99US-0137524	99US-0130077. 99US-0130510. 99US-0130510. 99US-0130891. 99US-0132449. 99US-0132407. 99US-0132484. 99US-0132486. 99US-0132486. 99US-0132486. 99US-0132486. 99US-0132487. 99US-0132486. 99US-0132486. 99US-0132486. 99US-0132486. 99US-0132487. 99US-0132486.	2000EP-0301439.  99US-0121825.  99US-0123180.  99US-0125788.  99US-012664.  99US-0126785.  99US-0127462.  99US-0128714.  99US-0128714.	(first entry) thaliana DNA fragment SEQ ID NO: 34823. n assay; genetic mapping; gene expression tification; signal transduction pathway; thway; promoter; termination sequence; ss. thaliana.
					n control;
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                                                                                      TCCGCTGCATTGATAGGCTTTCTCTGGATTCAGAGCGGCTGGATAGGCCACGACTCCGGC
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                                                            TCCGCCGTTTTACTCGGTCTCCTCTGGATCCAAAGCGCTTACGTCGGCCACGATTCCGGT
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Conservative
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Pred. No. 3.4e-60;
0; Mismatches 299;
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08-JAN-1992;
14-SEP-1994;
28-JAN-1997;
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    WPI; 2002-380944/41.
                                          Thomas TL
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91US-0774475.
92US-0817919.
92US-0307382.
97US-0789936.
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Sequence 1702 BP;
                                                                                                                   gamma
                                                                                                                 nucleic acid encoding evening primrose delta6-desaturase which rts linoleic acid to gamma linolenic acid useful for producing linolenic acid in transgenic plant or bacteria -
                                                                                                   2; Column
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The invention describes an isolated nucleic acid encoding an evening primrose Delta6-desaturase. The nucleic acid and a vector expressing the nucleic acid are useful for producing a plant such as sunflower, soybean, maize, tobacco, peanut, carrot or oil seed rape plant, with increased gamma linolenic acid (GLA) content, and also for inducing or increasing production of GLA in a bacteria or plant deficient, lacking in or producing low levels of GLA. The nucleic acid is also useful for inducing chilling tolerance in plants. This sequence encodes the evening primrose delta6 desaturase involved in the production of gamma linoleic acid. 41-46; 53pp; English

358 A; 471 C; 446 G; 427 T; 0 other;

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                                                        TGGACTTGGTTCCTCTTTTAGTGNCTTGCCTGCCAAATTGGGCCTGATAGGGGNATGTTT
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14-SEP-1994;
28-JAN-1997;
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19-SEP-1997;
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92US-0817919.
94US-0307382.
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Novel nucleic acid encoding evening primrose delta-6-desaturase, for producing plant with increased gamma linolenic acid content, for inducing octadecatetraenoic acid production in plant

Claim 2; Fig 10; 55pp; English

The invention relates to a nucleic acid encoding an evening primrose delta-6-desaturase polypeptide. The nucleic acid, a vector comprising the nucleic acid or a nucleic acid encoding delta-12-desaturase, is useful for producing a plant (such as sunflower, soybean, maize, tobacco, peanut, carrot or oil seed rape plant) with increased gamma-linolenic acid (GLA) content by transforming a plant cell with the nucleic acid or vector and regenerating a plant with increased GLA content from the plant cell, for inducing or increasing production of GLA in an organism lacking in or producing low levels of GLA and for inducing production of octadecatetraenoic acid in at least one of a plant deficient or lacking in or producing low levels of octadecatetraenoic acid, a bacterium which produces alpha-linolenic acid or a bacterium which exhibits a collar-15-desaturase activity on a GLA substrate. This sequence represents collar encoding an evening primrose delta-6-desaturase polypeptide.

Sequence 1702 BP; 358 Α; 471 Ç 446 ູດ 427 + 0

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RESULT 9
AAV34398
ID AAV3
XX
AC AAV3
XX
DT 02-M
XX
DE Bora
XX
KW Upst
KW 1ipi
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Best Local Similarity
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Upstream region; regulatory region; sunflower; albumin; lipid metabolism; delta-6 desaturase; transgenic plant;
                                             Borage delta-6 desaturase gene
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nilarity 59.6%;
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Pred. No. 2e-59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1684 BP;
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                                                AACCACAACGCCCACCACCATTGCATGCAACAGCCTCGACTATGACCCCTGATCTGCAGCAC
                                                                                        GCAATTCAGATTCTCTCCGGCAACATTCTCGCCGGAATCAGCATCGGCTGGTGGAAGTGG
                                                                                                                                                                              GGCTGGATAGGCCACGACTCCGGCCATTACAACGTGATGCTCAGCCGCCGCCCTCAACCGC
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                               AACCATAATGCACATCACATTGCCTGTAATAGCCTTGAATATGACCCTGATTTACAATAT
                                                                                                                                                  GGTTGGATTGGACATGATGCTGGGCATTATATGGTAGTGTCTGATTCAAGGCTTAATAAG
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complement (616..63
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Pred. No. 4.4e-52;
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                                            Nucleic acid containing oleosin 5'-regulatory region - useful modulating fatty acid synthesis and lipid metabolism in plants particularly to increase content of gamma-linolenic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                 Delta-6 desaturase; borage; oleosin; AtS21; promoter; transgenic plant; seed; lipid; fatty acid; oilseed; vegetable oil; gamma-linolenic acid; octadecatetraenoic acid; ds.
                 Example 2;
                                                                                                          P-PSDB;
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DB; AAW98130.
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                 Page
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                   59-61;
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43..1389
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Best Local Simi
Matches 497;
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AAW98130), an enzyme that catalyses the conversion of linoleic acid
to gamma-linolenic acid (GLA). Delta-6 desaturase CDNA was
isolated from a borage membrane-bound polysomal cDNA library
using a partial clone, obtained from an EST database search, as
probe The borage delta-6 desaturase nucleic acid can be
coperably linked to the seed-specific 5' regulatory region (see
AAX24916) of the Arabidopsis thaliana oleosin AtS21 gene in claimed
expression cassettes of the invention. Transgenic plants, e.g.
sunflower, soybean, maize, tobacco, cotton, peanut, oilseed
rape or Arabidopsis are obtained that show increased levels of
GLA or octadecatetraeonic acid. The levels of desirable fatty
coils of use in human health and industrial applications.
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                   GCTAGCTTTGCTGTTTGTNCCNATCCAGCACATTCAGTTCTGGTTGAATCACCTTGCTGA
                                                                                                     TGGTTCCTCTTTTAGTGNCTTGCCTGCCAAATTGGGCCTGATAGGGGNATGTTTGNGCTT
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57.7%;
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Pred. No. 4.4
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                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                      A DNA clone (AAT30395) codes for borage delta-6-desaturase (AAR98455), which catalyses the conversion of linoleic acid to gamma-linolenic acid (GLA). It was isolated from a borage membrane-bound polysomal library using probes based on abundantly expressed seed storage protein cDNAs and with an isolated partial cDNA clone. The gene can be incorporated into a vector, pref. incorporating a tissue-specific promoter, for the expression of delta-6-desaturase in transgenic plants, esp. sunflower, soybean, maize, tobacco, peanut, carrot or oilseed rape, resulting in increased GLA prodn. Alteration of plant lipids may also lead to improved chilling
                                                                                                                                                                                                                                                                                              Sequence 1685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Page 51-52; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transgenic plants comprising the borage delta-6-desaturase g show increased production of gamma linolenic acid and having increased resistance to chilling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-DEC-1994;
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Best Local Sim
Matches 497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention describes an isolated nucleic acid encoding an evening primrose Delta6-desaturase. The nucleic acid and a vector expressing the nucleic acid are useful for producing a plant such as sunflower, soybean, maize, tobacco, peanut, carrot or oil seed rape plant, with increased gamma linolenic acid (GLA) content, and also for inducing or increasing production of GLA in a bacteria or plant deficient, lacking in or producing low levels of GLA. The nucleic acid is also useful for inducing chilling tolerance in plants. This sequence encodes the borage delta6 desaturase involved in the production of gamma linoleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel nucleic acid encoding evening primrose delta6-desaturase which converts linoleic acid to gamma linolenic acid useful for producing gamma linolenic acid in transgenic plant or bacteria -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1685 BP; 431 A; 277 C; 357 G; 620 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 9; Column 29-32; 53pp; English.
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14-SEP-1994;
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10-OCT-1991;
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    AACCATAATGCACATCACATTGCCTGTAATAGCCTTGAATATGACCCTGATTTACAATAT
                             AACCACAACGCCCACACTTGCATGCAACAGCCTCGACTATGACCCTGATCTGCAGCAC
                                                                               TTTÄTGGGTÄTTTTTGCTGCAÄÄTTGTCTTTCAGGÄÄTAÄGTÄTTGGTTGGTGGÄÄÄÄTGG
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91US-0774475.
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/product= "delta6-desaturase"
/transl_except= (pos:1151..1153,
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Pred. No. 4.4e-52;
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08-JAN-1992;
14-SEP-1994;
28-JAN-1997;
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  Thomas
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19-SEP-1997;
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                                       (THOM/) THOMAS
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/product= "Borage delta-6-desaturase #1"
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a nucleic acid encoding an evening primrose delta-6-desaturase polypeptide. The nucleic acid, a vector comprising the nucleic acid or a nucleic acid or a mucleic acid or a sunflower, soybean, malze, tobacco, peanut, carrot or oil seed rape plant) with increased gamma-linolenic acid (GLA) content by transforming a plant cell with the nucleic acid or vector and regenerating a plant with increased GLA content from the plant cell, for inducing or increasing production of GLA in an organism lacking in or producing low levels of GLA and for inducing production of of GLA in an organism lacking in or producing low levels of GLA and for inducing production of or produces alpha-linolenic acid or a bacterium which exhibits a delta-15-desaturase activity on a GLA substrate. This sequence represents cDNA encoding a borage delta-6-desaturase polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acid encoding evening primrose delta-6-desaturase, for producing plant with increased gamma linolenic acid content, for inducing octadecatetraenoic acid production in plant
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)B; ABG73095.
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                                                                                                                                                                                                                                                                                                                                            GCAATTCAGATTCTCTCCGGCAACATTCTCGCCGGAATCAGCATCGGCTGGTGGAAGTGG
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                                                  TACCCTATTATGTGTGCTGCTAGGCTCAATATGTATGTACAATCTCTCATAATGTTGTTG
                                                                                                                   AMAAGGTTGACTTTTGACTCTTTATCAAGATTCTTTGTAAGTTATCAACATTGGACATTT
                                                                                                                                                                                  AACCATAATGCACATCACATTGCCTGTAATAGCCTTGAATATGACCCTGATTTACAATAT
                                                                                                                                                                                                                                                                               AACCACAACGCCCACCACATTGCATGCAACAGCCTCGACTATGACCCTGATCTGCAGCAC
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                                                                                                                                                Fig 5A; 55pp; English.
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57.7%;
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Pred. No. 4.4e-52;
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                             24-AUG-2000;
26-JAN-2001;
22-JUN-2001;
                     in methods of the invention.

Note: The sequence data for this patent is not representionation but is based on sequence information the European Patent Office.
                                                                                                                                                                                                                                                                           WPI;
                                                                   (b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used
                                                                                                                                      cell has been exposed, comprising:

(a) contacting nucleic acid representative of expressed in the plant cell with an array or probes representative
                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                      Identifying a and producing
                                                                                                                                                                                                                                                                                                  Harper JF,
                                                                                                                                                                                                                                                                                                                                                                                                              24-AUG-2001; 2001WO-US26685
                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200216655-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana stress regulated gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JAN-2003
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                                                                                                                                                                            invention relates to identifying
                                                                                                                              genome; and
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SYNGENTA PARTICIPATIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCTAGCTTTGCTGTTTGTNCCNATCCAGCACATTCAGTTCTGGTTGAATCACCTTGCTGA
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; 2001US-264647P.
; 2001US-300111P.
                                                                                                                                                                                                                                                                                                 Kreps J,
                                                                                                                                                                                                   ID NO 558; 577pp +
                                                                                                                                                                                                                                      stress condition to which a plant cell has been plants with increased tolerance to these abiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plant; gene; stress;
                                                                                                                                                                                                                                                                                                  Wang
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                                                                                                                                                                                                     Sequence
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                                                                                                                                           representative
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                                                                                                                                                                             condition to which a plant
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                                  the printed
o Derwent by
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Sequence 1350

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392

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other,

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RESULT 15
AAC51462
ID AAC51
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AC AAC51
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Arabi
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KW Hybri
KW prote
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Matches 469;
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Best Local
Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway;
                                 Arabidopsis thaliana DNA fragment SEQ ID NO: 68612.
                                                         18-OCT-2000
                                                                                AAC51462;
                                                                                                      AAC51462 standard; DNA; 1650
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                                                                                                                                                                              TTCTGGTTGAATCACCTTGCTGAAAATTTATATGNCGGGC 819
                                                                                                                                                                                                         ĊTĠĀĠĀĠĀTTCTŤCĠTCTŤCĀĊĀĀĠĊŤŤCĀĊĊĠ-ŤCĀCĠĠĊĠĊŤŤĊĀĀĊĀĊĀŤŤĊĀĀ
                                                                                                                                                                                                                                                         CCGGAATCTTAGTCTTCTGGACTTGGTTCCCCACTCTTAGTCTCATGTCTACCAAACTGGC
                                                                                                                                                                                                                                                                              TGGGGATCCTTGTGTTTTGGACTTGGTTCCTCTTTTAGTGNCTTGCCCCAAATTGGGC
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                                                                                                                                                                                                                                                                                                                                                   CATTGACCTCGAGATTCTACGATCGGAAACTCACGTTTGATCCAGTCGCGAGATTCTTAG
                                                                                                                                                                                                                                                                                                                                                                                                             CCATAACCTCTCATTNCTATGGGAGGAAGTTNGAGTTTGATTNCATTGCTANGTTCTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTACGATCCAGATCTACAACACATCCCTGTCTTCGCCGTCTCCACCAAATTCTTCTCCT
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                                                                                                                                                              TTCACGCTTAACCATTTCGCTGCTGATGTCTACGTTGGTC 1021
                                                                                                                                                                                                                                 CTGATAGGGGNATGTTTGNGCTTGCTAGCTTTGCTGTTTGTNCCNATCCAGCACATTCAG
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ilarity 57.2%;
Conservative
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Pred. No. 7.3e-52;
0; Mismatches 349;
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  28-MAY-1999;
01-JUN-1999;
03-JUN-1999;
04-JUN-1999;
07-JUN-1999;
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06-MAY-1999;
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                                           TAGGCTTTCTCTGGATTCAGAGCGGCTGGATAGGCCACGACTCCGGCCATTACAACGTGA
                                                                               CTGTCTGCGGCGTCCTCTCTCCCGACAGCACTTTCGTGCACGTGCATTCCGCTGCATTGA
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U025934 QHG12E03		U02593	13	S	ω	21	44
E445712 WHE1452		E44571	10	N	ω.		3
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24179 QHF16J2		U024	13	σ	٠.	$\mathbf{r}$	41
26884		U02688	13	4	4.	21	40
25712	.0	U0257	13	S	4.	15.	9
84487	7	D48448	14	9	4.	16.	38
၀ွ		BQ976973	13	748	24.8	217.8	37
81359		Q28135	13	4	4.	19.	36
86053		B086	14	o	4.	19.	35
05403	•	D00540	14	ū	'n	20.	34
97852		G09785	10	0	'n	20.	33
55838	_	E3558	10	0	'n	20.	32
74236		H67423	28	w	ŗ	22.	31
76		192176	12	9	ŗ	23.	30
6850		3685	9	9	ŗ	25.	29
74553		H57455	28	4	ŗ	26.	28
36433		3643	28	-	9	29.	27
21804 BOHOG43		H52180	28	9	6	23	26
29325 BNLGHil31		AI729325	9	σ	٥,	30.	25
87946 hk10c10.		B08794	14	0	σ,	32.	24
CB002410 VVB016E06		B00241	14	J	σ.		23
002504 VVB017E1		B00250	14	J	9	36.	22
81157		ᆲ	13	8	σ.	36.	21
BJ465389 BJ465389		46538	12	9	.7	39.	20
12771	-	771	12	9	7	40.	19
M87882		M878	12	9	7.	4	18
TPLC005	•	D03769	14	0	7.	41.	17
68200 odh53g04		6820	28	702	7.	ü	16
03445 EST43194		0344	10	J	8	47.	15
jNEST93	•	908	14	8	œ	51.	14
82077	7	820	12	9	œ	54.	7
47198		G64719	10	B	9	54.	12
48907 GM880016	7	U54890	13	0	9	56.	11
02431 GA_Ed00		4024	13	7	9	261	10
35212 sau50d04		A93521	14	4	0	σ	9
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TITLE JOURNAL COMMENT	REFERENCE AUTHORS	KEYWORDS SOURCE ORGANISM	ACCESSION VERSION	RESULT 1 CA785300 LOCUS DEFINITION
Public Soybean EST Project Unpublished Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project Public Soybean EST Project Public Soybean EST Project	l (bases 1 to 726) Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., A., Bolla, B., Warra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann	EST. Glycine max (soybean) Glycine max Glycine max Glycine max Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Varidiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids ; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;	Gm-c1062-9581 5' similar to TR:Q9ZTY9 Q9ZTY9 DESATURASE/CYTOCHROME B5 PROTEIN. ;, mRNA sequence. CA785300 CA785300.1 GI:26048847	CA785300 726 bp mRNA linear EST 04-DEC-2002 sau27h03.y1 Gm-c1062 Glycine max cDNA clone SOYBEAN CLONE ID:

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BASE COUNT
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                                                                         421 AATTCCCTCACTTCCAGATTCTACGACAGAAAGTTGAATTTCGATTCCTTTGCTAGGTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              237 TTGATAGGCTTTCTCTGGATTCAGAGCGGCTGGATAGGCCACGACTCCGGCCATTACAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 TTCAACCGCAAGGCCACACAACCTCCATCCTCCTCTCCCTTATTCTCACCCTTTTTCCT
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This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
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Seg primer: -40RP from Gibco
AATTCCATAACCTCTCATTNCTATGGGAGGAAGTTNGAGTTTGATTNCATTGCTANGTTC
                                                                                                                                                                CTCGACTATGACCCCGATCTCCAGCATTTGCCCTTCTTCGTCGTCTCCTCTAGGTTTTTC
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue type="stem tissue
/dev_stage="1 month old"
/lab_host="DH10B"
/clone_lib="Gm-c1062"
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/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID:
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82.8%;
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Pred. No. 1e-110;
0; Mismatches 120;
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of greenhouse
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	source	FEATURES			JOURNAL COMMENT		REFERENCE AUTHORS	ORGANISM	ACCESSION VERSION KEYWORDS SOURCE	RESULT 2 A1748200 LOCUS DEFINITION	Db 61	Qy 7:	Qy 6:	tri (	0y 4
/db xret='tayon: 3847" /db xret='taxon: 3847" /clone="GENOME SYSTEMS CLONE ID: Gm-c1011-238" /tissue_type="immature cotyledons of greenhouse grown /tissue_type="immature cotyledons of greenhouse grown /tissue_type="immature cotyledons of greenhouse grown /lab host="HOH10B" /clone_lib="Genocity II SK+; Site_1: EcoRI; Site_2: /note="Wector: pBluescript II SK+; Site_1: EcoRI; Site_2: /note="Wector: pBluescript II SK+; Site_1: EcoRI; Site_2: /note="Wector: pBluescript II SK+; Site_1: EcoRI; Site_2: /note="Wector: pBluescript II SK+; Site_1: EcoRI; Site_2: /note="This cDNA library was constructed_from mRNA isolated from immature cotyledons (100-200mgs) of greenhouse grown plants: The cDNA library was prepared using the Life Technologies pSuperScript cDNA library construction kit. /complementary DNA was synthesized from mRNA using a poly /(dT) sequence with a Not I restrictions // ilinkers adapters were ligated to the blunt-ended cDNA /fragments followed by NotI digestion. The cDNA fragments were directionally cloned into the NotI-SSAI I restriction site of the pSPORT 1 vector. The ligated cDNA fragments	1. 579 /organism="Glycine max" /mol type="mRNA"	sert Length: 1134 Std Error: gh quality sequence stop: 412. Location/Qualifiers	st@watson.wusi reversed clos through: Res untsville, Al	Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1810 Fax: 314 286 1810	<pre>Contact: Sheemaker R/Public Soybean EST Project Public Soybean EST Project</pre>	B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., con, R. and Wilson, R. san EST Project	elycine.  1 (bases 1 to 579)  1 (bases 1 to 579)  Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Allen,M., Bowers wylie.T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers	max ta; v ophyt ids I	AI748200 AI748200.1 GI:5126464 EST. Glycine max (soybean)	AI748200 579 bp mRNA linear EST 30-NOV-2001 8b49411.Y1 Gm-c1011 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1011-238 5' similar to TR:082348 082348 PUTATIVE CYTOCHROME B5:	61 TGGTGGGAGAGGCTTTTGTTTTGTTTTCCTGAGTTTCTCTGTT 702	16 GGGCCTGATAGGGGGNATGTTTGNGCTTGCTAGCTTTGCTGTT 757	656 ATAATGGGGATCCTTGTTTTTGGACTTGGTTCCTCTTTTAGTGNCTTGCCTGCCAAATT 715	TTTGCGCAGTCTTTTTCTTGTTGTCTAAGAGGAGGGTGGAGAACAGAGGCAGTGAG	481 TTGTTTAGTTACCAGCACTGGACTTTTTACCCTGTGATGTGTTTCGCTAGGGTTAATCTG 540 597 TATCTGCAGACAATTCTGCTATTGTTTTCGAGGNGAAAAGTGCAGGATAGA-GCTTGAAC 655

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ACCESSION
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ORGANISM
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Best Local Similarity
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                                                                             AUTHORS
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EST.
Glycine max (soybean)
Glycine max
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid;
eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
1 (bases 1 to 592)
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna Shoemaker,R., Keim,P., Hillier,L., Kucaba,T., Martin,J., Beck,C., A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,B., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
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sp06h07.y1 Gm-c1041 Glycine
Gm-c1041-2102 5' similar to
B5. ;, mRNA sequence.
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This library was constructed by Dr. Lila Vodkin and
Anu Khanna."
1 126 c 143 g 187 t 4 others
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Query Match
Best Local Simi
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Location/Qualifiers
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGCCTCAACCGCGCAATTCAGATTCTCTCCGGCAACATTCTCGCCGGAATCAGCATCGGC 371
                                                                                                            CTGCTATTGTTTCTCAGGCGAAAAGTGCAAGATAGAACCTTGAACATAATGGGGATCCTT
                                                                                                                                                                                                                                                                                                                                                                                 CATTNCTATGGGAGGAAGTTNGAGTTTGATTNCATTGCTANGTTCTTGATCTGCTACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                           GATCTGCAACATGCCGGTCTTTGCAGTTTCGTCGCGGGTTCTTCAATTCCATAACCTCT
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                         GTGTTTTGGACTTGGTTC-CTCTTTTAGTGNCTTGCCTGCCAAATTGGGCCTGATAGGGG
                                                                                                                                         CTGCTATTGTTTTCGAGGNGAAAAGTGCAGGATAG-AGCTTGAACATAATGGGGATCCTT
                                                                                                                                                                                                                    CACTITACTTTTTACCCTGTAATGTGAGTTGCCAGGGTCAACTTGTATCTGCAGACAATT
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//clone_lib="Gm-cl041"
//clone="Vector; pT773Pac (Pharmacia); Site_1: EcoRI;
//note="Vector; pT773Pac (Pharmacia); Site_1: EcoRI;
//clone="Vector; pT773Pac (Pharmacia); Site_1: EcoRI;
//clone="Vector"; ptain in the constructed from mRNA
isolated from senescing leaf tissue of mature greenhouse
grown plants of the cultivar Williams. Complementary DNA
was synthesized from mRNA using a 3' anchored poly(dT)
primer. EcoRI adapters were ligated to the blunt-ended
cDNA fragments followed by digestion with EcoRI and
HindIII. The cDNA fragments were directionally cloned
into the EcoRI-HindIII restriction site of the pT7T3-Pac
vector. The ligated cDNA fragments were transformed into
DH10B host cells. This library was constructed by Dr.
Randy Shoemaker."

32 a 124 c 139 g 197 t
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/mol_type="mRNA"
/db_xref="taxon:3847"
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83.7%;
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Pred. No. 7.8e-72;
0; Mismatches 79
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JOURNAL COMMENT
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ORGANISM
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       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
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1 (bases 1 to 414)

1 (bases 1 to 414)

Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., R., Bolla,B., Marra,M., Hillier,L., Theising,B., Allen,M., Bowers, T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R., and Wilson,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
Putative full length read
vector to vector length is 503 This clone is available through:
ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville,
35801 For further information call: (800)-533-4363 or contact via
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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Glycine max
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BI316528.1
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414 bp mRNA linear EST 29-NOV-2001
saf04e03.yl Gm-c1065 Glycine max cDNA clone GENOME SYSTEMS CLONE
ID: Gm-c1065-4445 5', similar to TR:Q9ZTY9 Q9ZTY9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                email: ccu@resgen.
Seq primer: -40RP
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DESATURASE/CYTOCHROME B5 PROTEIN. ;, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         quality sequence stop: 413.
Location/Qualifiers
                                                             36
                                                                                                                 /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: XhOI, The cDNA library was constructed from mRNA isolated germinating shoots of the cultivar Williams. The seeds were allowed to germinate for 24 hours prior to being cold stressed for 2 days at 4C. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhOI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhOI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhOI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library
                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="germinating shoots"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Glycine max"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                             /db xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1065-4445"
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       36.1%;
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BG882278.1 GI:142593
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Glycine max (soybean)
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                                                                                                                                                                                                                  Tel: 314 286 1800
Fax: 314 286 1810
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/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
                                                                               Location/Qualifiers
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61 CCGCCGCCTCCTCCGACTACCGCAAGCTCTTCTCCGACCTCTCCGCGCTCAACCTCTTCA
                           Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Cc
South Memorial Parkway Huntsville, AL 35801 For furthe
call: (800)-533-4363 or contact via email: ccu@resgen.
Insert Length: 1730 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                 Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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sae98b11.y1 Gm-c1065 Glycine max cDNA clone GENOME SYSTEMS
ID: Gm-c1065-3910 5' similar to TR:Q9ZTY9 Q9ZTY9
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quality sequence stop: 418.
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BASE COUNT

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AY103762
Zea mays
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
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a 134 c
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/clone lib="Gm.cl065"
/clone lib="Gm.cl065"
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhOI; The cDNA library was constructed from mRNA isolated germinating shoots of the cultivar Williams. The seeds were allowed to germinate for 24 hours prior to being cold stressed for 2 days at 4C. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhOI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhOI digestion. The cDNA fragments were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      was constructed in the laboratory of Dr. Randy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="germinating shoots"
/lab_host="DH10B"
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Matches 519;
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LOCUS DEFINITION ACCESSION RESULT 6 AY103762

VERSION KEYWORDS

ORGANISM

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Direct Submission
Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.rmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.mcbi.nim.nih.gov. When the source of the maize CDNA sequences is either Virginia Walbot, Stanford or Pat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schnable, Iowa State, www.zmdb.iastate.edu.
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Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design
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CCATAACCTCTCATTNCTATGGGAGGAAGTTNGAGTTTGATTNCATTGCTANGTTCTTGA
                                                                                         ACTATGACCCTGATCTGCAGCACATGCCGGTCTTTGCAGTTTTCGTCGCGGTTCTTCAATT
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3 602 c 456 g 396 t
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/db_xref="MaizeDB:634923"
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Pred. No. 4.3e-62;
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                                 439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brassica oleracea

Bukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eu
; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 823)

Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fras
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BOHSQ94TF BO 2 3 KB Brassica
genomic survivor
1 CCGCCTCCCTCCTCCCCGCCTTCTCCACCTCCCACCGTCTTTCCGACCACCACCGTCT
                                                                                                                                                                                                                                                                                         Seg primer: TF
Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                                                         Contact:
                                                                                                                                                                                                                                                                                                                                                                                                                                      Whole genome shotgun sequencing of Brassica oleracea Unpublished Other_GSSs: BOHSQ94TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genomic survey sequence.
BH687867
                                                                                                                                                                                                                                                                                                                       Email: cdtown@tigr.org
DNA is from a doubled haploid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brassica oleracea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BH687867.1 GI:18758304
                                             Similarity
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                                                                                                              182
                                                                                                                                                                                                                                                                                                                                                         301-838-3523
                                                                                                                                                                                                                                                                                                                                                                                       Medical Center Drive,
                                                                                                           /clone_lib="BO_2_3_KB"
/note="Vector: pHOS1, Site_1: BstXI; 2-3 kb
genomic DNA inserted into pHOS1 using BstXI
a 197 c 283 g 161 t
                                                                                                                                                                                                                                                                                                                                                                                                                         Chris Town
                                                                                                                                                                                          /mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                            organism="Brassica oleracea"
                                                                                                                                                                            clone="BOHSQ94"
                                                                                                                                                                                                                                                             . 823
                                             31.9%;
                         0;
                              Score 281; DB 28;
Pred. No. 3.8e-57;
0; Mismatches 250;
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BOHSQ94,
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Glycine max (soybean)
Glycine max
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                                         Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna, A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Marrin,J., Beck,C., Wylie,T., Underwood,K., Steptee,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R., and Wilson,R.
                                                                                                                                                                                                                                                                                                                      BM143768 588 bp mRNA linear ES saj48e09.y1 Gm-c1072 Glycine max cDNA clone SOYBEAN CI Gm-c1072-2921 5' similar to TR:082348 082348 PUTATIVE
                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
             Unpublished
                          Public Soybean EST Project
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This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington
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GCAATAGTCTTGACTATGATCCTGATCTCCAGCACATACCTGTCTTTGCCGTGTCGACAC
                                                       GCAACAGCCTCGACTATGACCCTGATCTGCAGCACATGCCGGTCTTTGCAGTTTCGTCGC
                                                                                                                                                                                                                                   ACTATGAGGTTATGTCTAGCCCTGGCTACAACAAATTGGCACAAATCCTTTGTGGCAATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp. glyvines (plant Cell Report 18:375-380). Cultivar PI 567374 is partially resistant to the disease SDS. Plant tissue (expanded leaves, folded leaves, and new shoots) were collected at 1, 6, 24, and 48 hrs. after inoculation and their mRNA pooled equally for cDNA construction. The library was prepared using the Stratagene pBluescript II SK(+) library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with an XhoI restriction site. EcoRI adaptors were ligated to the blunt-ended cDNA fragments followed by XhoI digestion via methylation during first strand synthesis. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into E.coli ElectroMax DHIOB host cells. Plants were inoculated by Shuxian Li (Glen Hartman lab, University of Illinois). Library was constructed by Steve Clough (Lila Vodkin lab, University of Illinois).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note=TVector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library wms constructed from mRNA isolated from 2-3 week old seedlings that were induced for symptoms of SDS (Sudden Death Syndrome) disease by the translocation of culture filtrate of Pusarium solani f.
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(Sudden_Death Syndrome) disease"
/dev_stage="2-3 weeks old"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntaville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C. Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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Glycine max (soybean)
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CA935212.1 GI:27423692
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449 bp mRNA linear EST 30-DEC-2002
8au50d04.y1 Gm-c1071 Glycine max cDNA clone SOYBEAN CLONE ID:
Gm-c1071-4376 5' similar to TR:082348 082348 PUTATIVE CYTOCHROME
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Public Soybean EST Project
                                                                                                                                                                                                                                                                                                                                                             Seq primer: -40RP from Gibco.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
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/clone_lib="Gm-c1071"
/note="Vector: pSPORT: Site_1: NotI; Site_2: SalI; The CDNA library was constructed_from mRNA isoTated from immature pods (approximately 2cm long) of greenhouse grown plants. The library was prepared using the Life Technologies pSuperScript cDNA library construction kit.
                                                                                                                                                          /lab_host="DH10B"
                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-c1071-4376"
                                                                                                                                                                                                          tissue_type="immature pods"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished Contact: Wing RA Clemson University Genomics Institute Clemson University Genomics 29634, US
                                                                                                                                                                                     An integrated analysis of the cotton fiber
                                                                                                                                                                                                             Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., ,D., Wood,T.C., Leslie,A. and Wilkins,T.A. an integrated analysis of the genetics, development, and evolutions of the genetics of the genetics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BQ402431 676 bp mRNA linear GA Ed0049E09f Gossypium arboreum 7-10 dpa fiber larboreum cDNA clone GA Ed0049E09f, mRNA sequence.
                                         Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                 BQ402431.1
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: rwing@clemson.edu
High Quality bases =
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complementary DNA was synthesized from mRNA using
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91.6%;
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Pred. No. 2.2e-53;
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COMMENT

ACCESSION VERSION KEYWORDS

mRNA sequence.
BU548907
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SOURCE

(soybean) GI:22931768 TITLE

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High quality sequence start: 5
High quality sequence stop: 641.
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/clome_lib="Gossypium arboreum 7-10 dpa fiber library"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
/note="Vector: pBK-CMV; 226 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tissue_type="Fibers isolated from bolls
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/db_xref="taxon:29729"
/clone="GA__Ed0049E09f"
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/mol_type="mRNA"
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Pred. No. 2.4e-52;
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Glycine
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycine max
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: 1-vodkin@uiuc.edu
Insert Length: 503 Std
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Soybean (NSF 9872565)
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Contact: Vodkin, L.O., PI, A Functional Genomics Program for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: (217) 333-4582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Edwin R.
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                        115
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                                                                                                                                                                                                                germinating seedlings, shoot tips, or leaves exposed to various stresses (source libraries Gm-c1064, Gm-c1065, Gm-c1066, and Gm-c1067; and Gm-c1068); and 963 cDNAs from young leaves exposed to bacterial and fungal pathogens (source libraries Gm-c1072, Gm-c1073, and Gm-c1074). The source libraries Gm-c1073, and Gm-c1074). The STS of the source clones from the different libraries was used to select singletons, or a representative of each contig, which were reracked to form library Gm-r1088 and the cDNA clones of the reracked Gm-r1088 library were then sequenced at the 3' end. The uniquene selection and 3' sequencing was funded by NSF Plant Genome project #9872565 (http://soybeangenomics.croppsci.uiuc.edu/) as part of creation of a low redundancy soybean cDNA set. The source cDNA libraries were constructed by the laboratories of Lila Vodkin, University of Illinois, Randy Shoemaker, Iowa State University, and Paul Keim, Northern Arizona University as part of the Public EST project, http://129.186.26.94/soybeanset.html. The contig analysis to select unique genes was performed by the laboratory of Ernest Retzel, Center for Computational Genomics and Bioinformatics, University of Minnesota, http://web.ahc.umm.edu/biodata/nefsoy/. Reracking and 3' sequencing were conducted by services of the University of Illinois Keck Center for Comparative and Functional Genomics http://www.hiotech.uiu.edu/keck.htm. Note. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (217) 244-6147
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                                                                   Genomics http://www.biotech.uiuc.edu/keck.htm. Note: The corresponding 5' EST from each clone in the Gm-r1088 library is listed in the 'OTHER EST' field. The detailed information on the source library for each clone can also be obtained by referring to the Genome Systems clone ID of the original cDNA library that is also listed under 'OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNAs from tissue culture derived somatic embryos (source libraries Gm-c1036 and Gm-c1075); 3,275 cDNAs from
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/note="The_library Gm-r1088 is a sequence-driven,
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Matches 352; Conserv
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                                                                                                                                                                                                                                                                                             Hahn, M.G., Ojanen-Reuhs, T., Samac, D., Utterback, T., Cho, J. and Fraser, C.M. ESTs from roots of Medicago truncatula oligogalacturonides of DP 6-20
                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Medicago truncatula (barrel medic)
Medicago truncatula
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EST508817 HOGA Medicago truncatula cDNA clone pHOGA-15P24 5' end,
available at: www.medicago.org
Seq primer: SKmod (CTA gAA CTA
Location/Qualifiers
                                                             Email: hahn@ccrc.uga.edu
G390804e TIGR sequence name: MTMBV96TK More information
                                                                                                                                                                        University of Georgia
220 Riverbend Road, A
                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                    Hahn, M.G.,
                                                                                                                       Fax: 706-542-4412
                                                                                                                                                      Tel: 706-542-4457
                                                                                                                                                                                                                           Complex Carbohydrate Research Center
                                                                                                                                                                                                                                                  Contact: Michael G. Hahn
                                                                                                                                                                                                                                                                                                                                                                                                                       Medicago
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//note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
//note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in SOLR cells."

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/tissue_type="3 day old seedling roots"
/tissue_type="3 day old seedling roots"
/dev_stage="24 hours after treatment in the dark at with 0.5 mg/ml oligogalacturonides (DP 6-20) in the presence of 100 ug/ml Gentamicin"
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/mol_type="mRNA"
/cultivar="A17"
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Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Martin, J., Beck, C., A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Xohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insert Length: 1782 Std Error: 0.00 High quality sequence stop: 415.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid
; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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Glycine max
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sae95g06.yl Gm-c1065 Glycine max cDNA clone GENOME SYSTEMS CLONE
ID: Gm-c1065-3779 5' similar to TR:082348 082348 PUTATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            call: (800)-533-4363 or contact via email: ccu@resgen.com
Insert Length: 1782 Std Error: 0.00
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                                                                                                                                                                                              Similarity
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                                                        AGCCCTGGCTACAACAAATTGGCACAAATCCTTTGTGGCAATTGCATGACTGGGATAAGC
                                                                                                            AGCCGCCGCCTCAACCGCGCAATTCAGATTCTCTCCGGCAACATTCTCGCCGGAATCAGC
                                                                                                                                                                                                                                                                                                          113
                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                  /clone lib="Gm-C1065"
//clone lib="Gm-C1065"
//note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
//note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
//note="Tector: pBluescript was constructed from mRNA isolated germinating shoots of the cultivar Williams. The seeds germinating shoots of the cultivar Williams. The seeds were allowed to germinate for 24 hours prior to being cold stressed for 2 days at 4C. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBR). This library
                                                                                                                                                                                                                                                                                                        Shoemaker.
a 106 c
                                                                                                                                                                                                                                                                                                                                                              was constructed in the laboratory of Dr. Randy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:3847"
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/lab_host="DH10B"
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                                                                                                                                                                                           28.9%;
70.6%;
                                                                                                                                                                  Score 254.2; DB 12;
Pred. No. 9.2e-51;
0; Mismatches 143;
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301 For further i
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Lotus japonicus
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Eukaryota, Magnoliophyta, eudicotyledons, core eudicots, rosid,
Spermatophyta, Magnoliophyta, eudicotyledons, toteae, Lotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 585 bp mRNA linear EST 16-MAY-2003 LiNEST93h9r Lotus japonicus nodule library 5 and 7 week-old Lotus japonicus cDNA 5', mRNA sequence.
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1 (bases 1 to 585)
Colebatch,G., Freund,S., Trevaskis,B and Udvardi,M.
                                                                                                                                                                                                                                          Molecular Plant Nutrition
Max Planck Institute of Molecular Plant Physiology
Am Muehlenberg 1, 14476 Golm, Germany
Fax: 49 331 567 8250
                                                                                                                                                                                                                                                                                              Contact: Udvardi MK
                                                                                                                                                                                                                                                                                                                                                                                                                                        CB829088.1 GI:29969635
                                                                                                                                                                                                                              Email: udvardi@mpimp-golm.mpg.de
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              122
                                                                                                                                                                                        quality sequence stop:
                                                                                        /clone_lik
week-old"
              strain R7A."
124 c
                                   /note="Organ: Nodule; Vector: pSPORT1; Site_1: SalI; Site_2: NotI; The library was prepared using mRNA extracted from nodules of 5 and 7 week-old Lotus plants. Nodules were induced by, and contained Mesorhizobium
                                                                                                              /organism="Lotus japonicus"

/mol type="mRNA"
/cultivar="Gifu (B-129)"
/db xref="taxon:34305"
/dev_stage="5 and 7 week-old plants"
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Matches 373; Conserv
                                                                                                                                          AUTHORS
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BF003445
Department of Plant Biology
University of Minnesota
220 BioSci Center, 1445 Gortner Ave,
Tel: 612 624 2755
Fax: 612 625 1738
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                                                                                       ESTs from roots of Medicago truncatula with Sinorhizobium meliloti
                                                                                                                                                                                                     Medicago truncatula
Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                              EST
                                                               Contact: VandenBosch
                                                                          Unpublished
                                                                                                                  Fraser, C.M.
                                                                                                                                                                    Medicago
                                                                                                                                                                                                                                Medicago truncatula
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135 ACAACCTCCATCCTCTCTCCCTTATTCTCACCCTTTTTCCTCTCTCTCTCTGCGGCGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     VandenBosch,K., Endre,G., Hur,J., Moore,J., Beremand,P., Ellis,L., Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and
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Pred. No. 3.7e-50;
0; Mismatches 207;
St.
                                                                                                                                                                                                                                                                                                                                                    24 hours
Paul, MN 55108, USA
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                         340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      472 TCTTCAATTCCATAACCTCTCATTNCTATGGGAGGAAGTTNGAGTTTGATTNCATTGCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Texas A&M University name: T267255e TIGR sequence name: MTIAP62TK More information is available at: http://chrysie.tamu.edu/medicago Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: kvandenb@cbs.umn.edu
CAGCACATTCAGTTCTGGTTGAATCACCTTGCTG 801
                                                                                                GCCAAATTGGGCCTGATAGGGGAATGTTTGNGCTTGCTAGCTTTGCTGTTTGTNCCNATC
                                                                                                                                                        TTTACAACATCATGGGTATCGGTGTGTTCTGGACTTGGTTCCCTCTGCTATTGTCAGCCC
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                                                                                                                                                                                                                                                   ACTTGTACCTTCAAACATTTTTGCTCTTGTTTTCGCCATCACGAAATGTTCCTGATAGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="E. coli strain XLOLR"
/clone lib="KVI"
/clone lib="KVI"
/clone lib="KVI"
/clone lib="KVI"
/note="Vector: pBluescript SK -; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA insers were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Medicago truncatula"
/mol type="mRNA"
/mol type="mRNA"
/cultivar="genotype A17"
/db xref="taxon:3880"
/clone="pKV1-514"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tissue_type="Seedling roots"
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Pred. No. 4.5e-49;
0; Mismatches 220;
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> Search completed: December 31, 2003, Job time : 1345.13 secs 23:59:21

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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Match
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*
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US-08-831-579-1
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US-08-36-779-4
US-08-36-779-4
US-08-38-23-463-14
US-08-232-463-14
US-09-249-585A-4
US-09-249-585A-4
US-09-249-586A-11
US-08-658-136-2
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US-09-618-166-209
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US-09-728-323A-1
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US-08-954-441-1	US-08-323-170B-1	US-09-262-610-2	US-08-766-738-2	US-08-997-467-1	US-09-078-166-1	US-08-858-003-1	US-09-357-014-6	US-08-574-959A-6	US-09-357-014-8	US-08-574-959A-8	PCT-US95-12414-1	US-08-466-743-1	US-08-466-717-1	US-08-468-066-1	US-08-314-503A-1	US-08-466-603-1	US-09-244-796-17
Sequence 1, Appli	,-	Sequence 2, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 6, Appli	Sequence 6, Appli	Sequence 8, Appli	Sequence 8, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 17, Appl

## ALIGNMENTS

LINOLENIC ACID BY A #88er on #1.25  DB 4; Length 1702;	254-26 26, Application US/08934254 o. 6355861 INFORMATION: CANT: Thomas, Terry L.	Thomas, Terry L.  NVENTION: PRODUCTION OF GAMMA	OF INVENTION: DELTA 6-DESATURASE	R OF SEQUENCES:	DENCE ADDRESS:	cott, Murphy &	1: 400 Garden City Plaza	Garden City	New Yo	 530	; COMPUTER READABLE FORM:		SYSTEM:	PatentIn Release #1.0,	ATA:	; APPLICATION NUMBER: US/08/934,254	CLASSIFICATION: 435	,	. PROTOTRATION NIMBER: 10 807	REFERENCE/DOCKET NUMBER: 8383ZYXWVU	ä	; TELEPHONE: (516) 742-4343	; TELEFAX: (516) 742-4366	N FOR SEQ	RISTICS:	; LENGTH: 1702 base pairs	nucleio	; STRANDEDNESS: both	ă		; NAME/KEY: CDS		EY:	; LOCATION: 481406	US-08-934-254-26	Query Match 31.2%; Score 274.2;
1.25 LENIC ACID E		GAMMA	TRASE			Murphy	laza					ble	/MS-DOS	se #1.0, Version		8/934,254			R37	8383ZYXWVU	ON:	ω		6:						Ö						274.2;
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RESULT 2
US-08-831-570-1
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                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
APPLICANT: Munberg, Andrew N.
APPLICANT: Munberg, Andrew D.
APPLICANT: Beremand, Phillip D.
TITLE OF INVENTION: A SUMPLOWER ALBUMIN 5' REGULATORY REGION TITLE OF INVENTION: FOR THE MODIFICATION OF PLANT SEED LIPID TITLE OF INVENTION: COMPOSITION NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
                                                                                                                                                                                                                                                                                                1046 CTCCGGCGACACATACGTGGGCCCCCCCAAGG 1077
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NAME: DIGIGIO, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 1054;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEPAX: (516) 743-4366
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1684 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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NAME/KEY:
LOCATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/831,570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STRANDEDNESS: doub
TOPOLOGY: linear
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CITY: Garden City
STATE: New York
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                                                               AACCATAATGCACATCACATTGCCTGTAATAGCCTTGAATATGACCCTGATTTACAATAT
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Pred. No. 1.1e-53;
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                                                                   ; NAME/KEY:
; LOCATION:
US-08-831-575-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08831575
Patent No. 5977436
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
APPLICANT: Li, Zhongsen
TITLE OF INVENTION: AN OLEOSIN 5'REGULATORY REGION FOR THE
TITLE OF INVENTION: MODIFICATION OF PLANT SEED LIPID COMPOSE
      Query Match 27.9%;
Best Local Similarity 57.7%;
Matches 497; Conservative
                                                                                                                                                                                                        TELEPAX: (516) 742-4366 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
                                                                                                                                                                                                                                                                                  CLASSIFICATION: 800
ATTORNBY/AGENT INFORMATION:
NAME: DIGIGIO: Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 100
                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDLIM TYPE: Flopby disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                     TELEPHONE: (516) 742-4343
                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 09-APP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                           LENGTH:
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                                                                                                                                                                                        1684 base pairs
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                                                                                                                             DNA (genomic)
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    Score 245.2; DB 2;
Pred. No. 1.1e-53;
0; Mismatches 359;
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                                                                                                                                                                                                                                                                                                                                                                                                              Version #1.30
                                 Length 1684;
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                                                GENERAL INFORMATION:
APPLICANT: Thomas,
APPLICANT: Reddy,
APPLICANT: Nuccio,
                                                                                                             Sequence 4,
Patent No. 5
                    APPLICANT:
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T: Thomas, Terry L.
T: Reddy, Avutu S.
T: Nuccio, Michael
T: Freyssinet, Georges L.
T: Nunberg, Andrew N.
INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID
                                                                                                                           Application US/08366779
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1685 base pairs
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ADDRESSEE: Scully, Scott, Mury
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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ATGCCGGTCTTTGCAGTTTCGTCGCGGTTCTTCAATTCCATAACCTCTCATTNCTATGGG
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57.7%;
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Pred. No. 1.1e-53;
0; Mismatches 359;
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US-08-789-936-4
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Patent No. 9
                                           TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO.
SEQUENCE CHARACTERISTICS:
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                                                                                               NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 8383
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID TITLE OF INVENTION: DELTA 6-DESATURASE NUMBER OF SEQUENCES: 25
                                                                                                                                                                                            FILING DATE: 30-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CTTY: Garden City
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TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 28-JA
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                                   ENGTH:
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400 Garden City Plaza
                                 1685 base pairs
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RESULT 6
US-08-934-254-4
; Sequence 4, Application US/08934254
; Patent No. 6355861
; GENERAL INFORMATION:
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                                                                                                                                  ATTGGATATCTCTTGTGNCCCT
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Pred. No. 1.1e-53;
0; Mismatches 359;
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Best Local (
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEPAX: (516) 742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Thomas, Terry L.
TITLE OF INVENTION: PRODUCT
TITLE OF INVENTION: DELTA 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
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TOPOLOGY: li
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Pred. No. 1.1e-53;
0; Mismatches 359;
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                                                                                                              APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991
ATTORNEY/ACENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMTELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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   LENGTH: /___
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PPLICANT: FALKNER, F. G.
TILE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                 TELEFAX:
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 STRANDEDNESS:
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1800 Diagonal Road, Suite 500
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APPLICANT: HOTICK, Robert
TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SEI
FILE REFERENCE: 0867/0D905
CURRENT APPLICATION NUMBER: US/09/249,585A
CURRENT FILLING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 1926
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                                                                                                                                                                                                                               ; ORGANISM: Epstein Barr Virus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1926)
; OTHER INFORMATION: template strand of EBNA-1 DNA
US-09-249-585A-4
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                                                                                                                                                                 Matches 183;
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Best Local (
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                                                                                                                                                                   Conservative
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                                                                                                                                                                               8.2%;
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                                                                                                                                                                             Score 72; DB 4;
Pred. No. 3.3e-09;
                                                                                                                                                                   Mismatches 185;
                                                                                                                                                                                                  DB 4; Length 1926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SELECTION OF EPISOMES
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RESULT 9
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; ORGANISM: EBNA
US-09-130-114-2
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CURRENT FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:

APPLICANT: Horlick, Robert A.

APPLICANT: Damaj, Bassam B.

APPLICANT: Robbins, Alan K.

TITLE OF INVENTION: Eukaryotic Cells Stably Expressing
TITLE OF INVENTION: From Multiple Transfected Episomes

FILE REFERENCE: 0867/1D903US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09130114
Patent No. 5976807
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1931
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Pred. No. 3.3e-09;
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US-08-658-136-2
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                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 53526 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2 Patent No.
                                                                                                                                                                                                                                                   Matches 118;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,136
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TOPOLOGY: lin
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: GETELECOMMUNICATION INFORMATION:
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NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,
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CITY: FRAMINGHAM
STATE: MASSACHUSI
                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 01701
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DACKOWSKI, WILLIAM
TOWTHO, GREGORY
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BURN, TIMOTHY C
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                                                                                                                                                                                                                                                                                                                                 DNA (genomic)
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53.4%;
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                                                                                                                                                                                                                                                                  Score 56.2; DB 3;
Pred. No. 0.00012;
                                                                                                                                                                                                                                                    Mismatches 103;
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US-08-658-136-1 ; Sequence 1, Application US/08658136 ; Patent No. 6071717

GENERAL INFORMATION:

RESULT 11

KLINGER, KATHERINE

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US-08-458-568A-11
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                                                                                                                                                                 RESULT 12
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; MOLECULE TYPE:
US-08-658-136-1
                                                                                             Sequence 11, Application US/08458568A
Patent No. 5821339
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 508-872-5415
INFORMATION FOR SEQ ID NO: 1:
                           APPLICANT: Schaffer, Priscilla A.
APPLICANT: Yell, Lily
TITLE OF INVENTION: Compositions
TITLE OF INVENTION: Infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: LASSEN, ELIZABETH REGISTRATION NUMBER: 31,845. REFERENCE/DOCKET NUMBER: GETELECOMMUNICATION INFORMATION: TELEPHONE: 508-872-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: GENZYME CORPORATION
STREET: ONE MOUNTAIN ROAD
CORRESPONDENCE ADDRESS:
               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                 34814
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                                              Compositions and Methods for Treatment of Herpesvirus
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Pred. No. 0.00012;
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                                                                                                                                             RESULT 13
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                                                                          Sequence 1, Application Patent No. 5968809
GENERAL INFORMATION:
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Best Local Similarity 52.2%;
Matches 121; Conservative
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: 1116-0
MOLECULE TYPE: D'
HYPOTHETICAL: NC
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ORGANISM: Herpes simplex virus
STRAIN: Herpes Simplex Virus Type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Leary Ph.D., Kathryn R.
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: DFCI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                APPLICANT:
                                APPLICANT:
                                                 APPLICANT:
                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: WordPerfect CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5821339ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 12001 base pairs
TYPE: nucleic acid
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 02-JU
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TELEFAX: (215) 568-3439
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                                                                                                                                                                                           CTGTCTGCGGCGTCCTCTTCCGACAGCACTTTCGTGCACGTGCTTTCCGC 232
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MURKERJI, PRADIP
HUANG, YUNG-SHENG
THURMOND, JENNIFER
CHAUDHARY, SUNITA
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                                                              KNUTZON, DEBORAH
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Pred. No. 0.00021;
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OF INVENTION:

METHODS AND COMPOSITIONS FOR SYNTHESIS OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS

NUMBER OF SEQUENCES:

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                                                                                                                                                                                                           sequence 1, Application US/08834033A Patent No. 6075183
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Best Local Similarity 51.0%;
Matches 125; Conservative
                                                                                                                                                                                         GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 1:
                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,655
FILING DATE: 11-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1617 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.124.00US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 328-4400
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ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
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ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
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                                                                                                                                              KNUTZON, DEBORAH
MUKERJI, PRADIP
                                                                                                                        HUANG, YUNG-SHENG
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Pred. No. 0.00023;
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US-09-363-574-1
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                                                                                                                                                                                                                                      Sequence 1, Application US/09363574 Patent No. 6136574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 51.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834
FILING DATE: 11-APR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REGERENCE/DOCKET NUMBER: CGAE
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEPAX: (415) 433-8716
                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: KNUTZO
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LENGTH: 1617 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic
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TELEX: N/A
INFORMATION FOR SEQ ID NO:
                                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
STREET: 2001 FERRY BUILDING
                                                             TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS NUMBER OF SEQUENCES: 18
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                                                                                                                    MURKERJI, PRADIP
HUANG, YUNG-SHENG
THURMOND, JENNIFER
CHAUDHARY, SUNITA
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                 KNUTZON, DEBORAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA (genomic)
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Pred. No. 0.00023;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 120; Indels
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; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1617 base pairs
; TYPE: nucleic acid
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-09-363-574-1
Search completed: January 1, 2004, 00:05:26 Job time: 45.6671 secs
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6.0%; Score 53; DB 3; Length 1617;
Best Local Similarity 51.0%; Pred. No. 0.00023;
Matches 125; Conservative 0; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,574
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
AREGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-202 USA
TELEPONE: (415) 433-4150
TELEPAN: N/A
TELEPAN: (415) 433-8716
                                                                                                                                                                                                                                                                                                                          330 CAGATTCTCTCCGGCAACATTCTCGCCGGAATCAGCATCGGCTGGAGGGAAGTGGAACCAC 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           518 ACCCTCGCCAACGTGCTCTCGGCTGCGCCTTTTGGGTCTGTTCTGGCAGCAGTGCGGATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               210 ACTITICGTGCACGTGCTTTCCGCTGCATTGATAGGCCTTTCTCTGGATTCAGAGCCGGCTGG
                                                                                                 758 CTGTT 762
                                                                                                                                                                                                                                             390 AACGCCCACCACATTGCATGCAACAGCCTCGACTATGACCCTGATCTGCAGCACATGCCG 449
                                                                                                                                                                                                                                                                                              638 GGCGCCTTCTTGGGAGGTGTCTGCCAGGGCTTCTCGTCGTCGTGGAAGGACAAGCAC
                                                                                                                                                                                                                                                                                                                                                                                             578 TTGGCTCACGACTTTTTGCATCACCAGGTCTTCCAGGACCGTTTCTGGGGTGATCTTTTC 637
                                                                                                                                                                                                                                                                                                                                                                                                                           270 ATAGGCCACGACTCCGGCCATTACAACGTGATGCTCAGCCGCGCGCCTCAACCGCGCAATT 329
                                                                                                                                               450 GTCTT 454
                                                                                                                                                                                             698 AACACTCACCACGCCGCCCCAACGTCCACGGCGAGGATCCCCGACATTGACACCCCACCCT 757
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Database :
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OM nucleic - nucleic search, using sw model
                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                December 31, 2003, 21:04:45; Search time 219.488 Seconds (without alignments)
13877.414 Million cell updates/sec
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Gapop 10.0 , Gapext 1.0
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880
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Published Applications NA:*
1: /cgn2_6/ptodata///pubpna/US07
2: /cgn2_6/ptodata//2/pubpna/US06_
3: /cgn2_6/ptodata//2/pubpna/US06_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                             /Ggn2_6/ptodata/2/pubpna/US09E_PUBCOMB.seq:*
/Ggn2_6/ptodata/2/pubpna/US09E_PUBCOMB.seq:*
/Ggn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
/Ggn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
/Ggn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
/Ggn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
/Ggn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
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/Ggn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
/Ggn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                           6/ptodata/2/pubpna/US09A
SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEW PUB. seq: *
PUBCOMB. seq: *
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S_PUBCOMB. seq: *
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15	C 14	c 13	c 12	11	c 10	9	8	7	თ	տ	4	u	N	1	Result No.
65.6	65.6	67.6	67.6	72.2	74.2	74.2	93	93	111.2	111.6	132.4	244.2	245.2	274.2	Score
7.5	7.5	7.7	7.7	8.2	8.4	8.4	10.6	10.6	12.6	12.7	15.0	27.7	27.9	31.2	Query
720	720	520	520	1059	9025608	1095	265	265	476	1098	263	1350	1685	1702	Query Match Length DB
1.4 4	14	15	15	15	11	15	12	9	9	12	10	10	14	14	
US-10-101-487-76	US-10-101-487-74	US-10-184-634-332	US-10-184-644-332	US-10-156-761-1580	5 US-10-156-761-1	US-10-156-761-2285	US-09-923-876-5116	US-09-923-876-5116	US-09-770-444-39	US-10-369-493-27824	US-09-878-574-9255	US-09-938-842A-558	US-10-029-756-4	US-10-029-756-26	ID
Sequence 76, Appl	Sequence 74, Appl	Sequence 332, App	Sequence 332, App	Sequence 1580, Ap	Sequence 1, Appli	Sequence 2285, Ap	Sequence 5116, Ap	Sequence 5116, Ap	Sequence 39, Appl	Sequence 27824, A	Sequence 9255, Ap	Sequence 558, App	Sequence 4, Appli	Sequence 26, Appl	Description

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53.4 53.4	53.4	53.4	54	54.2	54.6	54.6	54.6	54.6	54.8	55	55	55	55.4	56.2	56.6	56.6	56.6	56.6	56.6	58	58.2	58.4	58.4	58.6	58.6	59.4	59.4	60
6.1	6.1	6.1	6.1	6.2								6.2		6.4	6.4	6.4	6.4	6.4	6.4	6.6	6.6	6.6	6.6	6.7	6.7		6.8	6.8
42619 250000	31857	23088	437	154817	554	554	530	522	267	1362	1362	1362	1380	53522	5785	907	895	895	889	1687	895	1223197	1223197	9025608	1128	68233	3809	287
13 13	12	<u>1</u>	10	12	14	14	14	14	9	13	13	13	10	11	16	16	16	16	16	15	16	14	13	15	15	13	14	10
US-10-225-810-9 US-10-225-810-26	US-10-292-798-683	US-10-017-161-785	US-09-960-352-12835	US-10-085-117-334	US-10-101-487-106	US-10-101-487-69	US-10-101-487-73	US-10-101-487-71	US-09-864-761-27984	US-10-431-952-13	US-10-054-534B-13	US-09-769-863-13	US-09-967-477B-7	US-09-904-968A-1	US-10-273-334-1	US-10-273-334-6	US-10-273-334-23	US-10-273-334-21	US-10-273-334-3	US-10-163-198-40	US-10-273-334-15	US-10-027-632-179264	US-10-027-632-179264	US-10-156-761-1	US-10-156-761-2338	US-10-034-650-31	US-10-001-870-68	US-09-878-574-3260
Sequence 9, Appli Sequence 26, Appl	Sequence 683, App	Sequence 785, App	Sequence 12835, A	334,	106,				Sequence 27984, A	13,	Sequence 13, Appl	Sequence 13, Appl	7,	Sequence 1, Appli	Sequence 1, Appli	Sequence 6, Appli	Sequence 23, Appl	Sequence 21, Appl	Sequence 3, Appli	Sequence 40, Appl	Sequence 15, Appl	Sequence 179264,	Sequence 179264,	Sequence 1, Appli	Sequence 2338, Ap	•	Sequence 68, Appl	Sequence 3260, Ap

## ALIGNMENTS

	ZS.
STATE: New York  COUNTRY: United States  ZIP; 11530  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25  CURRENT APPLICATION NUMBER: US/10/029,756 FILING DATE: 21-Dec-2001 CLASSIFICATION NUMBER: UB/934,254 FILING DATE: -Unknown> PRIOR APPLICATION NUMBER: 08/934,254 FILING DATE: -Unknown> ATTORNEY/AGENT INFORMATION: NAME: Presser, Leopold REGISTRATION NUMBER: 19,827 REPERENCE/DOCKET NUMBER: 8383ZYXWVU TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: THE REPRESENTION: THE REPRESENT INFORMATION: THE REPRES	RESULT 1  US-10-029-756-26  ; Sequence 26, Application US/10029756  ; Publication No. US20020108147A1  ; GENERAL INFORMATION:  APPLICANT: Thomas, Terry L.  TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A  ; NUMBER OF SEQUENCES: 27  CORRESPONDENCE ADDRESS:  ; ADDRESSEE: Scully, Scott, Murphy & Presser  STREET: 400 Garden City Plaza  CITY: Garden City

LENGTH: 1702 base pairs

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US-10-029-756-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 48..1406
SEQUENCE DESCRIPTION: SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
1046 CTCCGGCGACACATACGTGGGCCCCCCCAAGG 1077
                                                                                                                                                                927
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                                                                                                                                                                                                                                                                                    819
                                                                                                                                                                                                                                                                                                                              807
                                                                                                                                                                                                                                                                                                                                                                                                                                        498 TATGGGAGGAAGTTNGAGTTTGATTNCATTGCTANGTTCTTGATCTGCTACCAGCACTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      438 CAGCACATGCCGGTCTTTTGCAGTTTCGTCGCGGTTCTTCAATTTCCATAACCTCTCATTNC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        387
                                      797
                                                                                                                                                                                                                                                                                                                                                                  558 ACTITITACCCCGGTAATGTGTTTGCCAGGGTCAACTTGTATCTGCAGACAATTCTGCTA 617
                                                                                                                                                                                                                                                                                                                                                                                                             747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       567 AACAGAATCACGCAACTCATAGCAGGCAACATCCTAACCGGAATCAGCATCGCGTGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       447 GCGTCGGAGTCCGGAGTTCACATGCTCTGCGGCGCACTGCTGGGCTTTGCTGTGGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             198 TTCTCCGACAGCACTTTCGTGCACGTGCTTTCCGCTGCATTGATAGGCTTTCTCTGGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            327 TACCGGAGGCTTTTGAACGAGATGTCGCGGTCCGGGATCTTCGAGAAGAAGGGCCACCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  267 CCGCTCTTCACCGGCTACTACTACCTCAAGGACTTCGAAGTGTCGGAGATCTCCAAGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78 TACCGCAAGCTCTTCTCCGACCTCTCCGCGCTCAACCTCTTCAACCGCAAGGGCCACACA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTGTTTTCGAGGNGAAAAGTGCAGGATAGAGCT-TGAACATAATGGGGATCCTTGTGTTT
                                      TGCTGAAAATTTATATGNCGGGCACNANTGGG 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                    GNGCTTGCTAGCTTTGCTGTTTGTNCCNATCCAGCACATTCAGTTCTGGTTGAATCACCT
                                                                                                                                                          TGGACGTGGTTCCCCGCTCTTCGTATCTTGTCTCCCGAACTGGCCTGAACGGTTCGGGTTC
                                                                                                                                                                                                    TGGACTTGGTTCCTCTTTTAGTGNCTTGCCTGCCAAATTGGGCCTGATAGGGGNATGTTT
                                                                                                                                                                                                                                            CTCCTCACCAGGCGCGACGTCCCTGACCGCGCTCTAAACTTAATGGGTATCGCGGTTTTC
                                                                                                                                                                                                                                                                                                                            ACCTACTACCCGGTCATGATCTTCGGCCGAGTCAACCTCTTCATCCAGACCTTTTTATTG
                                                                                                                                                                                                                                                                                                                                                                                                             TATGGCCGAGTCCTGAAATTCGACGAAGTGGCACGGTTCCTAGTCAGCTACCAGCACTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGCACATCCCCGTATTCGCCGTCTCCACCCGACTCTTCAACTCCATCACCTCGGTCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGTGGACCCACAACGCCCACCACCTCGCCTGCAACAGCCTCGACTACGACCCCGACCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGTGGAACCACAACGCCCACACATTGCATGCAACAGCCTCGACTATGACCCTGATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACCGCGCAATTCAGATTCTCTCCGGCAACATTCTCGCCGGAATCAGCATCGGCTGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAAGCCGCGTATGTGGGCCATGACTCCGGCCATTACCAGGTGATGCCAACCCGTGGATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGAGCGGCTGGATAGGCCACGACTCCGGCCATTACAACGTGATGCTCAGCCGCCGCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATCATGTGGACGTTCGTCGGCGTTGCGGTCATGATGGCGGCAATCGTCTACGGCGTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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48..1406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>,</u>
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Pred. No. 3.2e-74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 326; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 497; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDICATION.

GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID
DELTA 6-DESATURASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 230 901 SANS UR INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1685 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/934,254
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/10/029,756
FILING DATE: 21-Dec-2001
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: Scully, Scott, Murj
STREET: 400 Garden City Plaza
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                                                                                                                                                                                                  386 GCAACTTTGTGCTTTATAGCAATGCTGTTTGCTATGAGTGTTTATGGGGTTTTGTTTTGT 445
                                                                                                                                                                                                                                                                                 326 AAGCTTGTGTTTGAGTTTTCTAAAATGGGTTTGTATGACAAAAAAGGTCATATTATGTTT 385
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GCAATTCAGATTCTCTCCGGCAACATTCTCGCCGGAATCAGCATCGGCTGGTGGAAGTGG 383
                                                                                                                                                                                                                                          GGCTGGATAGGCCACGACTCCGGCCATTACAACGTGATGCTCAGCCGCCGCCCCAACCGC
                                                                                                                       GAGGGTGTTTTGGTACATTTGTTTTCTGGGTGTTTTGATGGGGTTTCTTTGGATTCAGAGT
                                                                                                                                         GACAGCACTTTCGTGCACGTGCTTTCCGCTGCATTGATAGGCTTTCTCTGGATTCAGAGC
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REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 8383ZYXWVU
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STATE: New York
                                       GGTTGGATTGGACATGATGCTGGGCATTATATGGTAGTGTCTGATTCAAGGCTTAATAAG
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Pred. No. 3.2e-65;
0; Mismatches 359;
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APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILLING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 558
LENGTH: 1350
TYPE: DNA
ORGANISM: Arabidopsis thaliana
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US-09-938-842A-558
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                                                                            Query Match
Best Local Similarity
                                                            Matches
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APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
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   1 CCGCCTCCCTCCCCCCGCCTTCTCCACCTCCCACCGTCTTTCCGACCACACCGTCT 60
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                                                                            27.7%;
                                                         Score 244.2; DB 10;
Pred. No. 5.9e-65;
0; Mismatches 349;
                                                                                             Length 1350;
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APPLICANT: Byrun, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/90/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 9255
LENGTH: 263
                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCGGAATCTTAGTCTTCTGGACTTGGTTCCCACTCTTAGTCTCATGTCTACCAAACTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCGCCGCCTCCTCCGACTACCGCAAGCTCTTCTCCGACCTCTCCGCGCTCAACCTCTTCA 120
                                                                                                                                                                                                                                                                                                                                                                           TTCACGCTTAACCATTTCGCTGCTGATGTCTACGTTGGTC 1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGCAGACAATTCTGCTATTGTTTTCGAGGNGAAAAGTGCAGGATAGAGC-TTGAACATAA
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; ORGANISM: Glycine n
; OTHER INFORMATION:
US-09-878-574-9255
                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Neurospora crassa
US-10-369-493-27824
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52652)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/0/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 27824
LENGTH: 1098
                                                                                                                                                                                                                                                                                                            Hest Local Similarity 53.2%;
Matches 231; Conservarion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 27824, Application US/10369493 Publication No. US20030233675A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 183;
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Best Local Similarity
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                                                                                                                                                                                                     227 TTCCGCTGCATTGATAGGCTTTCTCTGGATTCAGAGCGGCTGGATAGGCCACGACTCCGG
                                                                                                                                                                                                                                                                                      167 CCTTTTTCCTCTCTCTGTCTGCGGCGTCCTCTTCTCCGACAGCACTTTCGTGCACGTGCT 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          375 TGGAAGTGGAACCACAACGCCCACCACATTGCATGCAACAGCCTCGACTATGACCCTGAT
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                                                                             ACACATGGGCATCACGCACCATTTCCATGTCGATACTGTCATCGGCCATCATCATTGCCGA
                                                                                                                                                                TAGTGCGTTCTGGCTCTTTCTGGCACCAGCTAGTCTTCACTGCCCATGACGCCGG
                                                                                                                      CCATTACAACGTGATGCTCAGCCGCCGCCTCAACCGCGCAATTCAGATTCTCTCCGGCAA
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CTTCATCGGTGGTCTCAGTCTAGGTTGGTGGAAGCGAACCACAACGTTCACCATATCAT
                                    CATTCTCGCCGGAATCAGCATCGGCTGGTGGAAGTGGAACCACAACGCCCACACATTGC 406
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Pred. No. 1.3e-30;
0; Mismatches 70;
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                                                                                                                                                                                                                                                                                                                           Score 111.6; DB 12; Length Pred. No. 8.2e-24; O; Mismatches 203; Indels
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                                                                                                                                                                                                                                                                                                                                                                    Length 1098;
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TYPE: DNA
CAGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(476)
OTHER INFORMATION: n = A,T,C or G
US-09-770-444-39
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                                                                                                                                 Query Match
Best Local Simi:
Matches 221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 39, Application US/09770444
Patent No. US20020023280A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version SEQ ID NO 39
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2027 (PARA-016PRV)
CURRENT APPLICATION NUMBER: US/09/770,444
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,502
PRIOR FILING DATE: 2000-01-27
                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 999
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                                                                                                                                                                                                                                                                                                                       LENGTH: 476
                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      467 GCGGTTCTTCAATTCCATAACCTCTCATTNCTATGGGAAGGAAGTTNGAGTTTGATTNCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              407 ATGCAACAGCCTCGACTATGACCCTGATCTGCAGCACATGCCGGTCTTTTGCAGTTTTCGTC
                               61 CCGCCGCCTCCTCCGACTACCGCAAGCTCTTCTCCGACCTCTCCGCGCTCAACCTCTTCA 120
                                                                  70
                                                                                                  GGTCAACTTGTATC 600
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Kricker, Maja
Slader, Ted
Davis, Keith R.
Allen, Keith
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 CCGAAGTCTCACGCGATTACCGTCGTATGGCTGCCGAGTTTCGTAAACTCGGTCTCTTCG
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Hamilton, Carol M.
Price, Jennifer L.
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Woessner, Jeffrey P.
Haas, William David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matthew,
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Rameaka, Joshua G.
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                                                                                                                                     Conservative
                                                                                                                                                   12.6%;
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                                                                                                                                   0; Mismatches 185;
                                                                                                                                                   Score 111.2; DB 9
Pred. No. 6.9e-24;
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                                                                                                                                                                    DB 9;
                                                                                                                                                                    Length 476;
                                                                                                                                     Indels
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                                                                                                                                     Gaps
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Best Local (
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SOFTWARE: PERL Program
SEQ ID NO 5116
LENGTH: 265
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Patent No. US20020013958A1
GENERAL INFORMATION:
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CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/298,329
PRIOR FILING DATE: 1999-04-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/085,331 PRIOR FILING DATE: 1998-05-05
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TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED
FILE REFERENCE: PL-0012-1 CON
                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20020013958A1 700456385H1
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Local Similarity 60.7%;
es 147; Conservation
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i, Laura Y. (Ito)
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Pred. No. 2.3e-18;
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APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Kamigaki, Laura Y. (Ito)
APPLICANT: Kamigaki, Laura Y. (Ito)
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: PL-0012-1 CON
CURRENT APPLICATION UNUMBER: US/09/923,876
CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/298,329
PRIOR FILING DATE: 1999-04-21
PRIOR FILING DATE: 1999-04-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 6332
SOFTWARE: PERL PROGRAM
SEQ ID NO 5116
LENGTH: 265
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                               Sequence 2285, Application US/10156761
Publication No. US20030119018A1
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                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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Best Local 8
                                                                                                APPLICANT: SAKAKI, YOSHYUKI
APPLICANT: SAKAKI, YOSHYUKI
APPLICANT: HATTORI, MASHYUKI
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-272697 PRIOR FILING DATE: 2001-08-02 NUMBER OF SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                       APPLICANT: OMURA, SATOSHI APPLICANT: IKEDA, HARUO
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                                                             PRIOR APPLICATION NUMBER: JP 2001-204089 PRIOR FILING DATE: 2001-05-30
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Local Similarity 60.7%;
les 147; Conservative
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HORIKAWA, HIROSHI
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Pred. No. 2.3e-18;
0; Mismatches 95
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GENERAL INFORMATION:

APPLICANT: OMURA, SATOSHI

APPLICANT: ISHIKAWA, JUN

APPLICANT: ISHIKAWA, HIROSHI

APPLICANT: HORIKAWA, HIROSHI

APPLICANT: SHIBA, TADAYGSHI

APPLICANT: SHIBA, TADAYGSHI

APPLICANT: HATTORI, MASAHIRA

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

FILE REFERENCE: 249-262

CURRENT APPLICATION NUMBER: US/10/156,761

CURRENT FILING DATE: 2002-05-29

PRIOR APPLICATION NUMBER: JP 2001-204089

PRIOR APPLICATION NUMBER: JP 2001-272697

PRIOR APPLICATION NUMBER: JP 2001-272697

PRIOR APPLICATION NUMBER: JP 2001-272697
; NAME/KEY: misc feature
, LOCATION: (4187715)
; OTHER INFORMATION: a, t, c,
US-10-156-761-1
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; NAME/KEY: CDS
; LOCATION: (1)..(1095)
US-10-156-761-2285
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LENGTH: 1095
                                                                                                                                NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 1
LENGTH: 9025608
TYPE: DNA
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Publication No. US20030119018A1
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Best Local Similarity
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                                                                                       FEATURE:
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Pred. No. 3.
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3.4e-12;
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
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                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 1580
LENGTH: 1059
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Best Local S
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Best Local Similarity
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NAME/KEY: CDS
LOCATION: (1).
                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Streptomyces
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249 CTCTGGATTCAGAGCGGCTGGATAGGCCACGACTCCGGCCATTACAACGTGATGCTCAGC 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              419 CGACTATGACCCTGA
                                                                                          189 GGCGTCCTCTTCTCCGACAGCACTTTCGTGCACGTGCTTTCCGCTGCATTGATAGGCTTT
                                                           184 GECETÉCTECTEATGESTÁCETÉCTGETGÉSTECTÉCTECTÉCECEGÉTÉCTECÉCESTE 243
                                                                                                                                       137;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATGGGCCTGTGCGGCGGTCAGTCCGCCTTCATGTGGCACGACGCCGGCCACAAGGCCCAT 2800867
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                                                                                                                                       Score 72.2; DB 15;
Pred. No. 1.4e-11;
0; Mismatches 108;
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Pred. No. 4.8e-10;
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US-10-184-644-332/c
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; SEQ ID NO 332
; LENGTH: 520
; TYPE: PRT
; ORGANISM: Homo Sapien
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: 9343081227
CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT FILING DATE: 2002-06-28
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                                                                                                                                                                                                                                                                  CATC.SC.SC..CTYC.SCTSC..CMTC.DCBTC..C.BC..C..C.HCMTC..CT.C..
                                                               C.KCKTCMDC..C.TC..CM.Y.KC.N.A.NHBY...D.DSBYBWA..T..B..YSTC.T
                                                                                              AGGCTTTCTCTGGATTCAGAGCGGCTGGATAGGCCACGACTCCGGCCATTACAACGTGAT 301
                                                                                                                                   C..C.ACATC.MC.TC..C..CT.CMBC.
                                                                                                                                                                   TGTCTGCGGCGTCCTCTTCTCCGACAGCACTTTCGTGCACGTGCTTTCCGCTGCATTGAT 241
                                                                                                                                                                                                   C.YC.HCMSC.TC..CKBCTHCMKCYHCMSC..C.HCM.CMACA.CM.C..CCHCMSCM.
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                                                                                                                                                                                                                                                                                                     CGCCGCCTCCTCCGACTACCGCAAGCTCTTCTCCGACCTCTCCGCGCTCAACCTCTTCAA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCCGA 428
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                                                                                                                                                                                                                                                                                                                                     CSSCMBC.HCM.CT.C.TCM.CT.C.SC..CMBCT.C.BCS.CMYC..C..CAHCMSCM.
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.D.C.DTS...S.S.SH 90
                             GCTCAGCCGCCGCCTCA 318
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Gurney, Austin L.
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Goddard, Audrey
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US-10-101-487-74/c
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                                                                                                                                                             Sequence 74, Application US/10101487
Publication No. US20020169125A1
GENERAL INFORMATION:
APPLICANT: LEUNG, DAVID W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 332
LENGTH: 520
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Best Local Similarity
               APPLICANT: BERGMAN, PHILIP A.
APPLICANT: LOPQUIST, ALLAN
APPLICANT: PIETZ, GREGORY B.
APPLICANT: TOMPKINS, CHRISTOPHER K.
APPLICANT: TOMPKINS, CHRISTOPHER K.
APPLICANT: WAGGONER JR., DAVID W.
TITLE OF INVENTION: RECOMBINANT PRODUCTION
TITLE OF INVENTION: THERMED
FILE REFERENCE: 077319/0329
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CURRENT FILING DATE: 2002-06-28
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CURRENT APPLICATION NUMBER: US/10/101,487
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Godowski, Paul
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APPLICANT: LEUNG, DAVID W.
APPLICANT: BERGMAN, PHILIP A.
APPLICANT: LOFQUIST, ALAN
APPLICANT: LOFQUIST, ALAN
APPLICANT: TOMPKINS, CHRISTOPHER K.
APPLICANT: TOMPKINS, CHRISTOPHER K.
APPLICANT: WAGGONER JR., DAVID W.
TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 077319/0329
CURRENT APPLICATION NUMBER: US/10/101,487
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 60/277,705
PRIOR APPLICATION NUMBER: 60/277,705
PRIOR APPLICATION NUMBER: 60/277,705
PRIOR FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 116
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 76
LENGTH: 720
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PRIOR APPLICATION NUMBER: 60/277,705
PRIOR FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 116
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 74
LENGTH: 720
TYPE: DNA
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US-10-101-487-74
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Best Local Similarity
Matches 179; Conserv
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Search completed: January 1, 2004, 05:19:32 Job time: 238.488 secs

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Result
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Maximum DB seq length: 2000000000
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8. /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:
8. /SIDS1/gcgdata/
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                                                                                                                                                                                                                                                                                                                    Length
                                                                                                  4449
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         AAY71553
AAY71554
AAG29290
AAG07392
AAY51333
AAG07391
AAG53861
AAY51334
AAU79851
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Soybean sphingolip
Soybean sphingolip
Arabidopsis thalia
Arabidopsis thalia
B. napus sldl prot
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
A. thaliana sldl p
                                                                                                                                                                                                                                                                                                              Description
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## ALIGNMENTS

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RESULT 1
AAY71553
ID AAY71553
ID AAY71553
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AC AAY7
AC AAY7
AC AAY7
CX Soyk
XW Soyk
XW Soyk
XW Crar
XX Glyc
FT Misc
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FT Misc
                                                                                                                      /label= Unknown
/note= "Encoded by TNC"
Misc-difference 166
  Misc-difference
                                                                                                                                                                                                  Glycine max.
                                 Misc-difference
                                                                 Misc-difference 173
                                                                                                   Misc-difference 170
                                                                                                                                                                                                                      Soybean; sphingolipid desaturase; membrane-bound desaturase; transgenic plant; fatty acid.
                                                                                                                                                                                                                                                        Soybean sphingolipid desaturase #1.
                                                                                                                                                                                                                                                                              12-OCT-2000
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/note= "Encoded by NGA" 213
                                  206
                                                                                                           /label= Unknown
/note= "Encoded by TTN"
                                                                                                                                                                            Location/Qualifiers
                                           note= "Encoded
                                                                            label= Unknown
note= "Encoded
                                                      .abel= Unknown
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RESULT 2
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Best Local
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The present sequence is useful for producing transgenic plants having altered levels of sphingolipid desaturase which in turn would alter the fatty acid composition. The enzyme is also useful for producing polyclonal or monoclonal antibodies. The polymucleotide is useful as primer or probe for screening CDNA libraries to
                                                                                                                                                                                                                                                                                                                                                                                                                  Polynucleotide encoding delta-6 desaturase enzyme useful for producing transgenic plants and for producing antibodies specific to which is useful for screening cDNA expression libraries -
                                                                                                                                                                                                                                                                                                                                                                                                                 transgenic plants and useful for screening c
12-OCT-2000
                 AAY71554;
                                  AAY71554 standard;
                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                         FTFYPVMCVARVNLYLQTILLLFSRXKVQDRALNIMGILVFWTWFLFLLALLFVPIQHIQ
                                                                                                                                                 WKWNHNAHHIACNSLDYDPDLQHMPVFAVSSRFFNSITSHXYGRKXEFDXIAXFLICYQH
                                                                                                                                                             WKWNHNAHHIACNSLDYDPDLQHMPVFAVSSRFFNSITSHXYGRKXEFDXIAXFLICYQH
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                                                                                                                                                                                                LFSDSTFVHVLSAALIGFLWIQSGWIGHDSGHYNVMLSRRLNRAIQILSGNILAGISIGW
                                                                             FWLNHLAENLYXG 253
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TGATAGGGGNATGTTTGNGC"
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100.0%; Pr
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Pred. No. 3.7e-137;
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17-OCT-2000 AAG29290; AAG29290

(first

entry)

standard;

Protein;

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RESULT 3
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polynucleotide encoding delta-6 desaturase enzyme useful transgenic plants and for producing antibodies specific useful for screening cDNA expression libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-DEC-1998;
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                                                                                                                                                                                                                              WKWNHNAHHIACNSLDYDPDLQHMPVFAVSSRFFNSITSHXYGRKXEFDXIAXFLICYQH
                                                   FTFYPVMCVARVNLYLQTILLLFSRXKVQDRALNIMGILVFWTWF-----
                                                                                                                                                                                                       WKWTHNAHHIACNSLDHDPDLQHMPVFAVSSRFFNSITSHFYGRKLEFDFIARFLICYQH
                                                                                                                                                                                                                                                                              LRCTSVWAHLGSGMLLGLLWMQSAYVGHDSGHYVVMTTNGFNKVAQILSGNCLTGISIAW
                                                                                        FLLALLEY-PIQHIQFWLNHLAENLYXG 253
                                                                                                                              FTFYPVMCVARVNLYLQTILLLFSRRKVQDRALNIMGILVFWTWFPLLVSCLPNWPERVM
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Pred. No. 1.6e-
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Query Match 59.9%;
Best Local Similarity 54.9%;
Matches 147; Conservative 3
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hybridiaation assay; genetic mapping; gene expression control; promoter;
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                                                                                                                                                                        This invention describes a novel sphingolipid desaturase that selectively controduces a double bond into the sphingobase of the ceramide residue of sphingolipids and capnoids. A DNA sequence encoding the sphingolipid content of the sphingolipid control of the sphingolipid content of the sphingolipid content of the sphingolipid content of the sphingolipid content of the sphingolipid content of the sphingolipid content of the sphingolipid content of the sphingolipid content of the sphingolipid content of the sphingolipid content of the sphingolipid content of the sphingolipid content of the sphingolipid content of the sphingolipid conditions, cold or frost and/or phytopathogenic microorganisms or to conditions, cold or frost and/or phytopathogenic microorganisms or to conditions, cold or frost and/or phytopathogenic microorganisms or to conditions, cold or frost and/or phytopathogenic microorganisms or to conditions, cold or frost and/or phytopathogenic microorganisms or to conditions, cold or frost and/or phytopathogenic microorganisms or to conditions, cold or frost and/or phytopathogenic microorganisms or to conditions, cold or frost and/or phytopathogenic microorganisms or to conditions, cold or frost and/or phytopathogenic microorganisms or to conditions, cold or frost and/or phytopathogenic microorganisms or to conditions, cold or frost and/or phytopathogenic microorganisms or conditions, cold or frost and/or phytopathogenic microorganisms or conditions, cold or frost and/or phytopathogenic microorganisms or to conditions, cold or frost and/or phytopathogenic microorganisms or to conditions, cold or frost and/or phytopathogenic microorganisms or to conditions, cold or frost and/or phytopathogenic microorganisms or to conditions, cold or frost and/or phytopathogenic microorganisms or to conditions, cold or frost and/or phytopathogenic microorganisms or to conditions, cold or frost and/or phytopathogenic microorganisms or to conditions, cold or frost and/or phytopathogenic microorganisms or to conditions, col
                                           Matches 141;
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                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brassica napus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B. napus sldl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New sphingolipid desaturase that selectively introduces double bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAZ44832.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GVSE-) GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH.
                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sphingolipids and capnoids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
      HRLSDHTVSAASSDYRKLFSDLSALNLFNRKGHTTSILLSLILTLFPLSVCGVLFSDSTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fig 2; 62pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FTVTALQHIQFTLNHFAADVYVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VMCVARVNLYLQTILLLFSRXKVQDRALNIMGILVFWTWFLFLLALL------FV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----PIQHIQFWLNHLAENLYXG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zaehringer U,
                                                                                                                                                           sldl protein described in the method of the invention
                                                                                                                           449 AA;
                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
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                                                             59.2%;
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                                           44;
                                         Score 780.5; DB 21; Pred. No. 3.1e-78; 4; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         253
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                                                                             Length
                                                                                  449;
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                                                                                                                                                                                                                                                                                                                                                                                                                        16-APR-1999
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                                                                                                                                                                 -MAY-1999;
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99US-0132048
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99US-0126785
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RESULT 6
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01-APR-1999

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99US-0149333
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Matches 144
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                                                                     WPI; 2000-127549/12.
N-PSDB; AAZ44833.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sphingolipid desaturase; sld1; sphingobase; ceramide; capnoid; transgenic plant; crop plant; delta-8-unsaturated long-chain base; tolerance; resistance; soil salinity; ion stress; toxicity; drought; cold; frost; phytopathogenic microorganism; flowering time; cosmetic; pharmaceutical; food; chemical raw material.
New sphingolipid desaturase that selectively introduces double into sphingolipids and capnoids -
                                                                                                                                       Heinz E,
                                                                                                                                                                                                                                     27-JUN-1998;
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                                                                                                                                                                                       (GVSE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TFVHVLSAALIGFLWIQSGWIGHDSGHYNVMLSRRLNRAIQILSGNILAGISIGWWKWNH
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99US-0161405

99US-0161350

99US-0161361

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99US-0161361

99US-0161992

99US-0161992

99US-0161993

99US-0161993
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Pred. No. 5.1e-78;
37; Mismatches 67;
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                                                                                                                                       Sperling
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06-OCT-1999
06-OCT-1999
11-OCT-1999

23-JUL-1999 23-JUL-1999 26-JUL-1999 27-JUL-1999 27-JUL-1999 27-JUL-1999 27-JUL-1999 28-JUL-1999 28-JUL-1999 28-JUL-1999 29-AUG-1999 05-AUG-1999 06-AUG-1999 06-AUG-1999 10-AUG-1999 11-AUG-1999 11-AUG-1999 11-AUG-1999 11-AUG-1999 11-AUG-1999 12-AUG-1999 13-AUG-1999 13-AUG-1999 13-AUG-1999 14-AUG-1999 15-AUG-1999 17-AUG-1999 20-AUG-1999 20-AUG-1999 21-AUG-1999 21-AUG

S-0147204. S-0147302. S-0147192. S-0147260.

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RESULT 9
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XX Eve
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KW gea
KW gea
KW gea
KW ch
XX Oe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes a novel sphingolipid desaturase that selectively cc introduces a double bond into the sphingobase of the ceramide residue of c sphingolipids and capnoids. A DNA sequence encoding the sphingolipid cc desaturase, or a vector containing the DNA sequence, can be used to c produce transgenic plants, especially crop plants, with an increased or cc decreased delta-8-unsaturated long-chain base content or an altered content-sequence, can be used to compensate for a delta-8-unsaturated long-chain base deficiency, to cc exclude production of delta-8-unsaturated long-chain base deficiency, to cc exclude production of delta-8-unsaturated bases, to increase tolerance cc or resistance to soil salinity, ion stress or toxicity, drought, wet conditions, cold or frost and/or phytopathogenic microorganisms, or to calter size growth and flowering time. Cells, transgenic organisms or cc plants containing the DNA sequence can be used to produce sphingolipids can desponids with unsaturated sphingobases. The sphingolipids or capnoids can be used in cosmetics, pharmaceuticals and foods and as chemical raw can be used in cosmetics, pharmaceuticals and foods and as chemical raw desaturase sld1 protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 144
   13-OCT-1992;
10-OCT-1991;
08-JAN-1992;
                                                                                                                                                                                                                         delta6-desaturase; sunflower; soybean; maize; tobacco; peanut; carrot; oil seed rape; gamma linolenic acid; GLA; chilling tolerance; evening primrose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                          Oenothera biennis.
                                                                           19-SEP-1997;
                                                                                                                12-MAR-2002
                                                                                                                                                     US6355861-B1
                                                                                                                                                                                                                                                                                                   Evening primrose delta6-desaturase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 NAHHIACNSLDYDPDLQHMPVFAVSSRFFNSITSHXYGRKXEFDXIAXFLICYQHFTFYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138 VFAHQIAAALLGLLWIQSAYIGHDSGHYVIMSNKSYNRFAQLLSGNCLTGISIAWWKWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAHHLACNSLDYDDDLQHIPVFAVSTKFFSSLTSRFYDRKLTFDPVARFLVSYQHFTYYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TFVHVLSAALIGFLWIQSGWIGHDSGHYNVMLSRRLNRAIQILSGNILAGISIGWWKWNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGYHIRDFQVSEVSRDYRRMAAEFRKLGLFENKGHVTLYTLAFVAAMFLGVLYGVLACTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TSHRLSDHTVSAASSDYRKLFSDLSALNLFNRKGHTTSILLSLILTLFPLSVCGVLFSDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VMCFGRINLFIQTFLLLFSKREVPDRALNFAGILVFWTWPPLLVSCLPNWPERFFFVFTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59.1%; Score 778.5; DB 21 [larity 54.8%; Pred. No. 5.1e-78; Conservative 37; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; 62pp; German.
                                                                                                                                                                                                                                                                                                                                          (first entry)
 92US-0959952.
91US-0774475.
92US-0817919.
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                                                                           97US-0934254.
                                                                                                                                                                                                                                                                                                                                                                                                                    Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 21;
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RESULT 10
ABG73416
ID ABG73
XX ABG73
XX ABG73
XX 16-AP
DT 16-AP
DE Eveni
XX Delta
XX maize
KW maize
KW eveni
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Best Local Similarity
Matches 142; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention describes an isolated nucleic acid encoding an evening primrose Delta6-desaturase. The nucleic acid and a vector expressing the nucleic acid are useful for producing a plant such as sunflower, soybean, maize, tobacco, peanut, carrot or oil seed rape plant, with increased gamma linolenic acid (GLA) content, and also for inducing or increasing production of GLA in a bacteria or plant deficient, lacking in or producting low levels of GLA. The nucleic acid is also useful for inducing chilling tolerance in plants. This is the amino acid sequence of the evening primrose delta6 desaturase involved in the production of gamma linoleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acid encoding evening primrose delta6-desaturase which converts linoleic acid to gamma linolenic acid useful for producing gamma linolenic acid in transgenic plant or bacteria -
                                                  Oenothera biennis.
                                                                                                             Delta-6-desaturase; enzyme; delta-12-desaturase; sunflower; maize; tobacco; peanut; carrot; oil seed rape; gamma-linolen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                maize; tobacco; peanut; carrot; oil seed rape; gamma-linolenic acid;
octadecatetraenoic acid; alpha-linolenic acid; delta-15-desaturase;
                                                                                                                                                              Evening primrose
                                                                                                                                                                                                16-APR-2003
                                                                                                                                                                                                                                                               ABG73416 standard; Protein; 452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-SEP-1994;
28-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (RHON ) RHONE-POULENC AGROCHIMIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 ASESVGVHMLCGALLGLLWIQAAYVGHDSGHYQVMPTRGYNRITQLIAGNILTGISIAWW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Column 45-48; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N
                                                                               primrose
                                                                                                                                                                                                                                                                                                                                              VLISFAVTAIQHVQFTLNHFSGDTYVG
                                                                                                                                                                                                                                                                                                                                                                      -LLALLFVPIQHIQFWLNHLAENLYXG
                                                                                                                                                                                                                                                                                                                                                                                                              TYYPVMIFGRVNLFIQTFLLLLTRRDVPDRALNLMGIAVFWTWFPLFVSCLPNWPERFGF
                                                                                                                                                                                                                                                                                                                                                                                                                                 KWTHNAHHLACNSLDYDPDLQHIPVFAVSTRLFNSITSVFYGRVLKFDEVARFLVSYQHW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KWNHNAHHIACNSLDYDPDLQHMPVFAVSSRFFNSITSHXYGRKXEFDXIAXFLICYQHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FSDSTFVHVLSAALIGFLWIQSGWIGHDSGHYNVMLSRRLNRAIQILSGNILAGISIGWW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAFSTSHRLSDHTVSAASSDYRKLFSDLSALNLFNRKGHTTSILLSLILTLFPLSVCGVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLFTGYYYLKDFEVSEISKDYRRLLNEMSRSGIFEKKGHHIMWTFVGVAVMMAAIVYGVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          452
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97US-0789936
                                                                                                                                                                  delta-6-desaturase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.2%; Score 753.5; DB 2
53.2%; Pred. No. 3.2e-75;
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                                                                                                                                                                  世
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              452
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US2002108147-A1

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RESULT 11
AAY51348
ID AAY51
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AC AAY51
XX
AC AAY51
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DT 27-AF
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Best Local S
Matches 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a nucleic acid encoding an evening primrose delta-6-desaturase polypeptide. The nucleic acid, a vector comprising the nucleic acid or a nucleic acid or a nucleic acid or a nucleic acid or a sunflower, soybean, maize, tobacco, peanut, carrot or oil seed rape plant) with increased gamma-linolenic acid (GLA) content by transforming a plant cell with the nucleic acid or vector and regenerating a plant with increased GLA content from the plant cell, for inducing or increasing production of GLA in an organism lacking in or producing low levels of GLA and for inducing production of octadecatetraenoic acid in at least one of a plant deficient or lacking in or producing low levels of octadecatetraenoic acid, a bacterium which produces alpha-linolenic acid or a bacterium which exhibits a delta-15-desaturase activity on a GLA subscrate. This sequence represents an evening primrose delta-6-desaturase polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel nucleic acid encoding evening primrose delta-6-desaturase, useful for producing plant with increased gamma linolenic acid content, and for inducing octadecatetraenoic acid production in plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-066659/06.
N-PSDB; ABX15367.
 27-APR-2000
                              AAY51348;
                                                            AAY51348 standard;
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19-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-DEC-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 142;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                      VLISFAVTAIQHVQFTLNHFSGDTYVG
                                                                                                                                                                                                                 FSDSTFVHVLSAALIGFLWIQSGWIGHDSGHYNVMLSRRLNRAIQILSGNILAGISIGWW
                                                                                                                                                                                              TYYPVMIFGRVNLFIQTFLLLLTRRDVPDRALNLMGIAVFWTWFPLFVSCLFNWPERFGF
                                                                                                                                                                                                                                                                               KWNHNAHHIACNSLDYDPDLQHMPVFAVSSRFFNSITSHXYGRKXEFDXIAXFLICYQHF
                                                                                                                                                                                                                                                                                                                        ASESVGVHMLCGALLGLLWIQAAYVGHDSGHYQVMPTRGYNRITQLIAGNILTGISIAWW
                                                                                                                                                                                                                                                                                                                                                                                   PLFTGYYYLKDFEVSEISKDYRRLLNEMSRSGIFEKKGHHIMWTFVGVAVMMAAIVYGVL
                                                                                                                                                                                                                                                                                                                                                                                                                PAFSTSHRLSDHTVSAASSDYRKLFSDLSALNLFNRKGHTTSILLSLILTLFPLSVCGVL
                                                                                                                                                                   -LLALLFVPIQHIQFWLNHLAENLYXG
                                                                                                                                                                                                                                                            KWTHNAHHLACNSLDYDPDLQHIPVFAVSTRLFNSITSVFYGRVLKFDEVARFLVSYQHW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            452
                                                                                                                                                                                                                                                                                                                                                                                                                                              57.2%; ilarity 53.2%; Conservative 3
 (first entry)
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92US-0817919.
94US-0307382.
97US-0789936.
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97US-0934254
                                                            Protein; 458
                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 753.5; | Pred. No. 3.2e 37; Mismatches
                                                                                                                                      340
                                                                                                                                                                     253
                                                                                                                                                                                                                                                                                                                                                                                                                                                              .2e-75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24; Length 452;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              15;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes a novel sphingolipid desaturase that selectively cintroduces a double bond into the sphingobase of the ceramide residue of csphingolipids and capnoids. A DNA sequence encoding the sphingolipid cC desaturase, or a vector containing the DNA sequence, can be used to produce transgenic plants, especially crop plants, with an increased or decreased delta-8-unsaturated long-chain base content or an altered congensate for a delta-8-unsaturated long-chain base content or an altered compensate for a delta-8-unsaturated long-chain base deficiency, to cc compensate for a delta-8-unsaturated long-chain base tolerance cc exclude production of delta-8-unsaturated bases, to increase tolerance cc conditions, cold or frost and/or phytopathogenic microorganisms, or to cc alter size growth and flowering time. Cells, transgenic organisms or cc plants containing the DNA sequence can be used to produce sphingolipids and capnoids with unsaturated sphingobases. The sphingolipids or capnoids can be used in cosmetics, pharmaceuticals and foods and as chemical raw materials. This sequence represents a sphingolipid desaturase protein conditions.
                                                                                                                                                                                                                                                                                                                            Best Local Sir
Matches 140;
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sphingolipid desaturase; sld1; sphingobase; ceramide; capnoid; transgenic plant; crop plant; delta-8-unsaturated long-chain base; tolerance; resistance; soil salinity; ion stress; toxicity; drought; cold; frost; phytopathogenic microorganism; flowering time; cosmetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 15; 62pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heinz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New sphingolipid desaturase that selectively introduces double bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sphingolipid desaturase protein
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                   235
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                                                                                                                                                                                                                         64
                                                                                                                                                                                                                                                          87
                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                      NHNAHHIACNSLDYDPDLQHMPVFAVSSRFFNSITSHXYGRKXEFDXIAXFLICYQHFTF
                                                                                                                                                                                                                         DSTFVHVLSAALIGFLWIQSGWIGHDSGHYNVMLSRRLNRAIQILSGNILAGISIGWWKW
-----PIQHIQFWLNHLAENLYXG
                                                                                                                    THNAHHIACNSLDYDPDLQHLPMLAVSSKLFNSITSVFYGRQLTFDPLARFFVSYQHYLY
                                                                                                                                                                                       GSFWIHMLSGAILGLAWMQIAYLGHDAGHYQMMATRGWNKFAGIFIGNCITGISIAWWKW
                                                                                                                                                                                                                                                          TGYHLKDYQVSDISRDYRKLASEFAKAGMFEKKGH--GVIYSLCFVSLLLSACVYGVLYS
                                                                                                                                                                                                                                                                                          TSHRLSDHTVSAASSDYRKLFSDLSALNLFNRKGHTTSILLSLILTLFPLSVC--GVLFS
                                                    YPIMCVARVNLYLQTILLLISKRKIPDRGLNILGTLIFWTWFPLLVSRLPNWPERVAFVL
                                                                                    YPVMCVARVNLYLQTILLLFSRXKVQDRALNIMGILVFWTWFLFLLALL-----FV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zaehringer U,
                                                                                                                                                                                                                                                                                                                                                                                               458 AA;
                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                             56.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           German.
                                                                                                                                                                                                                                                                                                                             40;
                                                                                                                                                                                                                                                                                                                            Score 747.5; DB 2
Pred. No. 1.5e-74;
0; Mismatches 66
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                   253
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                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                               458;
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RESULT 12
AAG07393
ID AAG07393
ID AAG07393
ID AAG07393
ID AAG07393
ID AAG07393
ID AAG07393
ID AAG07393
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Query Match Best Local Similarity Matches 138; Conser	28-OCT-1999; 29-OCT-1999;	28-OCT-1999;	26-OCT-1999; 26-OCT-1999;	26-OCT-1999;	25-OCT-1999;	22-OCT-1999;	22-OCT-1999;	21-OCT-1999;	21-OCT-1999;	21-OCT-1999;	21-OCT-1999;	18-OCT-1999;	14-OCT-1999;	14-OCT-1999;	14-0CT-1999;	13-OCT-1999;	13-OCT-1999;	12-OCT-1999;	08-OCT-1999;	06-OCT-1999;	05-OCT-1999;	29-SEP-1999;	28-SEP-1999;	23-SEP-1999;	22-SEP-1999;	16-SEP-1999;	13-SEP-1999; 15-SEP-1999;	10-SEP-1999;	01-SEP-1999; 07-SEP-1999;	31-AUG-1999;	27-AUG-1999;	27-AUG-1999; 27-AUG-1999;	26-AUG-1999;	23-AUG-1999;	23-AUG-1999;	20-AUG-1999;	20-AUG-1999;	17-AUG-1999;	16-AUG-1999;	13-AUG-1999;	11-AUG-1999; 12-AUG-1999;	10-AUG-1999;	09-AUG-1999; 09-AUG-1999;
56.1%; 55.2%; vative	99US-0161993. 99US-0162142.	9908-0161920.	99US-0161360. 99US-0161361.	99US-0161359.	99US-0161405.	99US-0160989. 99US-0161404.	9903-0160981.	99US-0160815.	99US-0160814.	99US-0160768.	9908-0160767.	99US-0159584.	99US-0159638.	99US-0159331.	9908-0159330.	9908-0159295.	9908-0159294.	9905-0158369.																						99US-0148565.	99US-0148341.	99US-0148171.	99US-0147493. 99US-0147935.
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linoleic acid to gamma-linolenic acid (GLA). Its sequence was deduced from that of the delta-6-desaturase gene (AAT30395) isolated from that of the delta-6-desaturase gene (AAT30395) isolated from that of Synechocystis delta-6-desaturase (AAR98456). Expression of the desaturase in transgenic plants, esp. sunflower, soybean, maize, tobacco, peanut, carrot or oilseed rape, results in
                                                                                                                                                                                                                                                                                                                                                                                                                                         Delta-6-desaturase; gamma-linolenic acid; transgenic plant; borage; polyunsaturated fatty acid; octadecatetraeonic acid; chilling resistance; oilseed.
                                                                                                            Transgenic plants comprising the borage delta-6-desaturase grands increased production of gamma linolenic acid and having increased resistance to chilling
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                                                                                          Claim
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                                                               delta-6-desaturase (AAR98455) catalyses the conversion of
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                                                                                                                                                          AAT30395.
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                                                                                       Page 52-53; 75pp; English.
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NHFAADVYVG
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Best Local Similarity
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  New sunflower albumin 5' altered lipid metabolism
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DB; AAV34398.
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373..377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "His-rich metal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156..163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "cytochrome b5 haem-binding motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                Thomas
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Pred. No. 1.1e-72;
50; Mismatches 72;
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Search completed: January 1, 2004, 06:36:53 Job time: 24.293 secs 밁 밁 δ ঠ δ 문 S 밁 Query Match 55.4%; Score 730.5; DB 19; Length 448; Best Local Similarity 48.9%; Pred. No. 1.1e-72; Matches 131; Conservative 50; Mismatches 72; Indels 15; Gaps This sequence corresponds to the borage (Borago officinalis) delta-6 desaturase enzyme. The encoding lipid metabolism gene is an example of a heterologous gene which can be expressed at high levels in a seed-specific manner in transgenic plants, when placed under control of the sunflower albumin gene 5' regulatory region (AAV34397). Sequence Example 2; Fig 1; 38pp; English. 312 227 72 1 LPAFSTSHRLSDHTVSAASSDYRKLFSDLSALNLFNRKGHTTSILLSLILTLFPLSVCGV 60 FVIASLSVTGMQQVQFSLNHFSSSVYVG 339 LDKFFTGYYLKDYSVSEVSKDYRKLVFEFSKMGLYDKKGHIMFATLCFIAMLFAMSVYGV 131 FLLALLFVP-IQHIQFWLNHLAENLYXG 253 448 AA;

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 1, 2004, 06:29:49; Search time 9.52229 Seconds (without alignments) 2555.128 Million cell updates/sec

Title: Perfect score: US-09-857-524B-6 1318 1 LPAFSTSHRLSDHTVSAASS......VPIQHIQFWLNHLAENLYXG 253

Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 283308 segs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	ហ	4.	w	N	_	Result No.
87	87	87		88	88	88.5	88.5	8	90.5	94	97	97	98	103	107	110.5	114	157	162	170	188	201.5	224.5	377.5	747.5	778.5	780.5	789.5	Score
o. 6	6.6			6.7			٠	•	6.9		7.4	7.4	7.4	7.8	8.1	8.4		11.9		•	14.3	•	٠		σ.	59.1	9.	9	Query Match
424	350	350	368	501	501	546	359	199	438	522	549	352	287	387	359	482	359	345	444	444	454	447	473	523	458	449	449	449	Length
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T07742	AH2005	S43772	S54809	G86050	E91204	S52053	AG2005	H89781	T15039	T24027	D30010	B69901	T11959	T07687	852650	F71969	835157	T36617	T13155	JG0180	H88791	T43319	T26280	JC7556	S68358	T47950	T50555	A84900	ID
omegā-6 desaturase	phosphatidylcholin	phosphatidylcholin	74	prot	sensor histidine p	rome-c	~	etical p	yаc	unc-7 protein - Ca	cytochrome-c oxida	acid	ac	9			ÇD.	probable Delta6 fa	oyl-co			4	-CoA	æ	Delta8 sphingolipi	ta-8	delta-8 sphingolip	hypothetical prote	Description

RESULT 2
T50555
delta-8 sphingolipid desaturase [imported] - rape
C:Species: Brassica napus (rape)
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 15-Sep-2000
C:Accession: T50555

<b>4</b> 5	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
82	82.5	82.5	83	83	83	83.5	83.5	83.5	84	84	84.5	85	85.5	86	87
6.2	6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.4	6.4	6.4	6.4	6.5	6.5	6.6
387	468	378	644	549	382	685	581	351	443	302	509	643	379	501	448
N	Ŋ	N	N	1	N	N	N	N	N	N	N	N	N	_	N
T47632	T25475	T14269	B97885	ODUTMB	AF0612	C70678	B90539	S54259	T08136	D82351	F71526	S70592	JC2555	RGECUB	D85362
hypothetical prote	hypothetical prote	Deltal2 fatty acid	transporter, trunc	cytochrome-c oxida	probable transport	probable electron	hypothetical prote	Deltal2 fatty acid	probable omega-6 d	rarD protein VC019	hypothetical prote	NADH2 dehydrogenas	omega-3 fatty acid	sensor protein uhp	hypothetical prote

## ALIGNMENTS

DЪ	Q	dg Qy	g Q	д Qy	рь	Query Match Best Local : Matches 14	RESULT 1 A84900 hypothetical protein C;Species: Arabidops C;Date: 02-Feb-2001 C;Accession: A84900 R;Lin, X.; Kaul, S.; M.; Koo, H.; Moffat, euss, D.; Nierman, W Nature 402, 761-768, A;Title: Sequence an A;Reference number: A;Accession: A84900 A;Status: preliminar A;Molecule type: DNA A;Residues: 1-449 <s 2<="" a;cross-references:="" a;gene:="" a;map="" at2946210="" c;genetics:="" position:="" th=""></s>
313 FVFVSFAVTAIQHVQFCLNHFAADVYTG 340	233FVPIQHIQFWLNHLAENLYXG 253	181 FTFYPVMCVARVNLYLQTILLLFSRXKVQDRALNIMGILVFWTWFLFLLALL 232               :	121 WKWNINAHHIACNSLDYDPDLQHMPVEAVSSREFNSITSHXYGRXXEFXIAXFLICYQH 180 	61 LFSDSTFVHYLSAALIGFLWIQSGWIGHDSGHYNVMLSRRLNRAIQILSGNILAGISIGW 120     :   :	1 LPAFSTSHRLSDHTVSAASSDYRKLFSDLSALNLFNRKGHTTSILLSLILTLFPLSVCGV 60 	Query Match 59.9%; Score 789.5; DB 2; Length 449; Best Local Similarity 54.9%; Pred. No. 5.1e-68; Matches 147; Conservative 38; Mismatches 68; Indels 15; Gaps 2;	RESULT 1 A84900 hypothetical protein At2g46210 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C;Accession: RA4900 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; white, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 199 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Raccession: A8990 A;Raccession: A8990 A;Residues: 1-494 <sto> A;Cross-references: GB:AE002093; NID:g3702328; PIDN:AAC62885.1; GSPDB:GN00139 C;Genetics: At2g46210 A;Map position: 2</sto>

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A; Map position: 3
A; Note: F2A19.180
C; Function: (EC
A; Description: (EC
C; Keywords: oxidor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Sperling, P; Zaehringer, U; Heinz, E.

J. Biol. Chem. 273, 28590-28596, 1998
A;Title: A sphingolipid desaturase from higher plants. I
A;Reference number: Z22986; MUID:99003197; PMID:9786850
A;Accession: T50555
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-449 <SPE>
                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:AL132962; PIDN:CAB71088.1
A;Experimental source: cultivar Columbia; BAC clone F2A19
R;Spering, P.; Zaehringer, U.; Heinz, E.
J. Biol. Chem. 273, 28590-28596, 1998
A;Title: A sphingolipid desaturase from higher plants. Ide
A;Reference number: Z22986; MUID:99003197; PMID:9786850
                                                                                                                                                                               A;Cross-references: EMBL:AJ224161; PIDN:CAA11858.1
A;Experimental source: cultivar Columbia; mainly green parts, some flowers, C;Genetics:
                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-449 <SPE>
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A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: T47950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: Z24480
                                         Description: (EC 1.14.99.-); delta-8 sphingolipid desaturase (validated, Keywords: oxidoreductase; unsaturated fatty acid biosynthesis
                                                                                                                                                          Gene:
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59.1%;
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A;Residues: 1-458 <SPE>
A;Cross-references: EMBL:X87143; NID:g1040728; PIDN:CAA60621.1; PID:g1040729
C;Superfamily: cytochrome b5 core homology
C;Keywords: heme; iron; metalloprotein; oxidoreductase
F;16-90/Domain: cytochrome b5 core homology <CB5>
F;51,74/Binding site: heme iron (His) (axial ligands) #status predicted
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Eur. J. Biochem. 232, 798-805, 1995
A;Title: A cytochrome-b(5)-containing fusion protein similar
A;Reference number: S68358; MUID:96028121; PMID:7588718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Delta8 sphingolipid desaturase (EC 1.14.99.-) [similarity] - common sunflower C;Species: Helianthus annuus (common sunflower) C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000 C;Accession: S68358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary
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Best Local S
Matches 140
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                                      235
                                                                                                184 YPVMCVARVNLYLQTILLLFSRXKVQDRALNIMGILVFWTWFLFLLALL-----FV-
                                                                                                                                                         205
                                                                                                                                                                                             124
                                                                                                                                                                                                                                  145 GSFWIHMLSGAILGLAWMQIAYLGHDAGHYQMMATRGWNKFAGIFIGNCITGISIAWWKW
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                                                                                                                                                                                                                                                                                                                                                                                           140;
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                                                                                                                                                                                                                                                        64 DSTFVHVLSAALIGFLWIQSGWIGHDSGHYNVMLSRRLNRAIQILSGNILAGISIGWWKW 123
                                                                                                                                                                                                                                                                                                              87
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                                                                                                                                                         THNAHHIACNSLDYDPDLOHLPMLAVSSKLFNSITSVFYGRQLTFDPLARFFVSYQHYLY 264
                                                                                                                                                                               NHNAHHIACNSLDYDPDLQHMPVFAVSSRFFNSITSHXYGRKXEFDXIAXFLICYQHFTF 183
                                                                                                                                                                                                                                                                                                              TGYHLKDYQVSDISRDYRKLASEFAKAGMFEKKGH--GVIYSLCFVSLLLSACVYGVLYS
                                                                                                                                                                                                                                                                                                                                      TSHRLSDHTVSAASSDYRKLFSDLSALNLFNRKGHTTSILLSLILTLFPLSVC--GVLFS
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  VSFCVTGIQHIQFTLNHFSGDVYVG
                                      -----PIQHIQFWLNHLAENLYXG
                                                                            YPIMCVARVNLYLQTILLLISKRKIPDRGLNILGTLIFWTWFPLLVSRLPNWPERVAFVL
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52.8%;
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7; Mismatches 67
                                                                                                                                                                                                                                                                                                                                                                                                             Score 747.5; DB 2
Pred. No. 5.6e-64;
                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
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RESULT 5 JC7556 linoleoyl-CoA desaturase (EC 1.14.19.3) N;Alternate names: delta6-desaturase

Mucor

rouxii

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RESULT 6
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Biochem. J. 330, 611-614, 1998
A;Title: Identification of a caenorhabditis elegans Delta6-fatty-acid-desaturase
A;Reference number: Z21637; MUID:98149727; PMID:9480865
A;Accession: T37238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linoleoyl-CoA desaturase (EC 1.14.19.3) W08D2.4 - N;Alternate names: Delta6 fatty acid desaturase C;Species: Caenorhabditis elegans
                                                               A;Map position: 4
A;Introns: 13/3; 39/2; 234/3; 277/3; 378/1; 413/3
C;Superfamily: Caenorhabditis elegans Delta6 fatty acid desaturase
                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-38,69-430,'V',432-473 <NAP>
A;Cross-references: EMBL:AF031477; NID:g3
                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-473 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: Z20188
A; Accession: T26280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Swinburne, J.; Ainscough, R. submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: T26280; T37238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000
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A;Title: Delta6-desaturase of Mucor rouxii with high similarity to plant delta6-desatura
A;Reference number: JC7556; MUID: 20563795; PMID:11112411
A;Accession: JC7556
A;Accession: UC7556
A;Residues: 1-523 <LAO>
A;Cross-references: GB:AF290983
                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: clone W08D2
                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:Z70271; PIDN:CAA94233.1; GSPDB:GN00022; CESP:W08D2
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                                           C; Keywords: alternative splicing; oxidoreductase; unsaturated
                                                                                                                                     A; Gene: CESP: W08D2.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status: translated from GB/EMBL/DDBJ
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                                                                                                                                                            Genetics:
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      Query Match
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      17.0%;
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    Score 224.5;
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Pred. No. 2.1e-28;
                                                                                                                                                                          NID:g3088519; PIDN:AAC15586.1; PID:g3088520
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    DB 1;
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A;Residua: 1-197, VSHIFNN',198-447 <WIL>
A;Cross-references: EMBL:Z81122; PIDN:CAB03352.1; GSPDB:GN00022; CESP:T13F2.1
A;Experimental source: clone T13F2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Delta5 fatty acid desaturase (EC 1.14.99.-) T13F2.1 [validated] - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000 C;Accession: T43319; T24875
                       á
                                                                                                                                                                                                                                                                                                                                                                                                                     A;Introns: 43/3; 80/3; 197/3; 295/3; 318/2; 349/1; 384/3 C;Superfamily: Caenorhabditis elegans Delta6 fatty acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: A; Accession: T24875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, A;Reference number: Z19947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Swinburne, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNA
A;Residues: 1-447 <MIC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Functional identification of a fatty acid delta5 A;Reference number: Z22422; MUID:99059458; PMID:9845325 A;Accession: T43319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Michaelson, L.V.; Napier, J. FEBS Lett. 439, 215-218, 1998
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                                                                                                                                                                                                                                                                                                               64;
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                     VNLYLQTILLL----
                                                                                                                                                                                       SAALIGFLWIQSGWIGHDSGHYNVMLSRRLNRAIQILSGNILAGISIGWWKWNHNAHHIA 131
                                                                                                                                                                                                                                SAQINKSFTDLRMRVRAEGLMD--GSPLFYIRKILETIFT-----ILFAFYLQYHTYYLP
                                                                                                                                                                                                                                                                      SSDYRKLFSDL----SALNLFNRKGHTTSILLSLILTLFPLSVCGVLFSDSTFVHVL---
                                                                                                         CNSLDYDPDLQHMPVFAVSSRFFNSITSHXYGRKXEFDXIAXFLICYQHFTFYPVMCVAR
                                                                                                                                                SAILMGVAWQQLGWLIHEFAHHQLFKNRYYNDLASYFVGNFLQGFSSGGWKEQHNVHHAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FLLPTWPLRVAYFIISQMGGGL
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                                                                  TNVVGRDGDLDLVPFYATVAEHLNNYSQ-
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                                                                                                                                                                                                                                                                                                                    Conservative
  15.3%; Score 201.5; DB 1; 25.1%; Pred. No. 1.4e-11;
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                                                                                                                                                                                                                                                                                                                 43; Mismatches 101;
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86; Mismatches 115;
FSRXKVQDRALNIMGILVEWTWFL----FL----LALLF:
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                                                                -DSWVMTLFRWQHVHWTFMLPFLR
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A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Accession: H88791
A;Accession: H88791
A;Status: preliminary
A;Molecule type: DNA
A;Residues: T-454 <STO>
A;Cross-references: GB:chr_IV; PIDN:CAB03352.1; PID:g3879828; GSPDB:GN00022; CESP:T13F2.C;Genetics:
A;Cross-references: DDBJ:AB021980; NID:g4514721; PIDN:BAA75496.1; PID:g4514722 C;Superfamily: cytochrome b5 core homology C;Keywords: heme; iron; metalloprotein; oxidoreductase; unsaturated fatty acid F;18-94/Domain: cytochrome b5 core homology <CB5> F;53,76/Binding site: heme iron (His) (axial ligands) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: T13F2.1
A;Map position: 4
C;Superfamily: Caenorhabditis elegans Delta6 fatty acid desaturase
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                                                                                                        A; Molecule type: mRNA
A; Residues: 1-444 < AKI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAILMGVAWQQLGWLIHEFAHHQLFKNRYYNDLASYFVGNFLQVSHIFNNGFSSGGWKEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SAALIGFLWIQSGWIGHDSGHYNVMLSRRLNRAIQILSGNILA-----GISIGWWKWN 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAQINKSFTDLRMRVRAEGIMD--GSPLFYIRKILETIFT----ILFAFYLQYHTYYLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                WSTRIMFFLVSHLVGGFLLSHV
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A;Cross-references: GDB:9956652
A;Note: DKF25586C201.1
C;Superfamily: cytochrome b5 core homology
C;Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase; unsaturated
C;Keywords: cytochrome b5 core homology <CB5>
F;18-94/Domain: cytochrome b5 core homology <CB5>
F;53,76/Binding site: heme iron (His) (axial ligands) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linoleoyl-CoA desaturase (BC 1.14.19.3) [validated] - human N;Alternate names: Delta6 fatty acid desaturase; protein DKFZp58 C;Species: Homo sapiens (man) C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change C;Accession: T13155; T08765 R;Cho, H.P.; Nakamura, M.T.; Clarke, S.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 'RTRG',138-428,'D',430,'M',432-444
A;Cross-references: EMBL;AL050118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:AF126799; NID:g4406527; PID:g4406528; PIDN:AAD20018.1 R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, March 1999 A;Reference number: Z16471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Title: Cloning, expression, and nutritional regulation A;Reference number: Z17612; MUID:99085046; PMID:9867867 A;Accession: T13155
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A; Residues: 1-444 < CHO>
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135 LDYDPDLQHMPVFAVSSRFFNSITSHXYGRKXEFDXIAXFLICYQHFTFYPVMCVARVNL | | | | : : : : | | | : : : : : |
                                                                  167
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                                                                  VLATSQAQAGWLQHDYGHLSVYRKPKWNHLVHKFVIGHLKGASANWWNHRHFQHHAKPNI 226
                                                                                                                                                         SKITEDFRALRKTAEDMNLFKTNHVFFLLLLAHIIALESIAWFTVFYFGNGWIPTLITAF
                                                                                                                                                                                                SAASSDYRKLFSDLSALNLFNRKGHTTSILLSLILTLFPLSVCGVLFSDSTFVHVL-SAA
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C;Species: Synechocystis sp.
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-(C;Accession: S35157; S76243
R;Reddy, A.S.; Nuccio, M.L.; Gross, L.M.; Thomas, T.L.
Plant Mol. Biol. 22, 293-300, 1993
A;Title: Isolation of a Delta(6) desaturase gene from the cyanobact.
A;Reference number: S35157; MUID:93283633; PMID:8389613
A;Accession: S35157
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-359 <RED
A;Cross-references: GB:L11421; NID:g349562; PIDN:AAA27286.1; PID:g3-A;Cross-references: GB:L11421; NID:g349562; PIDN:AAA27286.1; PID:g3-R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamui
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T36617
A;Reference number: A;Accession: S76243
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                                                                                         A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                  DNA Res.
                                                                                                                                  (Cross-references: GB:L11421; NID:g349562; PIDN:AAA27286.1; PID:g349563; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; Kaneko, T.; Sato, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasud Na Res. 3, 109-136, 1996
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Best Local :
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23.7%; Pred. No. 2e-07;
                           MUID:97061201;
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C; Superfamily:
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Rature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: F71969
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C;Species: Helicobacter pylori
A;Variety: strain J99

C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 20-Aug-1999

C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 20-Aug-1999

C;Accession: F71969

R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, R;Alm, R.A.; Ling, R.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Taylor, D.E.; Vovis, C.; Texton, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, C.; Texton, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, C.; Texton, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, C.; Texton, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, C.; Texton, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, C.; Texton, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, C.; Texton, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, C.; Texton, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, C.; Texton, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, C.; Texton, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, C.; Texton, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, C.; Texton, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, C.; Texton, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, C.; Texton, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, C.; Texton, R.; Merberg, D.; Mills, S.D.; Jiang, R.; Texton, R.; Merberg, D.; Mills, S.D.; Jiang, R.; Texton, R.; Merberg, D.; Mills, S.D.; Jiang, R.; Texton, R.; Merberg, D.; Mills, R.; Merberg, R.; Merberg, R.; Merberg, R.; Merberg, R.; Merberg, R.; Merberg, R.; Merberg, R.; Merberg, R.; Merberg, R.; Merberg, R.; Merberg, R.; Merberg, R.; Merberg, R.; Merberg, R.; Merberg, R.; Merberg, R.; Merberg, R.; Merberg, R.; Merberg, R.; Merberg, R.; Merberg, R.; Merberg, R.; Merberg, R.; Merberg, R.; Merberg, R.; Merberg, R.; Merberg, R.; Merberg, R
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-359 <KAN'
A;Residues: 1-359 <KAN'
A;Crose-references: EMBL.D90914; GB:AB001339; NID:g1653477; PIDN:BAA18502.1; PID:d101923:
A;Experimental source: PCC 6803
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Keywords: oxidoreductase; unsaturated fatty acid biosynthesis
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A;Molecule type: DNA
A;Residues: 1-482 <ARN>
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A;Experimental source: strain J99
                                                                                                                                                                                                                                                                                                                                  365 HLDPLIAVLFIVALFYLSHYFFASITAHVSA-----LFALFVGIGSH------IQGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            264 ELESMGRFSLKE-----ILMLSLTL--LALLGWIFGKSLGLHASATALIVMVLMAFCKIV 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148 MSPEQEHVGIYR-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28 DISALNIENRKGHTTSILISLILIFPISVCGVLFSDSTFVHVLSAALI-----GFLWIQ
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                                                                                                                                             NLQELSLFLMLS - -
                                                                                                                                                                                                                                     NLYLQTILLLESRXKVQDRALNIMGILV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -YEDIIKNKSAFNIFLLLGSLLTMAGGLKNVGFLNFIGNA---AQNFLEHA 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.6%; Score 114; DB 2,
20.1%; Pred. No. 0.0027
tive 39; Mismatches
                                                                                                                               - LG MGILTPYGTGPSTIYYGSGYIQSKDPWKWGFIFGFLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 110.5; DB Pred. No. 0.0081;
                                                243
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R;Heppard, E.P.; Kinney, A.J.; Stecca, K.L.; Miao, G.H. Plant Physiol. 110, 311-319, 1996
A;Title: Developmental and growth temperature regulation A;Reference number: Z16095; MUID:96151506; PMID:8587990
A;Rcccession: T07687
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                               omega-6 desaturase FAD2-1, microsomal - soybean
C;Species: Glycine max (soybean)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 11-May-2000
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A;Residues: 1-359 <SAK>
A;Residues: 1-359 <SAK>
A;Cross-references: GB:Dl3780; NID:g600596; PIDN:BAA02924.1; PID:g600598
A;Note: the authors translated the initiation codon GTG for residue 1 as Val
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miy
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamızu, E.; Nakamura, X.; Piyajima, A.; o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                             A; Molecule type: mRNA
A; Residues: 1-387 < HEP>
                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
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  A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:D90913; GB:AB001339; A;Note: the nucleotide sequence was submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Cloning of omega-3 desaturase from cyanobacteria and its use in altering the A;Reference number: S52649; MUID:95035996; PMID:7524725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Synechocystis sp.
A;Variety: PCC 6803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Note: the nucleotide sequence was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-359 <KAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: S74322;
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Matches
                                                                                                                                                                                                                                                             Accession:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000 Accession: S52650; S75843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Superfamily: omega-3 fatty acid desaturase Keywords: oxidoreductase; unsaturated fatty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Accession: S52650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  166 XEFDXIAXF---LICY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107 GHLSHTPIL-VPYHGWRISHRTHHANTGNIDTDES------WYPVSEQKYNQM 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 VGLIAGFYALAA----YLDSWFFYPIFWLIQGTLFWSLFVVGHDCGHGSFSKSKTLNNWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46 LSLILTLFPLSVCGVLFSDSTFVHVLSAALIGFLWIQSGWIGHDSGHYNVMLSRRLNRAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S75843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AWYEKILRFYLPLIAYPIYLFRRSPNRQGSHFMPGSPLFRPGEKAAVLTSTFALAA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALNIMGILVFWTW---FLFLLALLFVPIQHIQFW-----LNHLAENL--YXG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QILSGNILAGISIGWWKWNHNAHHIACNSLDYDDDLQHMPVFAVSSRFFNSITSHXYGRK 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA
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EMBL:L43920; NID:g904151; PIDN:AAB00859.1; PID:g904152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.1%; Score 107; DB 2; Length 359; 21.9%; Pred. No. 0.013; tive 32; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MUID:97061201; PMID:8905231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QHFTFYPVMCVARVNLYLQTILLLFSRXKVQDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Experimental source: seed
C;Genetics:
A;Gene: FAD2-1
C;Function:
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Best Local S
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                                                                                                     179
267
                                                                  214 ----YHPYAPIYSNRERLLIYVSDV-ALFSVTYSLYRVATLKGLV--WLLCVYGVPLLIV 266
                                                                                                                                                                       146
                                                                                                                                                                                                          113 HHAFSKYQWVDDVVGLTLHSTLL-VPYFSWKISHRRHHSNTGSLDRDEVFVPKPKSKVAW
                                                                                                                                   172 FSKYLNNPLGRAVSLLVTLTIGWPMYLAFNVSGRPYDSFASH-----
                                                                                                                                                                                                                                                                            53 SLLTSFSYVVYDLSFAFIFYIATTYFHLLDQPFSLIAWPIWVLQGCLLTGVWVIAHECG
                                                                                                                                                                                                                                          92 HYNVMLSRRLNRAIQILSGNILAGISIGWWKWNHNAHHIACNSLDYDPDLQHMP-----
                                                                                                                                                                                                                                                                                                               43 SILLSLILTLFPLSVCGVLFSDSTFVHVLSA--ALIGF--LWIQSG-----W-IGHDSG
                                                                                                                                                                                                                                                                                                                                               52;
                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                  P-----IQHIQFWLNH 245
                                                                                                 QHFTFYPVMCV----ARVNLYLQTILLLFSRXKVQDRALNIMGILVFWTWFLFLLALLFV
NGFLVTITYLQHTHFALPH
                                                                                                                                                                                                                                                                                                                                                                                                                  omega-3 fatty acid desaturase
                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                              7.8%; Score 103; DB 2; 20.1%; Pred. No. 0.034;
                                                                                                                                                                                                                                                                                                                                             37; Mismatches
                                                                                                                                                                       -----VFAVSSRFFNSITSHXYGRKXEFDXIAXFLICY
                                                                                                                                                                                                                                                                                                                                                   88;
                                                                                                                                                                                                                                                                                                                                                                                  Length 387;
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Search completed: January 1, 2004, 06:39:41
Job time: 10.5223 secs

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Result
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Listing first 45 summaries
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Maximum DB
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Perfect score:
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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length: 2000000000
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1318
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       GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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DESA SPIPL
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RM11 ACACA
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FD62 SYDN
UHPB SALTY
FD62 SOYBN
COXN BRAJA
Y006 BORBU
COXN BRAJA
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Q08871 synechocyst
Q9y8h5 mortierella
P59668 mortierella
P48630 glycine max
Q44261 alcaligenes
P54972 agrobacteri
P14544 leishmania
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5 escherichia a
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1 brassica na
4 spirulina p
1 trypanosoma
6 acanthameeb
1 phaseolus a
8 salmonella
1 slycine max
0 bradyrhizob
9 borrelia bu
1 saccharomyc
2 schizosacch
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ALIGNMENTS	CLC2_CAVPO	ARAB_YERPE	ACOD_HUMAN	FD3C_BRANA	T2RD_HUMAN	ACH4_DROME	COX1_PLACH	NU5M_ASCSU	YCAD_ECOLI	LGT_MYCGE	YI35 MYCTU	YMN2_CAEEL
	Q9wu45 cavia porce	P58543 yersinia pe	000767 homo sa	P48618 brassic	Q9nyv9 homo sa	P25162 drosophila	O99255 plasmod	P24884 ascaris	P21503 escherichia		Q50598 mycobacter:	P54246 caenorhabd
	orce	a pe	pien	a na	pien	ila	lium	Buu	chia	sma	teri	abdi

#### TT GNWENT

Query Match

12.1%; Score 159;

DB 1;

Length 444;

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01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Linoleoyl-CoA desaturase (EC 1.14.19.3) (Delta(6)-desaturase).
DES6 OR SIL10262.
                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., N
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimu
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo
Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A
Yamada M., Yasuda M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=93283633; PubMed=8389613; Reddy A.S., Nuccio M.L., Gross L.M., Tho "Isolation of a delta 6-desaturase gene Synechocystis sp. strain PCC 6803 by gai Anabaena sp. strain PCC 7120."; Plant Mol. Biol. 22:293-300(1993).
                               InterPro; IPR005804; FA desat fam. pF00487; FA desaturase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        COFACTOR: IRON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY: Linoleoyl-CoA + AH(2) + O(2) = gamma-linolenoyl-CoA + A + 2 H(2)O.
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                                                                                          L11421; AAA27286.1;
D90914; BAA18502.1;
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         PD001081;
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                                                                                                                                                                                           email to license@isb-sib.ch).
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Matches 45
                                                                               Liu L., Li M., Xing L., Hu G.;
"Delta 12 fatty acid desturase gene of Mortierella alpina.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Catalyzes the desaturation of oleic acid (delta9-1
to linoleic acid (delta9, delta12-18:2).
-!- PATHWAY: C20 polyunsaturated fatty acid biosynthesis.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential)
-!- DOMAIN: The histidine box domains may contain the active sit and/or be involved in metal ion binding.
-!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Identification of deltal2-fatty acid desaturase from arachidonic acid-producing Mortierella fungus by heterologous expression in the yeast Saccharomyces cerevisiae and the fungus Aspergillus oryzae."

Eur. J. Biochem. 261:812-820(1999).
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15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last seguence update)
15-SEP-2003 (Rel. 42, Last annotation updat
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its the Ew by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.,
STRAIN=ATCC 32221;
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                                                                                                                                                                                                                                                                                                                                and recombinant production
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                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99406036; PubMed=10478922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=1S-4
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Mortierellaceae; Mortierella.
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Pred. No. 0.0028;
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or send a
                                                      15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last amotation update)
15-SEP-2003 (Rel. 42, Last amotation update)
Delta-12 fatty acid desaturase (EC 1.14.99.-).
Mortierella isabellina (Umbelopsis isabellina).
Eukaryota, Fungi, Zygomycota, Zygomycetes; Mucorales;
Mucorales incertae sedis; Umbelopsis.
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GO; GO:0006633; P:fatty acid biosynthesis;
InterPro; IPR005804; FA_desat_fam.
Pfam; PF00487; FA_desaturase; 1.
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EMBL; AF110509; AAF08684.1; -.
EMBL; AF417744; AAL13300.1; -.
            SEQUENCE FROM N.A. STRAIN=M6-22;
                                         NCBI_TaxID=91625;
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BOX-2.
BOX-3.
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Matches 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Delta 12 fatty acid desturase mRNA of Mortierella isabellina.";
Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: Catalyzes the desaturation of oleic acid (delta9-18:1)
to linoleic acid (delta9, delta12-18:2) (By similarity).
-!- PATHWAY: C20 polyunsaturated fatty acid biosynthesis.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- DOMAIN: The histidine box domains may contain the active site and/or be involved in metal ion binding.
-!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
                                                                        Omega-6 fatty
(EC 1.14.19.-)
                                                                                                  01-FEB-1996 (Rel. 33,
01-FEB-1996 (Rel. 33,
28-FEB-2003 (Rel. 41,
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DOMAIN
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GO; GO:0006633; P:Eatty acid biosynthesis;
InterPro; IPR005904; FA desat-fam.
Pfam; PF00487; FA desaturase; 1.
ProDom; PD001081; FA desat_fam; 1.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as modified and this statement is not removed. Use this requires a license agreement (See htter)
                                           Glycine max (Soybean)
                                                            FAD2-1.
                                                                                                                                               P48630;
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"Developmental and growth temperature regulation of two different microsomal omega-6 desaturase genes in soybeans.";
Plant Physiol. 110:311-319(1996).

-i- FUNCTION: ER (MICROSOMAL) OMEGA-6 FATTY ACID DESATURASE INTROFTHE SECOND DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS, IMPORTANT CONSTITURIS OF PLANT MEMBRANES. IT IS THOUGHT TO USE CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS ESTERIFIED TO PHOSPHATIDYLICHOLINE AND, POSSIBLY, OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; T07687; T07687.

PIR; T07687; T07687.

InterPro; IPR005804; FA_desat_far
Pfam; PF00487; FA_desat_fam;
PD001081; FA_desat_fam;
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SUBCELLULAR LOCATION: Endoplasmic reticulum
TISSUE SPECIFICITY: STRONGLY EXPERSSED IN DEVELOPING
DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AND/ OR BE INVOLVED IN METAL ION BINDING. SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
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52; Conserv
NGFLVTITYLQHTHFALPH
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                                                         ----YHPYAPIYSNRERLLIYVSDV-ALFSVTYSLYRVATLKGLV--WLLCVYGVPLLIV
                                                                                                                   FSKYLNNPLGRAVSLLVTLTIGWPMYLAFNVSGRPYDSFASH
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                                                                                   QHETFYPVMCV----ARVNLYLQTILLLESRXKVQDRALNIMGILVEWTWFLFLLALLEV
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HISTIDINE
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Pred. No. 0.031;
7; Mismatches
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BOX-3.
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01-NOV-1997
01-NOV-1997
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01-OCT-1996
01-OCT-1996
28-FEB-2003
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"Canthaxanthin biosynthesis by the conversion of methylene to keto groups in a hydrocarbon beta-carotene by a single gene.";

Biochem. Biophys. Res. Commun. 209:867-876(1995).

-i- FUNCTION: CONVERTS BETA-CAROTENE TO CANTHAXANTHIN VIA ECHINENONE.

-i- PARTHMAY: CAROTENOID BIOSYNTHESIS. INVOLVED IN ASTAXANTHIN BIOSYNTHETIC PATHWAY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
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ProDom; PD001081; FA_desat_fam; 1.
Carotenoid biosynthesis; Oxidoreductase.
                           Rhizobiaceae;
                                                  Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                           Agrobacterium aurantiacum.
                                                                                                                                Beta-carotene
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Misawa N., Kajiwara S., Kondo K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 AA;
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(Rel. 35, Last sequence update)
(Rel. 41, Last annotation update)
ne ketolase (EC 1.13.-.-) (Beta-carotene oxygenase).
                                                                                                                                (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 41, Last annotation updat
ne ketolase (EC 1.13.-.-) (Beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                      Rhizobium/Agrobacterium
                                                                                                                                                                                                                                                                        STANDARD;
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28.6%;
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Pred. No. 0.0
                                                                                                                                                                                                                                                                        PRT;
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(Beta-carotene
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                      group;
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COX1_LEITA
P14544;
01-JAN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Structure and functional analysis of a marine bacterial carotenoid biosynthesis gene cluster and astaxanthin biosynthetic pathway proposed at the gene level.";
J. Bacteriol. 177:6575-6584(1995)
-!- FUNCTION: CONVERTS BETA-CAROTENE TO CANTHAXANTHIN VIA ECHINENONE.
de la Cruz V.F., Neckelmann N., Simpson L.;
"Sequences of six genes and several open reading frames in the
kinetoplast maxicircle DNA of Leishmania tarentolae.";
J. Biol. Chem. 259:15136-15147(1984).
-!- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. CO IS THE
CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
                                                                                                                                                                 sukaryota; Euglenozoa;
NCBI_TaxID=5689;
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ProDom; PD001081; FA_desat_fam; 1.

Carotenoid biosynthesis; Oxidoreductase.
SEQUENCE 242 AA; 27128 MW; 6AEBB5BF0
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15-SEP-2003
                                                                                                                                                                                                                                                    Cytochrome
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Misawa N., Satomi Y., Kondo K., Yokoyama
                                                                                                                         MEDLINE=85079995; PubMed=6096360;
                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                        Mitochondrion.
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                                                                                                                                                                                                                       Leishmania tarentolae
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                                                                                                                                                                                                                                                               (Rel. 13, Created)
(Rel. 13, Last sequence up
(Rel. 42, Last annotation
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                                                                                                                                                                                                                                                    oxidase
                                                                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                                                                                                                                                                 polypeptide I (EC 1.9.3.1).
                                                                                                                                                                                                                     (Sauroleishmania tarentolae)
                                                                                                                                                                                      Kinetoplastida; Trypanosomatidae; Leishmania.
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Pred. No. 0.03
30; Mismatches
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DUFF MOUSE
ID DUFF M
AC Q9QUI6
AC Q9QUI6
DT 28-FEB
DT 15-SEP
DE Duffy
GN FY OR
OS Mus mu
OC Eukary
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Best Local S
Matches 64
"Cloning, character gene: hor
chemokine receptor gene: hor
rea Res. 7:932-941(1997)
                                                                                                                                                                                                   DUFF_MOUSE STANDARD; PRT; 334 AA Q9QUI6; 035970; 091VB6; 0920X0; 0920X1; Q92 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METAL
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METAL
                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                          Duffy antigen/chemokine FY OR DFY OR DARC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METAL
                                                   Pogo A.O.;
                                                               SEQUENCE FROM N.A. MEDLINE=97458170; Luo H., Chaudhuri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CROSSLNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oxidoreductase; Heme; Copper; Mitochondrion;
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                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Respiratory chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INNER MEMBRANE. CONSIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PATHWAY: Respiratory chain; terminal step.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
INNER MEMBRANE. CONTAINS 12 POTENTIAL TRANSMEMBRANE DOWAINS.
SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY
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Pro; 1PR000883; COX1.
PF00115; COX1; 1.
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                                    characterization,
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549
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                                                              PubMed=9314499;
A., Johnson K.R.,
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IRON (HEME A AXIAL
                         Soromon
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COPPER B (PROBABLE).
COPPER B (PROBABLE).
COPPER B (PROBABLE).
IRON (HEME A3 AXIAL LIGAND) (PROBABLE).
IRON (HEME A AXIAL LIGAND) (PROBABLE).
1'-histidyl-3'-tyrosine (By similarity).
MW; F6DD04815A4917C2 CRC64;
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                         of a murine
human Duffy
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                                                                  Zbrzezna
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                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are nuse by non-profit institutions as long as its comodified and this statement is not removed. Usage entities requires a license agreement (See http://worsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [2]
SEQUENCE FROM N.A.
TISSUE=Skeletal muscle;
Colin Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIINE=99449053; PubMed=10520743; Tang T., Owen J.D., Du J., Walker C.L., Richmond A.; "Molecular cloning and characterization of a mouse g to the Duffy-antigen receptor for chemokines.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glycoprotein (DARC).
Submitted (NOV-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tournamille C., Colin Y.; "Murine skeletal muscle duffy antigen/receptor for chemokine glycoprotein (DARC).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 five Mus musculus subspecies. Submitted (FEB-2000) to the E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NJL/Msf, pgn2, and SWN/Msf;
Liu Y., Kitano T., Koide T.
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                                                                                                                                                                                                                                                                                  similarity).
SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Expressed in liver and brain.
SIMILARITY: BELONGS TO FAMILY DUFFY OF G-PROTEIN COUPLED
        Seq. 9:129-143(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C57BL/10SnJ, CAST/Ei, HMI/Msf, MSM/Msf,
. . . . . . . . . . . . . . . . . . .
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GO; GO:0006554; P:infilammatory response; IMP.
InterPro, IPR005384; Duffyantigen.
PRINTS; PR01559; DUFFYANTIGEN.
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GPWVSVLWIWFIF
                                                                                                                                                                                                                                                                                                    SDHTVSAASSDYRKLFSDLSALNLFNRKG-----HTTSILLSLILTLFPLSVC-----
                             ---ILVFWTWFLF 227
                                                              TFPSSRDMEALKYTHYAICFTIFTVLPLTLLAAKGLKI--
                                                                                             SHXYGRKXEFDXIAXFLICYQHFTFYPVMCVARVNLYLQTILLLFSRXKVQDRALNIMG-
                                                                                                                                                                                                    ELAVGSALFSIAVPILAPGLHSAHSTALCNLGY
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N-LINKED (GLCNAC. ...) (POTENTIAL).

N-LINKED (GLCNAC. ...) (POTENTIAL).

1 -> N (IN STRAINS BLG2/MSF, C57BL/10SNJ,

HMI/MSF, MSM/MSF, NJL/MSF AND SWN/MSF).

D -> G (IN STRAINS BLG2/MSF, C57BL/10SNJ,

HMI/MSF, MSM/MSF, NJL/MSF AND SWN/MSF).

CAST/EI, HMI/MSF, MSM/MSF, NJL/MSF AND

CAST/EI, HMI/MSF, MSM/MSF, NJL/MSF AND
                                                                                                                                                                                                                                                                                                                                   35;
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S -> L (
CAST/EI,
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CAST/EI,
SWN/MSF)
T -> A (
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HMI/MSF, MSM/MSF, UJL/MSF AND SWN/MSF).
M -> I (IN STRAIN UJL/MSF).
T -> I (IN STRAINS BLG2/MSF, C57BL/10SNJ
HMI/MSF, MSM/MSF, UJL/MSF AND SWN/MSF).
                                                                                                                                                                                                                                                                                                                                                     Score 94.5;
Pred. No. 0.
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T -> M (IN STRAINS C57BL/10SNJ, HMI/MSF,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND SWN/MSF)
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JL/MSF, PGN2
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UNC7_CAEEL
Q03412;
01-OCT-1993
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SEQUENCE
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16-OCT-2001
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EMBL; Z70685; CAA94607.1;
PIR; T24027; T24027.
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STRAIN=Bristol NZ;
STRAIN=9202469; PubMed=7681023;
MEDLINE=93202469; PubMed=7681023;
Starich T.A., Herman R.K., Shaw J.E.;
"Molecular and genetic analysis of unc-7, a Caenorhabditis elegans gene required for coordinated locomotion.";
Genetics 133:527-541(1993).
                                                                                                                                                                                                                                                                  Gap
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                                                                                                                                                                                                                                                                                                                                                                                                    between the Swiss Institute of Bioinformat:
the European Bioinformatics Institute. The:
use by non-profit institutions as long a
modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (APR-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Smye R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans.
                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>-</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UNC-7 OR R07D5.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Innexin unc-
                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                 WormPep; R07D5.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Integral membrane protein.
DEVELOPMENTAL STAGE: PRESENT IN ALL DEVELOPMENTAL STAGES
ABUNDANT IN L1-L3 LARVAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: STRUCTURAL COMPONENTS OF THE GAP JUNCTIONS. COORDINATED LOCOMOTION.
SUBUNIT: HETEROOLICOMER OF UNC-7 AND UNC-9 (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Belongs to the innexin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TaxID=6239;
                                       138
                                                                                                                                                                                                                                                                  unction;
                                                                                                                                                                                                                                                                              PF00876; Innexin; :
S; PR01262; INNEXIN
               78
                                                               30
                                                                                       78
                                                                                                                                        68;
                                                                                                              1 LPAFST----SH--RLSDHTVSAA----
                                                                                                                                                     Similarity
FLWIQSG-WIGHDSGHYNVMLSRRLNR: |:|: |: | | | | |
                                    DDDFVDKLNYY----YTTTILASFALLVSAKQYVGFPIQ-CWV---PATFTDAMEQYTEN
                                                                                       LPSYQAQKLLDGSHQLRIDSHHVGSAGHGAGQGHGHKKEFGPAMILYYLASAFRALYPRL
                                                             ----SALNLFNRKGHTTSILLSLILTL-----
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151
221
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(Rel.
(Rel.
                                                                                                                                                                                                                                                                 Transmembrane.
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27, Last sequence up
40, Last annotation
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241
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                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Delta(12) fatty acid dehydrogenase (EC 1.14.99.33) (Crepenynate synthase) (Delta-12 fatty acid acetylenase).
                                                TRANSMEM TRANSMEM
                                                                                                                                                                  Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; campanulids; Asterales; Asteraceae; Cichorioideae;
                                                                                                                                                                                                                     EMBL; Y16285; CAA76158.2;
                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and epoxy group formation.";
Science 280:915-918(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nilsson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE=9872738;
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                           TRANSMEM
                                                                                                                       Oxidoreductase; Fatty
                                                                                                                                           roDom; PD001081;
                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lee M., Lenman M., Banas A., Bafor M., S.
Nilsson R., Liljenberg C., Dahlqvist A.,
                                                                                                TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chorieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: CHANGES THE DELTA-12 DOUBLE BOND OF LINOLEIC ACID INTO TRIPLE BOND IN THE BIOSYNTHESIS OF CREPENYNIC ACID.

CAPALYTIC ACTIVITY: Linoleate + AH(2) + O(2) = crepenynate + A +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE SPECIFICITY: Seed.

DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PATHWAY: Polyunsaturated fatty SUBCELLULAR LOCATION: Integral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COFACTOR: Iron.
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0487; FA_desaturase; 1.
D001081; FA_desat_fam; 2.
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., Gummeson P.O., Sjoedahl S.,
                                                                                                                       Transmembrane; Iron
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                                                                                           EMBL; L29215; AAA50158.1; -.
plr; T07742; T07742.
InterPro; IPR005804; FA_desat_fam.
Pfam; PF00487; FA_desat_fam; Pr0Dom; PD001081; FA_desat_fam; 2.
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                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstating the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine
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01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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Glycine max (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94345008; PubMed=8066133; Hitz W.D., Carlson T.J., Booth J.R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Its expression in a cyanobacterium.";

Its expression in a cyanobacterium.";

It Physiol. 105:635-641(1994)

FUNCTION. CHLOROPLAST OMEGA-6 FATTY ACID DESATURASE INTRODUCES THE SECOND DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS EXTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL. SUBCELULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE). DOWAIN: THE HISTIDINE BOX DOWAINS MAY CONTAIN THE ACTIVE SITE AND/ OR BE INVOLVED IN METAL ION BINDING.

SIMILARITY: BEHONGS TO THE FATTY ACID DESATURASE FAMILY.
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peptide.
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                                                                                                                                                                                                                                                            s requires a license agreement (S
an email to license@isb-sib.ch).
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HISTIDINE BOX-2.
HISTIDINE BOX-3.
HISTAG64DD0C2926 CRC64;
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CHLOROPLAST (BY SIMILARITY)
OMEGA-6 FATTY ACID DESATURA
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chloroplast precursor (EC 1.14.19.-).
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A Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
A pohl T., Duesterhoeft A., Stiekema W., Enian K.-D., Terryn N.,
A Harris B., Ansorge W., Brandt P., Grivell L., Rieger M.,
A Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,
A Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T.,
A Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T.,
A Kreis M., Delseny M., Puigdomenech P., Watson M., Bancroft I.,
A Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P.,
A Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P.,
A Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
A Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
A Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
A Weitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
A Holzer E., Berandt A., Petters S., van Staveren M., Dirkse W.,
A Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
A Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
A Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
A Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
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P46312; 09M094;
10-NOV-1995 (Rel. 32, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Omega-6 fatty acid desaturase, chloroplast precursor (EC 1.14.19.-).
FAD6 OR FADC OR AT4630950 OR F6618.140.
Arabidopsis thaliana (Mouse-ear cres.14)
Arabidopsis thaliana (Mouse-ear cres.14)
                                                                                                                                                                                                                                                                                                                                                    Falcone D.L., Gibson S., Lemieux B., Somerville C.K., "Identification of a gene that complements an Arabidopsis mutant deficient in chloroplast omega 6 desaturase activity."; plant Physiol. 106:1453-1459(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=cv. Columbia;
MEDLINE=95148736; PubMed=7846158;
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Spermatophyta; Magnoliophyta; eudicotyledons;
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edons; core e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tracheophyta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rosidae;
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RA SHINDZAKI K., Davis R.W., Ecker J.R., Theologis A.;
RA ShinDZAKI K., Davis R.W., Ecker J.R., Theologis A.;
RA ShinDZAKI K., Davis R.W., Ecker J.R., Theologis A.;
RT "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the RT SSP consortium (Salk/Stanford/PGEC).";
SUDMITTION: CHLOROPLAST OMEGA-6 FATTY ACID DESATURASE INTRODUCES THE SECOND DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -I- DETERLIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -I- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -I- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -I- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE CC -I- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE CC -I- SIMILARITY: BELLONGS TO THE FATTY ACID DESATURASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RA Gabel C., Fuchs M., Fartmann B., Grander M., Mueller-Auer S., Ce Haan M., Maarse A., Schaefer M., Dauner D., Herzl A., RA Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A., RA Neumann S., Argiriou A., Vitale D., Liguori R., Piravandi E., RA Neumann S., Argiriou A., Vitale D., Liguori R., Piravandi E., RA Neumann S., Hiller R., Schmidt W., Lecharny A., Aubourg S., Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E., Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E., RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E., RA Chefdor F., Weber N., Vandenbol M., Bargues M., Terol J., Torres A., Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T., RA Heijnen L., Schwarz S., Scholler P., Hober S., Francs P., Bielke C., Frishmann D., Haase D., Lemcke K., Mewes H.-W., Stocker S., RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L., Schutz K., Huang E., Spiegel L., Schutz K., Huang E., Spiegel L., Schutz K., Huang E., Spiegel L., Schutz K., Huang E., Spiegel L., RA Schone M., Murray J., Sheet P., Cordes M., Abu-Threideh J., RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D., RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D., RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K., Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Joshu C., RA Nelson J., Seybotf A., Jones K., Drone K., Cotton M., Joshu C., RA Nelson J., Seybotf A., Jones K., Drone K., Cotton M., Joshu C., RA Nelson J., Stong J., Preston R., Vil D., Shekher M., Matero A., Shah R., Racker J., Marra M., Martienseen A., Hameed A., Lochi M., Johnson A., Ra R., McChai E., Marra M., Martienseen A., Hameed A., Lochi M., Johnson A., Ra Nelson J., Shattenseen A., Hameed A., Lochi M., Johnson A., Ra Nelson J., Shattenseen A., Hameed A., Lochi M., Johnson A., Ra Nelson J., Shattenseen A., McChen E., Marra M., Martienseen A., McChen E., McChen E., McChen E., McChen E., McChen E., McChen E., McChen E., McChen E., McChen E., McChen E
                                                                                                                                                                                                                                                                    EMBL; U09503; AAA92800.1; -. EMBL; AL022198; CAA18198.1; -. EMBL; AL161578; CAB79813.1; -. EMBL; AY045621; AAX73979.1; -. EMBL; AY058078; AAL24186.1; -. EMBL; AY058852; AAL24240.1; -.
  DOMAIN
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                                                                                                                                                                     Pfam; PF00487; FA_desaturase; ProDom; PD001081; FA_desat_fa
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Borkova D.,
                                                                                                                                                        Oxidoreductase;
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  peptide.
1 10
70
171
207
367
                                                                                                                                        IPR005804; FA_desat_fam.
10487; FA_desaturase; 1.
10001081; FA_desat_fam; 2.
1001081; Fatty acid_biosynthesis; Chloroplast; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bloecker
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  69
448
175
211
371
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                    CHLOROPLAST (BY SIMILARITY).
OMEGA-6 FATTY ACID DESATURAS
HISTIDINE BOX-1.
HISTIDINE BOX-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Benes V.,
BOX-1.
BOX-2.
BOX-3.
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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01-MAR-1989 (Rel. 10, Created)
01-BUG-1992 (Rel. 23, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Sensor protein uhpB (EC 2.7.3.-).
                                                                                                              Burland V.D., Plunkett G. III, Daniels D.L., Blattner F.R.; "DNA sequence and analysis of 136 kilobases of the Escherichia coligenome: organizational symmetry around the origin of replication."; Genomics 16:551-561(1993).
                                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE=92234930; PubMed=1569007;

ISLAND., Wei B.-Y., Kadner R.J.;

ISLINDE and function of the uhp genes

transport system in Escherichia coli and

J. Bacteriol. 174:2754-2762(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
This SWISS-PROT entry

    -!- SUBCELLULAR LOCATION: Integral membrane protein.
    -!- SIMILARITY: Contains 1 histidine kinase domain.

                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=93315143; PubMed=7686882;
                                                                                                                                                                                                                                                                                                                                   Submitted (AUG-1990)
                                                                                                                                                                                                                                                                                                                                                                                           Friedrich M.J., Kadner R.J.;
"Nucleotide sequence of the uhp region
J. Bacteriol. 169:3556-3563(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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                                                                                                                                                                                                                                                                                                                                                                REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=87279903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UHPB OR B3668
                                                     UHPB FUNCTIONS AS A MEMBRANE-ASSOCIATED PROTEIN KINASE THAT PHOSPHORYLATES UHPA IN RESPONSE TO ENVIRONMENTAL SIGNALS.
                                                                                   FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM UHPB/UHPA INVOLVED IN THE REGULATION OF THE UPTAKE OF HEXOSE PHOSPHATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246
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                                                                                                                                                                                                                                                                                                                                                                                                         of Escherichia coli.";
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Salmonella typ
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produced through
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                                         Inner
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a collaboration
                                           membrane
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RESULT 15
FD3E_TOBAC
ID FD3E_TOBAC
AC P486Z6;
DT 01-FEB-1996
DT 01-FEB-2003
DE OMEGA-3 fatt
GN FAD3.
OS Nicotiana ti
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OS Nicotiana ti
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OS NICOTIANA ti
GN FAD3.
OS SPERMATOPIA;
OC SPERMATOPIA;
OC SPERMATOPIA;
OC ASTECTIANE;
OX NCBI_TAXID=
RP SEQUENCE FRI
RC STRAIN=CV.
RX MEDLINE=950
RA Hamada T.
RT "Cloning of
RI Gene 147:29
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Best Local Similarity
Matches 51; Conserv
                                                                                                                                                                                                       01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
Omega-3 fatty acid desaturase.
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MOD_RES
SEQUENCE
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PIR; E65168; RGECUB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its upon the profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 SEQUENCE FROM N.A.
STRAIN-CV. SR1; TISSUE-Leaf;
MEDLINE-95011632; PubMed-7926817;
Hamada T., Kodama H., Nishimura M
"Cloning of a cDNA encoding tobacc
Gene 147:293-294(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00387; HATPase_c; 1.

PROSITE; PS50109; HIS_KIN; 1.

Sensory transduction; Transferase; Kinase; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M17102; AAA24721.1; ALT_SEQ.
EMBL; M89479; AAA24725.1; ---
EMBL; L10328; AAA62030.1; ALT INIT.
EMBL; AE000444; AAC76691.1; ALT_INIT.
                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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SMART; SM00387; HATPase c
                                                                                                                                                                                            Nicotiana tabacum (Common
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TRANSMEM
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InterPro; IPR005467; His_kinase.
                                                                                                                    NCBI_TaxID=4097;
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Pred. No. 1
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52 CRC64;
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the European Bioinformatics Institute. The
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                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR005804; FA_desat_fam.
Pfam; PF00487; FA_desat_trase; 1.
ProDom; PD001081; FA_desat_fam; 2.
Oxidoreductase; Patty acid_biosynthesis;
                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AND/ OR BE INVOLVED IN METAL ION BINDING. SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHOLIPIDS.

PATHWAY: Polyunsaturated fatty acid biosynthesis.

SUBCELLULAR LOCATION: Endoplasmic reticulum.

DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE

AND/ OR BE INVOLVED IN METAL ION BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: ER (MICROSOMAL) OMEGA-3 FATTY ACID DESATURASE INTRODUCES THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
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230
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                          LLLFSRXKVQDRALNIMGILVFWTWFLFLLAL
                                                    KIPFPLLAYPMYLMKRSPGKSGSHFNPYSDLFQPHERKYVVTSTLCWTVMAALLLYLCTA
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POTENTIAL.
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HISTIDINE
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                    SPTREMBL_23:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2004 Compugen Ltd.
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# SUMMARIES

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	568	573	523	448	469	448	448	448	448	458	446	446	449	449	449	446	Query Match Length
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	OBnkg9 saccharomyc	Q8nkq8 kluyveromyc	Q9hdg8 mucor rouxi	Q817i7 argania spi	Q9ztu8 triticum ae	O04353 borago offi	Q9sau5 borago offi	Q8vzzl echium pita	Q8vzz2 echium gent	Q43469 helianthus	Q8lld7 aquilegia v	·	Q9zrp7 arabidopsis	Q9zrp8 brassica na	Q8lb96 arabidopsis	Q9zty9 ricinus com	Description

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SEQUENCE
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01-OCT-2002 (TrEMBLrel. 23, Last sequence update)
01-MAR 2003 (TrEMBLrel. 23, Last sanctation update)
01-MAR 2003 (TrEMBLrel. 23, Last annotation update)
Delta-8 sphingolipid desaturase.
Arabidopsis thaliana (Mouse-ear cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Q8LB96;
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD000612; Cyt B5; 1.
ProDom; PD001081; FA Gesat fam; 1.
PROSITE; PS50255; CYTOCHROME B5_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR-2002) to the EMBL/GenBank/D

:- SIMILARITY: BELONGS TO THE CYTOCHROME

EMBL; AY087345; AAM04895.1; --

InterPro; IPR001199; Cyt B5.

InterPro; IPR005804; FA desat_fam.

Pfam; PF00487; FA desaturase; 1.

Pfam; PF00173; heme_1; 1.
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Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N.,
Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
"Full-length messenger RNA sequences greatly improve genome
annotation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Full-Length cDNA from Arabidopsis thaliana."; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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NAHHIACNSLDYDPDLQHMPVFAVSSRFFNSITSHXYGRKXEFDXIAXFLICYQHFTFYP
                                                      VFAHQIAAALLGLLWIQSAYIGHDSGHYVIMSNKSYNRFAQLLSGNCLTGISIAWWKWTH
                                                                                         TFVHVLSAALIGFLWIQSGWIGHDSGHYNVMLSRRLNRAIQILSGNILAGISIGWWKWNH
                                                                                                                                                                    TGYHIRDFQVSEVSRDYRRMAAEFRKLGLFENKGHVTLYTLAFVAAMFLRVLYGVLACTS
                                                                                                                                                                                                    TSHRLSDHTVSAASSDYRKLFSDLSALNLFNRKGHTTSILLSLILTLFPLSVCGVLFSDS
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                                                                                                                                                                                                                                                                                                                                                                                             449 AA;
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                                                                                                                                                                                                                                                                                                                                                                                             51744 MW;
                                                                                                                                                                                                                                                                               59.2%; Score 780.5; DB 54.8%; Pred. No. 5e-66; :ive 37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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Best Local Similarity
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Q1-MAY-1999
Q1-MAY-1999
Q1-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brassica napus (Rape).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                          Pfam; PF00173; heme 1; 1.
ProDom; PD000612; Cyt B5; 1.
ProDom; PD001081; FA desat fam; 1.
PROSITE; PS50255; CYTOCHROME_B5_2;
                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001199; Cyt B5.
InterPro; IPR005804; FA_desat_
Pfam; PF00487; FA_desaturase;
Pfam; PF00173; heme 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: BELONGS TO THE CYTOCHROME EMBL; AJ224160; CAA11857.1; -- HSSP; P82291; ICXY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sperling P., Zaehringer U., Heinz E.;
"A Sphingolipid Desaturase from Higher Plants Identification Cytochrome b5 Fusion Protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99003197; PubMed=9786850;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=3708;
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320
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                                                                                                                                                                68 VHVLSAALIGELWIQSGWIGHDSGHYNVMLSRRLNRAIQILSGNILAGISIGWWKWNHNA 127
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                                                                                                               HHIACNSLDYDDDLQHMPVFAVSSRFFNSITSHXYGRKXEFDXIAXFLICYQHFTFYPVM
                                                                                                                                                   AHLISAVLLGLLWIQSAYVGHDSGHYNVTSTKPCNKLVQLLSGNCITGISIAWWKWTHNA
                                                                        CVARVNLYLQTILLLFSRXKVQDRALNIMGILVFWTWFLFLLA------LLFV----
                                                                                                  HHISCNSLDHDPDLQHIPVLAVSNKFFKSMTSRFYGRKLTFDPLARFLISYQHWSFYPIM
 VTAIQHVQFCLNHFAADVYTG
                     --PIQHIQFWLNHLAENLYXG
                                                 CVGRINLFIQTLLLLFSRRYVPDRALNIAGILVFWTWFPLLVSFLPNWQERIIFVFLSMA
                                                                                                                                                                                                      YHVKDHHVSDVSRDYRRLAAEFSKRGLFDKKGHVTLYTLTCVAAMLAAVVYGVVACTSIW
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                                                                                                                                                                                                                                                                                                       449 AA;
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                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                       51490 MW;
                                                                                                                                                                                                                                                                 59.2%; Score 780.5; 54.0%; Pred. No. 5e-
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Last annotation update)
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340
                        253
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Carninci P., Chen H., Cheuk R., Chan M., Chang C.H., Dale J.M.,
A Deng J.M., Hayashizaki Y., Heuan V.W., Lee J.M., Ishida J., Kamiya A.,
Kawai J., Kim C.J., Narusaka M., Quach H.L., Sakurai T., Satou M.,
Seki M., Shinn P., Tang C.C., Toroumi M., Wallender E.K., Wong C.,
Wu H.C., Yamada K., Yu G., Yuan S., Shinozaki K., Ecker J.,
Theologis A., Davis R.W.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
-- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
EMBL; AJ224161; CAA11858 1; --
EMBL; AF428420; AAN17419 1; --
DR EMBL; AF428420; AAN17419 1; --
EMBL; BT000442; AAN17419 1; --
EMBL; BT000171; 115U.
                                Matches 144;
                                                                  Query Match
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Q9ZRP7;
01-MAY-1999 (TYEMBLrel. 10, Created)
01-WAY-1999 (TYEMBLrel. 10, Last sequence update)
01-MAY-1999 (TYEMBLrel. 23, Last annotation update)
01-MAR-2003 (TYEMBLrel. 23, Last annotation update)
Delta-8 sphingolipid desaturase (AT3G61580/FZA19_180).
SLD1 OR FZA19.180 OR AT3G61580.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidieurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.K., Jones T., Kamilya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=cv. Columbia; TISSUE=Flower, MAI
MEDLINE=99003197; PubMed=9786850;
Sperling P., Zaehringer U., Heinz E.;
"A sphingolipid desaturase from higher
cytochrome b5 fusion protein.";
J. Biol. Chem. 273:28590-28596(1998).
                                                                                                                                Pfam; PF00487; FA_desaturase; 1.
Pfam; PF00173; heme 1; 1.
Pr0D0m; PD000612; CVt B5; 1.
ProDom; PD001081; FA_desat_fam; 1.
PROSITE; PS50255; CYTOCHROME_B5_2; 1.
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Mayer K.F.X., Quetier F., Salanoubat M.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Arabidopsis cDNA clones."; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EU Arabidopsis sequencing project;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ
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                                                                                                       SEQUENCE
                                                                                                                                                                                                                                           InterPro;
                                                                                                                         {eme
                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FROM N.A.
TSHRLSDHTVSAASSDYRKLFSDLSALNLFNRKGHTTSILLSLILTLFPLSVCGVLFSDS
                                                                                                                                                                                                                       IPR001199; Cyt_B5.
IPR005804; FA_desat_fam.
                                                                                                       449 AA;
                                  Conservative
                                                                                                     51675 MW; 145048F9F1D35964 CRC64;
                                                59.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Flower, MAINLY
                                37;
                                Score 778.5; DB 1
Pred. No. 7.7e-66;
7; Mismatches 67
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                                                               DB 10;
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                                                                                                                                    Query Match
Best Local S
Matches 147
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Q9FR82;
01-MAR-2001
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SEQUENCE
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; lamiids; Boraginaceae; Borago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                          InterPro; IPRO01199; Cyt B5.
InterPro; IPRO05804; FA desat fai
Pfam; PF00487; FA desaturase; 1.
Pfam; PF00173; heme_1; 1.
                                                                                                                                                                                                                                                                                                                MEDINE-21260464; PubMed-1136816
Sperling P., Libisch B., Zaehrin
"Functional identification of a
Borago officinalis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Libisch B., Michaelson L.V., Lewis M.J., Shewry P.R., N
"Chimeras of Delta6-fatty acid and Delta8-sphingolipid
Biochem. Biophys. Res. Commun. 279:779-785(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=21092516; PubMed=11162428;
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=13363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Delta 8-sphingolipid desaturase.
                                                                                                                                                                                                                   PROSITE;
 126
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                                                                                                                                     al Similarity
147; Conserv
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                                                                                                                                                                                                            F00173; heme 1; 1.

PD000612; CYt_B5; 1.

PD001081; FA desat fam; 1.

PD001255; CYTOCHROME_B5_2; 1.
                          LWVHMLSGAMLGMCFIQAAYLGHDSGHYTMMSSKGYNKFAQVLNGNCLTGISIAWWKWTH
                                          TFVHVLSAALIGFLWIQSGWIGHDSGHYNVMLSRRLNRAIQILSGNILAGISIGWWKWNH
                                                                                                    TSHRLSDHTVSAASSDYRKLFSDLSALNLFNRKGHTTSILLSLILTLFPLSVCGVLFSDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VFAHQIAAALLGLLWIQSAYIGHDSGHYVIMSNKSYNRFAQLLSGNCLTGISIAWWKWTH
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NAHHIACNSLDYDPDLQHMPVFAVSSRFFNSITSHXYGRKXEFDXIAXFLICYQHFTFYP
                                                                                TGYHLEDYLVSEISKDYRKLASEFSKAGLFEKKGHTVIYCLSFIALLLCGCVYGVLCSNS
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                                                                                                                                                                                           446 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=11368168;
                                                                                                                                                                                           50926 MW;
                                                                                                                                    58.3%; Score 768.5;
55.9%; Pred. No. 6.9;
tive 35; Mismatches
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on of a delta 8-sphingolipid
                                                                                                                                                                                           EBD579F035A3AF0C CRC64;
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Matches 140
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Pfam; PF00173; heme 1; 1.
PRINTS; PR00363; CYTOCHROMEB5.
ProDom; PD000612; Cyt_B5; 1.
ProDom; PD001081; FA_desat_fam; 1.
PROSITE; PS50255; CYTOCHROME_B5_2
Q43469;
Q43469;
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Spermatophyta; Magnoliophyta;
Ranunculaceae; Aquilegia.
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01-OCT-2002 (TrEMBLrel 22, L
01-MAR-2003 (TrEMBLrel 23, L
01-MAR-2003 (TrEMBLrel 23, L
Sphingolipid long chain base
Aquilegia vulgaris
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01-OCT-2002
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                                                                                                                                                                                                                                                                                                                               IAVNSLDYDPDLQHIPFLAVSSDIFSSLTSKFYGRKMTFDPIARFLISFQHWTFYPVMAI
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                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58.1%; Score 765.5; DB 1
54.1%; Pred. No. 1.3e-64;
tive 43; Mismatches 61
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Matches 140
Q8VZZ2
Q8VZZ2;
01-MAR-2002
01-MAR-2002
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-!- SIMILARITY: BELONGS TO THE CYTOCHROME
EMBL; X87143; CAA60621.1; -.
HSSP; P00171; 1F03.
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ProDom; PD000612; Cyt B5; 1.
ProDom; PD001081; FA desat fam;
PROSITE; PS50255; CYTOCHROWE B5
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TISSUB=Cotyledons of developing sun
MEDLINE=96028121; PubMed=7588718;
Sperling P., Schmidt H., Heinz E.;
"A cytochrome b5-containing fusion
desaturases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Helianthus annuus (Common sunflower).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; campanulids; Asterales; Asteraceae; Asteroideae;
Heliantheae; Helianthus.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence up
01-OCT-2002 (TrEMBLrel. 22, Last annotation
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InterPro; IPR005804; FA_desat_
Pfam; PF00487; FA_desaturase;
Pfam; PF00173; heme_1; 1.
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STRAIN=cv. inbred line HA89;
TISSUE=Cotyledons of developing sunflower
MEDLINE=21116801; PubMed=11171153;
MEDLINE=21116801; PubMed=1171153;
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(TrEMBLrel.
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01-OCT-2002 (TrEMBLrel.

Last

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"Cloning and Molecular Characterization of the D6-Desaturase fro
TEchium: Functional Expression in Yeast and Tobacco.";
L Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
C -!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
EMBL; ANOS5117; AAL23580.1; -.
R InterPro; IPR001199; Cyt B5.
RR InterPro; IPR005804; FA_Gesat_fam.
Pfam; PF00407; FA_desaturase; 1.
RPfam; PF00407; FA_desaturase; 1.
RPfam; PF0010612; Cyt B5; 1.
RP ProDom; PD001081; FA_Gesat_fam; 1.
RP PODOm; PD001081; FA_Gesat_fam; 1.
RR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
RR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
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SEQUENCE FROM N.A.

MAROTO F.G., Alonso D.L., Garrido J.-A.S., Ferron M.V., Ruiz "Cloning and Molecular Characterization of the D6-Desaturase Echium: Functional Expression in Yeast and Tobacco."; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
EMBL; AY055118; AAL23581.1; -.
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SEQUENCE
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Boraginaceae; Echium.
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Spermatophyta; Magnoliophyta; eudicotyledons;
Asteridae; lamiids; Boraginaceae; Echium.
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Pred. No. 3.2
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Best Local S
Matches 129
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InterPro; IPR005804; FA_desat_fam
Pfam; PF00487; FA_desaturase; 1.
Pfam; PF00173; heme_1; 1.
ProDom; PD000612; Cyt_B5; 1.
ProDom; PD001081; FA_desat_fam; 1
PROSITE; PS50255; CYTOCHROME_B5_2
                                                                                                                                                                                                 Submitted (JUN-1997) to the EMBL/Gen-
-!- SIMILARITY: BELONGS TO THE CYTOC
EMBL; APO07561; AADO1410.1; -
InterPro; IPR001199; Cyt B5.
InterPro; IPR005804; FA desat_fam.
Pfam; PF00487; FA desat_urase; 1.
Pfam; PF00173; heme_1; 1.
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Q9SAU5;
01-MAY-2000
                                                                                          Heme.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE-Seed;
Nunberg A.N., Beremand P.D., Thomas
"Engineering of Plant Seed Oils to
(GLA).";
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Borago officinalis (Bourrache) (Borage).

Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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01-MAY-2000 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
                                                                                                                               ProDom; PD000612; Cyt_B5; 1.
ProDom; PD001081; FA desat fam; 1.
PROSITE; PS50255; CYTOCHROME_B5_2;
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NCBI_TaxID=13363;
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  cal Similarity
131; Conserv
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  55.4%; Score 730.5; llarity 48.9%; Pred. No. 2.98 Conservative 50; Mismatches
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THE CYTOCHROME B5 F
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Last annotation updat
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Pred. No. 9.5e
59; Mismatches
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2.9e-61;
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RESULT 11
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Borago officinalis (Bourrache) (Borage).

Bukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnoliophyta; eudicotyledons;
Asteridae; lamiids; Boraginaceae; Borago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE-97268723; PubMed-9108131;

Sayanova O., Smith M.A., Lapinskas P., Stobart A.K., Dobson G.,

Christle W.W., Shewry P.R., Napier J.A.;

"Expression of a borage desaturase cDNA containing an N-terminal

cytochrome b5 domain results in the accumulation of high levels of

delta6-desaturated fatty acids in transgenic tobacco.";

Proc. Natl. Acad. Sci. U.S.A. 94:4211-4216(1997).

-I-SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
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ProDom; PD001081; FA desat fam; 1.
PROSITE; PS50255; CYTOCHROME B5_2; 1.
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InterPro; IPR001199; Cyd_BS.
InterPro; IPR005804; FA_desat_fam.
Pfam; PF00487; FA_desaturase; 1.
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                                                                                                                                                                                 121 WKWNHNAHHIACNSLDYDPDLQHMPVFAVSSRFFNSITSHXYGRKXEFDXIAXFLICYQH
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Q9ZTU8;
01-MAY-1999
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ProDom; PD000611; Cyt B5; 1.
ProDom; PD001081; FA deast fam; 1.
PROSITE; PS50255; CYTOCHROME_B5_2; 1.
PROSITE; PS00038; HLH_1; 1.
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InterPro; IPR001092; HLH basic.
InterPro; FA desaturase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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"Aluminum tolerance in yeast conferred by over-expre
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Delhaize E.,
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                                                                                                                                                                                                                                                                                             100 RLTDYTVPPASADFRRLLAQLSSAGLFERVGHTPKFLLVAMSVLFCIALYCVLACSSTGA 159
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                                   VPIQHIQFWLNHLAENLYXG
                                                                                                          VARVNLYLQTILLLFSRXKVQDRALNIMGILVFWTWFLFLLALL---
                                                                                                                                                                      HIACNSLDYDPDLQHMPVFAVSSRFFNSITSHXYGRKXEFDXIAXFLICYQHFTFYPVMC
                                                                         FARINLLVQSIVFLITQKKVRQRWLEIAGVAAFWVWYPLLVSCLPNWWERVAFVLASFVI
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TGIOHVOFCLNHFSSAVYVG
                                                                                                                                              HISCNSLDHDPDLQHLPLFAVSTKLFNNLWSVCYERTLAFDAISKFFVSYQHWTFYPVMG
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IPR005804; FA_desat_fam.
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                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                           52617 MW; 16F223CC1F79740D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                     52.1%; Score 686.5; DB 10; 48.1%; Pred. No. 4.6e-57;
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Q9HDG8;
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01-MAR-2001 (TrEMBLr
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Delta-6 desaturase.
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ProDom; PD001081; FA desat fam; 1.
PROSITE; PS50255; CYTOCHROME B5_2;
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-!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
EMBL; AY131238; AAM94345.1; -.
                                        Biochem. Biophys. Res. Commun.
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=ATCC 24905;
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Delta-6-desaturase.
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InterPro; IPR005804; FA_desat_fam
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                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=29923;
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      AF296076; AAG36960.1;
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wTFYTIMCAARLNMYVQSLIMLLTKRNVSYRAHELLGCLVFSIWYPLLVSCLPNWGERIM
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                                                                                                                                                                                                                                                                                                                                                                                                                        Fungi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ericales; Sapotaceae; Argania.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        448 AA; 51304 MW; 0B46F81B7DEE29EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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tion and c
                                                                                                                                                                                                                                                                                                                                                                                                                            Zygomycota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51.5%;
46.6%;
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cloning of
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16,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49;
                                 THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 2.5e
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 678.5;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                        Zygomycetes; Mucorales; Mucoraceae;
                                 279:17-22(2000)
CYTOCHROME B5 F
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delta-6-desaturase in
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.es 79; Indels
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Best Local
                                                                                                                                                                                                                                                                    QBNKG8;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative delta 8-sphingolipid desaturase.
Kluyveromyces lactis (Yeast).
Eukaryota; Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
NCBI_TaxID=28985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD000612; Cyt B5; 1.
ProDom; PD001081; FA desat fam; 1.
PROSITE; PS00095; C5_MTASE_2; 1.
PROSITE; PS00191; CYTOCHROME_B5_1;
PROSITE; PS50255; CYTOCHROME_B5_2;
                                                                                       Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
-- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
EMBL, AB085690; BAB93118.1; --
InterPro; IPR001199; Cyt B5.
InterPro; IPR001199; Cyt B5.
Pfam; PF00487; FA desaturase; 1.
Pfam; PF00487; FA desaturase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001199; Cyt B5-
InterPro; IPR005804; PA_desat_fam.
Pfam; PF00487; PA_desaturase; 1.
Pfam; PF00173; heme_1; 1.
                                      SEQUENCE
                                                              PROSITE;
                                                                                                                                                                                            Takakuwa N., Kinoshita M., Oda Y., Ohnishi M.;
"Isolation and characterization of the genes encodir
sphingolipid desaturase from Saccharomyces kluyveri
                                                                                                                                                                                                          Takakuwa N., Kinoshita M., Oda Y., Ohni
"Isolation and characterization of the
                                                                                                                                                                                                                                  STRAIN-IFO 1090;
                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                              Q8NKG8
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                                                              PD001081;
}; PS50255;
Similarity
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                                      573
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Ş
                                                          FA_desat_fam;
CYTOCHROME_B5
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                                      67065 MW;
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32.5%;
26.0%;
29.2%;
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Score 342.5; DB 3
Pred. No. 3.1e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 377.5;
Pred. No. 1.:
                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                      9383EBA4323F1A57
                                                             ۱<sub>2</sub>
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Search com Job time :	B .	g Q	ОУ	Фу	ОУ	Matches
Search completed: January 1, 2004, 06:33:55 Job time : 23.907 secs	236IQHIQFWLNHLA 247 	194 LY-LQTILLLESRXKVQDRALNIMGILVFWTWFLFLLALLFVP	134 SLDYDPDLOHMPVFAVSSRFFNSITSHXYGRKXEFDXIAXFLICYQHFTFYPVMCVARVN 193     :  :  :       :::      ::   ::  ::         306 DPVHDPDIQHLPFFAVSTRLFHNVYSTYYDKFLWFDKFAQKVVPIQHYLYYPILCFGRFN 365	74 ALIGFLWIQSGWIGHDSGHYNVMLSRRLNRAIQILSGNILAGISIGWWKWNHNAHHIACN 133 	19 SSDYRKLFSDLSALNLFNRKGHTTSILLSLILTLFPLSVCGVLFSDSTFVHVLSA 73	75; Conservative 53; Mismatches 92; Indels 37; Gaps 5;

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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PAFSTSHRLSDHTVSAASSDYRKLFSDLSALNLFNRKGHTTSILLSLILTLFPLSVCGVL 	nilarity Conservat	OR SEQ ARACTER 452 ami ino aci linea PE: pr	NAME: Presser, Leopold REGISTRATION NUMBER: 19,827 REFERENCE/DOCKET NUMBER: 83 TELECOMMUNICATION INFORMATION: TELEPHONE: (516) 742-4343 TELEFAX: (516) 742-4366 TELEFAX: 230 901 SANS UR	MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compati OPERATING SYSTEM: PC-DOS SOFTWARE: PATENTIN Relea CURRENT APPLICATION NUMBER: US/OFILING DATE: CLASSIFICATION: 435	ADD Scul Sar Gar York ited	0220°° (		111112222222233466 1111122222222233466
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APPLICANT: Thomas
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/366,779
FILING DATE: 30-DEC-1994
                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                          NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 83
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
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CORRESPONDENCE ADDRESS:
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APPLICANT: Numberg, Andrew N.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINGLENIC ACID BY A
TITLE OF INVENTION: DELTA 6-DESATURASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
                                                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                     Matches 131;
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                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                       TELEX: 230 901 SANS UR INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/3
FILING DATE: 30-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (516) 742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Presser, Leope
REGISTRATION NUMBER:
                                                                                                                                                                                                                                        TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
                                                                                                                                                                                                                                                                         LENGTH: 448 amino acids
                                                                                                                                                                                                                                                                                                                                           TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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 132 LFCEGVLVHLFSGCLMGFLWIQSGWIGHDAGHYMVVSDSRLNKFMGIFAANCLSGISIGW
                     61 LFSDSTFVHVLSAALIGFLWIQSGWIGHDSGHYNVMLSRRLNRAIQILSGNILAGISIGW 120
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                                                                  LDKFFTGYYLKDYSVSEVSKDYRKLVFEFSKMGLYDKKGHIMFATLCFIAMLFAMSVYGV
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                                                                                                                                                                                                                                                                                                                                              (516) 742-4366
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Freyssinet, Georges L.
                                                                                                                                     Conservative
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                                                                                                                                  55.4%; Score 730.5; DB 1;
48.9%; Pred. No. 4e-74;
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                                                                                                                                     Indels
                                                                                                                                                                   Length 448;
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Patent No. 6355861
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                           Matches 131;
                                                                                                                                                                                                                                                                                                                                               Query Match
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Presser, Leopold
REGISTATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 83
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,254
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STATE: New York
Timited St
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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TYPE: amino acid
TOPOLOGY: linear
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WTFYPIMCAARLNMYVQSLIMLLTKRNVSYRAQELLGCLVFSIWYPLLVSCLPNWGERIM
                    FTFYPVMCVARVNLYLQTILLLFSRXKVQDRALNIMGILVFWTWF----
                                                                        WKWNHNAHHIACNSLEYDPDLQYIPFLVVSSKFFGSLTSHFYEKRLTFDSLSRFFVSYQH
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400 Garden City Plaza
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US-08-833-610-5
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Best Local Similarity
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LENGTH: 446 amino acids
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APPLICATION NUMBER: US,
FILING DATE: 11-APR-199
CLASSIFICATION: 435
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REFERENCE/POCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)328-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,7'
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ADDRESSEE: RAE-VENTER LAW
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STRANDEDNESS: not
TOPOLOGY: linear
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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FLLALLFVP-IQHIQFWLNHLAENLYXG 253
                                                                        FTFYPVMCVARVNLYLQTILLLFSRXKVQDRALNIMGILVFWTWF-----
                                                                                                                                      WKWNHNAHHIACNSLDYDPDLQHMPVFAVSSRFFNSITSHXYGRKXEFDXIAXFLICYQH
                                    WTFYPIMCAARLNMYVQSLIMLLTKRNVSYRAQELLGCLVFSIWYPLLVSCLPNWGERIM 311
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MURKERJI, PRADIP

HUANG, YUNG-SHENG

THURMOND, JENNIFER

CHAUDHARY, SUNITA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  not relevant
                                                                                                                                                                                                                                                                                                                                               54.7%; Score 721.5; DB 2
48.5%; Pred. No. 4.1e-73;
ative 50; Mismatches 73
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P.O. BOX 60039
                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                     Length 446;
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                                                                                                                                                                                                                                                                                                                                                              Matches 130;
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-300.USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
STREET: 2001 FERRY BUILDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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APPLICANT: CHAUDHARY, SUNITA

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS

FITTLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                               132 LFCEGVLVHLFSGCLMGFLWIQSGWIGHDAGHYMVVSDSRLNKFMGIFAANCLSGISIGW
                                          252 WTFYPIMCAARLNMYVOSLIMLLTKRNVSYRAQELLGCLVFSIWYPLLVSCLPNWGERIM
                                                                                                                        192 WKWNHNAHHIACNSLEYDPDLQYIPFLVVSSKFFGSLTSHFYEKRLTFDSLSRFFVSYQH
                                                                                                                                            121 WKWNHNAHHIACNSLDYDPDLQHMPVFAVSSRFFNSITSHXYGRKXEFDXIAXFLICYQH 180
                                                                                                                                                                                                                                                                                     72
                                                                                                                                                                                                                                          61 LESDSTFVHVLSAALIGFLWIQSGWIGHDSGHYNVMLSRRLNRAIQILSGNILAGISIGW 120
                                                                                                                                                                                                                                                                                                                       1 LPAFSTSHRLSDHTVSAASSDYRKLFSDLSALNLFNRKGHTTSILLSLILTLFPLSVCGV
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6075183
FLLALLFVP-IQHIQFWLNHLAENLYXG
                                                                                 FTFYPVMCVARVNLYLQTILLLFSRXKVQDRALNIMGILVFWTWF------L
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      253
                                                                                                                                                                                                                                                                                                                                                              73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     446;
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US-08-834-655-7
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Best Local Similarity
Matches 125; Conserv
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: MURKERJI, FRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND
TITLE OF INVENTION: OF LONG CHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDLIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,655
FILING DATE: 11-APR-1997
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 328-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAB-VENTER LAW GROUP, P.C.
ADDRESSEE: 260 SHERIDAN AVENUE, P.O. BOX 60039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
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CITY: PALO ALTO
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: not
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                                                                           125
                                                                                              179 QHFTFYPVMCVARVNLYLQTILLLFSRXKVQDRALNIMGILVFWTWFLFLLALL-----
                                                                                                                                                                        119 GWWKWNHNAHHIACNSLDYDDDLQHMPVFAVSSRFFNSITSHXYGRKXEFDXIAXFLICY 178
                                  233 --FV-----PIQHIQFWLNHLAENLYXG
                                                                                                                                                                                                                                                 59 GVLFSDSTFVHVLSAALIGFLWIQSGWIGHDSGHYNVMLSRRLNRAIQILSGNILAGISI
                                                                                                                                                   65 AWWKWTHNAHHLACNSLDYDPDLOHIPVFAVSTKFFSSLTSRFYDRKLTFGPVARFLVSY
                                                                                                                                                                                                                          5 GVLACTSVFAHQIAAALLGLLWIQSAYIGHDSGHYVIMSNKSYNRFAQLLSGNCLTGISI 64
                                                                         QHFTYYPVNCFGRINLFIQTFLLLFSKREVPDRALNFAGILVFWTWFPLLVSCLPNWPER 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/08834655
FFFVFTSFTVTALQHIQFTLNHFAADVYVG
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linear
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OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS
                                                                                                                                                                                                                                                                                              51.8%; Score 682.5; DB 2; 59.5%; Pred. No. 4.7e-69; tive 27; Mismatches 43;
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RESULT 8 US-08-834-033A-8

Sequence 8, Application US/08834033A Patent No. 6075183

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US-09-363-574-7
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                                                                                                      Sequence 7, Application US/09363574 Patent No. 6136574
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Best Local Similarity
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                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY AVNUMBER OF SEQUENCES: 26
                                                     APPLICANT:
                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (415) 433-4150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/834,033A FILING DATE: 11-APR-1997 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGTH:
                                                                                                                                                                                                                                        233 -- FV----- PIQHIQFWLNHLAENLYXG 253
                                                                                                                                                                                                                                                                                                                                                             119 GWWKWNHNAHHIACNSLDYDPDLQHMPVFAVSSRFFNSITSHXYGRKXEFDXIAXFLICY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125;
                                                                                                                                                                                                                                                                                                        179 QHFTFYPVMCVARVNLYLQTILLLFSRXKVQDRALNIMGILVFWTWFLFLLALL-----
                                                                                                                                                                                                                                                                                                                                           65 AWWKWTHNAHHLACNSLDYDPDLQHIPVFAVSTKFFSSLTSRFYDRKLTFGPVARFLVSY 124
                                                                                                                                                                                                                                                                                                                                                                                                                                  59 GVLFSDSTFVHVLSAALIGFLWIQSGWIGHDSGHYNVMLSRRLNRAIQILSGNILAGISI 118
                                                                                      INFORMATION:
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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THURMOND, JENNIFER CHAUDHARY, SUNITA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THURMOND, JENNIFER CHAUDHARY, SUNITA
                   HUANG, YUNG-SHENG
THURMOND, JENNIFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HUANG,
                                                   KNUTZON, DEBORAH
MURKERJI, PRADIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MUKERJI
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YUNG-SHENG
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Pred. No. 4.7e-69;
7; Mismatches 43;
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                                                                                                                                                                                                                                                          RESULT 10
US-09-363-526-7
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Best Local Similarity
                                                                                                                                                                                                                      Patent No. 6410288
                                                                                                                                                                                                                                       Sequence 7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERRINCE/DOCKET NUMBER: CGAB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433,4150
                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                    APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND CO
TITLE OF INVENTION: OF LONG CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
STREET: 2001 FERRY BUILDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/363,574
FILING DATE:
CLASSIFICATION:
                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 433-8716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: SAN FRANCISCO
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                                                                                                                                                                                                                                                                                                                                     185
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                                                         OF SEQUENCES:
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                                                                                                                                                                                                                                       Application US/09363526
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                                                                                                         KNUTZON, DEBORAH
MURKERJI, PRADIP
HUANG, YUNG-SHENG
THURMOND, JENNIFER
CHAUDHARY, SUNITA
: LIMBACH AND LIMBACH L.L.P. 2001 FERRY BUILDING
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OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51.8%; Score 682.5; DB 3
59.5%; Pred. No. 4.7e-69;
tive 27; Mismatches 43
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                                                                        COMPOSITIONS FOR SY IN POLY-UNSATURATED
                                                                                                                                                                                                                                                                                                                                   214
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                                                                        FATTY ACIDS IN PLANTS
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

94113

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                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/08834655 Patent No. 5968809
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                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: N/A
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,526
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                           NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:
ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
                                                                                                                                                                                                                  APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                  STATE:
                                                                                                       STREET: 260 SHEE
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 51.8%; Score 682.5; DB 4
Local Similarity 59.5%; Pred. No. 4.7e-69;
les 125; Conservative 27; Mismatches 43
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH:
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                                                                                                                                                                                                                                                             THURMOND, JENNIFER CHAUDHARY, SUNITA
                                                                                                                                                                                                                                                                                                            HUANG,
                                                                                                                                                                                                                                                                                                                            KNUTZON, DEBORAH
MURKERJI, PRADIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (415) 433-8716
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Best Local S
                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDERRECT 5.1

CURRENT APPLICATION DATA:

APPLICATION UMBER: US/08/834,033.

PILING DATE: 11-APR-1997

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: WARD, MICHAEL R.

REGISTRATION NUMBER: 38,651

REGISTRATION NUMBER: 38,651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: not
TOPOLOGY: linear
MOLECULE TYPE: pept:
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APPLICANT:
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APPLICANT:
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ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION UNBER: US/08/834,655 FILING DATE: 11-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY A
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REFERENCE/DOCKET NUMBER: CGN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 328-4400
REFERENCE/DOCKET NUMBER: CG
FELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                  STREET: 2001 FERRY CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: LIMBACH AND LIMBACH, L.L.P. STREET: 2001 FERRY BUILDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX:
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55; Conserv
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HUANG, YUNG-SHENG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KNUTZON, DEBORAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.1%; Score 291; DB 2; 52.4%; Pred. No. 2.3e-25; tive 15; Mismatches 25
                                                                                                                                                                        US/08/834,033A
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                                              CGAB-300.USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FATTY ACIDS IN PLANTS
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                Query Match
Best Local
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                                                                                                                                  TELEX: N/A
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acid
                                                                                                                                                                                                                         CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATMAE: WARD, MICHAEL R.

REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB
TELECOMPUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                               TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                            TELEPHONE: (415) 433-8716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: LIMBACH AND LIMBACH L.L.P. STREET: 2001 FERRY BUILDING CITY: SAN FRANCISCO
Local Similarity tes 55; Conserv
                                                                                                           STRANDEDNESS:
                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 55; Conserv
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TOPOLOGY: lir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 NNXFAQLLSGNCLTGI-IAWWKWTHNAHHLACNSLDYGPNLQHIP 104
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MURKERJI, PRADIP
HUANG, YUNG-SHENG
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                                                                                                           not relevant
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y 52.4%; Pred. No. ...
              22.1%; Score 291; DB 3; 52.4%; Pred. No. 2.3e-25;
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 Mismatches
                               DB 3; Length 104;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amin
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                                                                                                                                                                                         Query Match
                                                                                                                                                      Matches
                                                                                                                                                                      Query Match 22.1%; Score 291; DB 4; Length 104; Best Local Similarity 52.4%; Pred. No. 2.3e-25;
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CG
                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 433-4150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
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                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: not
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 2001 FERRY
CITY: SAN FRANCISCO
STATE: CA
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                                  101 LURAIQILSGNILAGISIGWWKWNHNAHHIACNSLDYDPDLQHMP 145
61 NNXFAQLLSGNCLTGI-IAWWKWTHNAHHLACNSLDYGPNLQHIP 104
                                                                                               50 LTLFPLS------VCGVLFSDSTFVHVLSAALIGFLWIQSGWIGHDSGHYNVWLSRR 100
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US-08-834-655-2

Sequence 2, Application US/08834655 Patent No. 5968809

GENERAL INFORMATION:

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APPLICANT:
APPLICANT:
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TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: PALO ALTO
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: US
ZIP: 94306
276 WCLQSILFVLPNGQAHKPSGARVPISLVEQUSLAMHWTWYLATM-FLFIKDPVNMLVYFL 334
                           194 LYLQTILLLF------SRXKVQDRALNIMGILVFWTWFLFLLALLFV--PIQHIQFWL 243
                                                        221 EDPDIDTHPLLTWSEHALEMFSDVPDEELTRMW-----SRFMVLNQTWFYFPILSFARLS
                                                                         137 YDPDLQHMPVFAVSS---RFFNSITSHXYGRKXEFDXIAXFLICYQHFTFYPVMCVARVN 193
                                                                                                                    161 GLFWQQCGWLAHDFLHHQVFQDRFWGDLFGAFLGGVCQGFSSSWWKDKHNTHHAAPNVHG 220
                                                                                                                                                                          101 AAEVRKLRTLFQSLGYYDSSKAYYAFKVSFNLCIWGLSTVIVAKWGQTSTLANVLSAALL 160
                                                                                                                                       77 GFLWIQSGWIGHDSGHYNVMLSRRLNRAIQILSGNILAGISIGWWKWNHNAHHIACNSLD 136
                                                                                                                                                                                                    19 SSDYRKLFSDLSALNLFNRKGHTTSILLSLILTLFPLS--VCGVLFSDSTFVHVLSAALI
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MURKERJI, PRADIP
HUANG, YUNG-SHENG
THURMOND, JENNIFER
CHAUDHARY, SUNITA
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Search completed: January 1, 2004, 06:38:14 Job time : 9.98981 secs

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Minimum DB
Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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747.5
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seq length: 2000000000
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Match Length
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1: /cgn2_6/ptodata/1/pubpaa/US07_

2: /cgn2_6/ptodata/1/pubpaa/PCT N

3: /cgn2_6/ptodata/1/pubpaa/US06_
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/cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
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US-10-029-756-27

US-10-340-779A-11

US-10-340-779A-13

US-10-340-779A-13

US-10-369-493-4137

US-09-769-863-14

US-10-054-534B-14

US-10-431-952-14

US-10-278-391-4

US-10-191-513A-41

US-10-191-513A-41

US-10-191-513A-41

US-10-191-513A-41

US-10-191-513A-41

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                 Sequence 27, Appl
Sequence 11, Appl
Sequence 5, Appli
Sequence 13, Appl
Sequence 4137, Ap
Sequence 14, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 17, Appl
Sequence 17, Appl
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Sequence 17, Appl
Sequence 18, Appli
Sequence 20, Appli
Sequence 20, Appl
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e 12, App e 2766, A	equence 2586, A	equence 650, Ap	equence 15,	equence 14,	equence 19,	equence 4,	equence 40,	equence 18,	equence 20,	equence 33,	equence 35,	equence 55,	equence 69,	equence 1,	equence 42,	equence 31,	equence 3,	equence	equence 29,	equence 29,	equence 38,	equence 9, 1	equence 12, App	equence 39, Ap	equence 9130,	equence 9	ence 6107,	equence 4

## ALIGNMENTS

	D: 27	
	TELEFAX: (516) /42-4343 TELEFAX: (516) 742-4366 TELEX: 230 901 SANS UR	
	TELECOMMUNICATION INFORMATION:	••
	REGISTRATION NUMBER: 19,827 REFERENCE/DOCKET NUMBER: 8383ZYXWVU	٠. ٠.
	NAME: Presser, Leopold	••
	ATTORNEY/AGENT INFORMATION:	•• ••
	APPLICATION NUMBER: 08/934,254	-
	PRIOR APPLICATION DATA:	•••
	CLASSIFICATION: <unknown></unknown>	
	APPLICATION NUMBER: US/10/029,756	٠.
		••
	SOFTWARE: PatentIn Release #1.0, Version #1.25	
	COMPUTER: IBM PC compatible	•
	MEDIUM TYPE: Floppy disk	
	COMPUTER READABLE FORM:	٠.
	COUNTRY: United States	
	STATE: New York	
	CIMP: Garden City staza	
	SS:	-
	NUMBER OF SEQUENCES: 27	
	DELTA 6-DESATURASE	
ACID BY	TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC AC	
	Publication No. US20020108147A1	
	Sequence 27, Application US/10029756	
	US-10-029-756-27	77
	RESULT 1	÷

LENGTH: 452 amino

acids

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GENERAL INFORMATION:

APPLICANT: Napier, Johnathan A.

APPLICANT: Michaelson, Louise

APPLICANT: Stobart, Keith

TITLE OF INVENTION: Desaturase

FILE REFERENCE: 005407.00004

CURRENT APPLICATION NUMBER: US/10/340,779A

CURRENT FILLING DATE: 2003-03-24

PRIOR APPLICATION NUMBER: US 09/582,034
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MOLECULE TYPE: protein
;
SEQUENCE DESCRIPTION: SEQ ID
US-10-029-756-27
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                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11, Application US/10340779A Publication No. US20030152983A1
                                                                                                                                                                                          Matches
                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: PCT/GB98/03895
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: UK 9814034.6
PRIOR APPLICATION NUMBER: UK 9727256.1
PRIOR APPLICATION NUMBER: UK 9727256.1
PRIOR FILING DATE: 1997-12-23
                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ
                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                  ORGANISM: Helianthus
                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                          LENGTH: 458
                                   145 GSFWIHMLSGAILGLAWMQIAYLGHDAGHYQMMATRGWNKFAGIFIGNCITGISIAWWKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      314 VLISFAVTAIQHVQFTLNHFSGDTYVG 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 TFYPVMCVARVNLYLQTILLLFSRXKVQDRALNIMGILVFWTWF-LF--------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 NHNAHHIACNSLDYDPDLQHMPVFAVSSRFFNSITSHXYGRKXEFDXIAXFLICYQHFTF 183
                                                                                                                                                                                          140;
                                                                        64 DSTFVHVLSAALIGFLWIQSGWIGHDSGHYNVMLSRRLNRAIQILSGNILAGISIGWWKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 FSDSTFVHVLSAALIGFLWIQSGWIGHDSGHYNVMLSRRLNRAIQILSGNILAGISIGWW
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                                                                                                                                       6 TSHRLSDHTVSAASSDYRKLFSDLSALNLFNRKGHTTSILLSLILTLFPLSVC--GVLFS
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                                                                                                             TGYHLKDYQVSDISRDYRKLASEFAKAGMFEKKGH--GVIYSLCFVSLLLSACVYGVLYS
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53.2%; Pred. No. 2.8e-70;
53.2%; Mismatches 73;
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                                                                                                                                                                                      Score 747.5;
Pred. No. 1.2e
40; Mismatches
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nes 66; Indels
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Sequence 5, Application US/10029756
Publication No. US20020108147A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 131; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEPAR: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: Protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Thomas, Terry L.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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                                                                          132
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                                                                                              61 LFSDSTFVHVLSAALIGFLWIQSGWIGHDSGHYNVMLSRRLNRAIQILSGNILAGISIGW 120
                                                                                                                                                    72 LDKFFTGYYLKDYSVSEVSKDYRKLVFEFSKMGLYDKKGHIMFATLCFIAMLFAMSVYGV
                                                                                                                                                                                      1 LPAFSTSHRLSDHTVSAASSDYRKLFSDLSALNLFNRKGHTTSILLSLILTLFPLSVCGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
                                                                          LFCEGVLVHLFSGCLMGFLWIQSGWIGHDAGHYMVVSDSRLNKFMGIFAANCLSGISIGW
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WKWNHNAHHIACNSLEYDPDLQYIPFLVVSSKFFGSLTSHFYEKRLTFDSLSRFFVSYQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/934,254 FILING DATE: <Unknown>
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CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/10/029,756
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                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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                                                                                                                                                                                                                            55.4%; Score 730.5; DB 1
48.9%; Pred. No. 6.9e-68;
ative 50; Mismatches 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (516) 742-4343
516) 742-4366
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                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                  Length 448;
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RESULT 5
US-10-369-493-4137
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APPLICANT: Michaelson, Louise
APPLICANT: Michaelson, Louise
APPLICANT: Stobart, Keith
TITLE OF INVENTION: Desacurase
FILE REFERENCE: 005407.00004
CURRENT APPLICATION NUMBER: US/10/340,779A
CURRENT FILING DATE: 2003-03-24
PRIOR APPLICATION NUMBER: US 09/582,034
PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: PCT/GB98/03895
PRIOR APPLICATION NUMBER: UX 9814034.6
PRIOR FILING DATE: 1998-12-23
PRIOR FILING DATE: 1998-06-29
PRIOR FILING DATE: 1998-06-29
PRIOR FILING DATE: UX 9814034.6
PRIOR APPLICATION NUMBER: UX 9727256.1
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Best Local S
Matches 131
                                                                                                                                             Sequence 4137, Application US/10369493 Publication No. US20030233675A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 1997-12-23
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13, Application US/10340779A Publication No. US20030152983A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
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                                                                                                                                                                                                                                                                                                     312 FVIASLSVTGMQQVQFSLNHFSSSVYVG 339
                                                                                                                                                                                                                                                                                                                                                                                         252 WTFYPIMCAARLNMYVQSLIMLLTKRNVSYRAHELLGCLVFSIWYPLLVSCLPNWGERIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 WKWNHNAHHIACNSLDYDPDLQHMPVFAVSSRFFNSITSHXYGRKXEFDXIAXFLICYQH 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 LFSDSTFVHVLSAALIGFLWIQSGWIGHDSGHYNVMLSRRLNRAIQILSGNILAGISIGW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WKWNHNAHHIACNSLEYDPDLQYIPFLVVSSKFFGSLTSHFYEKRLTFDSLSRFFVSYQH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.3%; Score 729.5; DB 12; Length 448;
48.9%; Pred. No. 8.8e-68;
tive 50; Mismatches 72; Indels 15;
                                                                                                                                                                                                                                                                                                                                            253
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; ORGANISM: Neurospora crassa
US-10-369-493-4137
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PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 4137
                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
                                                                                                                                                                                                      Query Match
Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Thurmond, Jennifer
APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
FILE REFERENCE: 6763.US.01
CURRENT APPLICATION NUMBER: US/09/769,863
CURRENT FILING DATE: 2001-01-25
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CURRENT FILING DATE: 2003-02-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Huang, Yung-Sheng
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                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Saprolegnia diclina
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TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                           LENGTH: 453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142 QHMPVFAVSSRFFNSITSHXYGRKXEFDXIAXFLICYQHFTFYPVMCVARVNLY-LQTIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  239 IOFWLNHLA 247
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143 C--LHFDSTAMYMVAAVILGLFYQQCGWLAHDFLHHQVFENHLFGDLVGVMVGNLWQGFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82 QSGWIGHDSGHYNVMLSRRLNRAIQILSGNILAGISIGWWKWNHNAHHIACNSLDYDPDL 141
                                          58 CGVLFSDSTFVHVLSAALIGFLWIQSGWIGHDSGHYNVMLSRRLNRAIQILSGNILAGIS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 QLVFTAHDAGHMGITHHFHVDTVÍGÍIIADFIGGLSLGWWKRNHNVHHIITNSPEHDÞDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 YRKLFSDLSALNLFNRKGHTTSILLSLILTLFPLSVCGVLFSDSTFVHVLSAALIGFLWI
                                                                                           85 AVDTS--ISDEVKKSQSDFIASYRKLRLEVKRLGLYDSSKLYYLYKCASTLSIALVSAAI
                                                                                                                                                                                         69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78; Conservative
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                                                                                                                                          AFSTSHRLSDHTVSAAS---SDYRKLFSDLSALNLF--NRKGHTTSILLSLILTLFPLSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Das, Tapas
                                                                                                                                                                                         Conservative
                                                                                                                                                                                                             19.6%; Score 258.5; DB 1
26.3%; Pred. No. 1.5e-18;
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                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                         DB 12;
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                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                    Length 453;
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US-10-431-952-14
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US-10-054-534B-14
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                                                                                                    GENERAL INFORMATION:
                                                                                                                     Sequence 14, Application US/10431952 Publication No. US20030190733A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
FILE REFERENCE: 6763.US.P1
CURRENT APPLICATION NUMBER: US/10/054,534B
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: US 09/769,863
PRIOR FILING DATE: 2001-01-25
NUMBER OF SEQ ID NOS: 55
NUMBER OF SEQ ID NOS: 55
                                                        APPLICANT: Abbott Laboratories APPLICANT: Mukerji, Pradip
                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 453
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                               312
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                                                                                                                                                                                                                                                                                    WFLFLL------ALLFV 234
                                                                                                                                                                                                                                               WNLGLVYAANMSLLQAAAFLFV 333
                                                                                                                                                                                                                                                                                                                                                                  IAXFLICYOHFTFYPVMCVARVNLYLQTILLLF-----SRXKVQDRALNIMGILVFWT 223
                                                                                                                                                                                                                                                                                                                                                                                                          VQWWKNKHNTHHAIPNLHATPEIAFHGDPDIDTMPILAWSLK----MAQHAVD-----SP 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C--LHFDSTAMYMVAAVILGLFYQQCGWLAHDFLHHQVFENHLFGDLVGVMVGNLWQGFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AVDTS--ISDEVKKSQSDFIASYRKLRLEVKRLGLYDSSKLYYLYKCASTLSIALVSAAI 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AFSTSHRLSDHTVSAAS----SDYRKLFSDLSALNLF--NRKGHTTSILLSLILTLFPLSV
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                  Mukerji, France, Mukerji, France, France, Yung-Sheng
                                                                                                                                                                                                                                                                                                                        VGLFFMRYQAYLYFFILLFARISWVIQSAMYAFYNVGPGGTFDKVQYPLLERAGLLLYYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WNLGLVYAANMSLLQAAAFLFV 333
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Mukerji, ria-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thurmond, Jennifer M. Pereira, Suzette L.
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Jennifer
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26.3%; Pred. No. 1.5e-18;
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RESULT 9
US-10-278-391-4
US-10-278-391-4
; Sequence 4, Application US/10278391
; Publication No. US20030159164A1
; Publication No. US20030159164A1
GENERAL INFORMATION:
GENERAL TOWN J.
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
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TITLE OF INVENTION: DESATURASE GENES AND USES
FILE REFERENCE: 6763.US.O1
CURRENT APPLICATION NUMBER: US/10/431,952
CURRENT FILING DATE: 2003-05-08
PRIOR APPLICATION NUMBER: US/09/769,863
PRIOR FILING DATE: 2001-01-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Saprolegnia diclina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 453
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                                                                                                                        ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTMARE: PATENTIA Release #1.0,

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL,
STREET: 220 MONTGOMERY STREE
                                                                                                                                                                                                                                                                                                                                                                                                                      MUKERJI, PRADIP
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
SYNTHESIS OF FATTY ACIDS, THEIR DERIVATIVES AND DOWNSTREAM
                                        PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 CGVLFSDSTFVHVLSAALIGFLWIQSGWIGHDSGHYNVMLSRRLNRAIQILSGNILAGIS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85 AVDTS--ISDEVKKSQSDFIASYRKLRLEVKRLGLYDSSKLYYLYKCASTLSIALVSAAI 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 AFSTSHRLSDHTVSAAS----SDYRKLFSDLSALNLF---NRKGHTTSILLSLILTLFPLSV
                                                            APPLICATION NUMBER: US/10/278,391 FILING DATE: 23-Oct-2002 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VGLFFMRYQAYLYFFILLFARISWVIQSAMYAFYNVGPGGTFDKVQYPLLERAGLLLYYG 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IGWWKWNHNAHHIACN-----SLDYDPDLQHMPVFAVSSRFFNSITSHXYGRKXEFDX 170
                                                                                                                                                                                                                                                                                                    STREET: 220 MONTGOMERY STREET, CITY: SAN FRANCISCO STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WNLGLVYAANMSLLQAAAFLFV 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WFLFLL-----ALLFV 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VQWWKNKHNTHHAIPNLHATPEIAFHGDPDIDTMPILAWSLK----MAQHAVD-----SP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C--LHFDSTAMYMVAAVILGLFYQQCGWLAHDFLHHQVFENHLFGDLVGVMVGNLWQGFS
APPLICATION NUMBER: US/09/087,578 FILING DATE: 29-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IAXFLICYQHFTFYPVMCVARVNLYLQTILLLF-----SRXKVQDRALNIMGILVFWT
                                                                                                                                                                                                                                                                              COUNTRY: UNITED STATES OF AMERICA
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HUANG, YUNG-SHENG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KIRCHNER, STEPHEN J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.6%; Score 258.5; DB 1
26.3%; Pred. No. 1.5e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52; Mismatches
                                                                                                                                                 #1.0,
                                                                                                                                                                                                                                                                                                                                               SUITE
                                                                                                                                                   Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 12;
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APPLICANT: Huang, Yung-Sheng
APPLICANT: Tapas, Das
ITITLE OF INVENTION: HUMAN DESATURASE GENE AND USI
FILE REFERENCE: 6295.US.D3
CURRENT APPLICATION NUMBER: US/10/191,513A
CURRENT FILING DATE: 2002-09-25
PRIOR APPLICATION NUMBER: US 09/227,613
PRIOR FILING DATE: 1999-01-08
PRIOR APPLICATION NUMBER: PCT/US98/07422
PRIOR APPLICATION NUMBER: US 08/833,610
PRIOR APPLICATION NUMBER: US 08/833,610
PRIOR FILING DATE: 1997-04-11
NUMBER OF SEQ ID NOS: 54
SCQ ID NO 11
LENGTH: 458
TYPER: PRT
                                                                                 ; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (458) ... (458)
; OTHER INFORMATION: Xaa = Unknown or other at position
US-10-191-513A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
US-10-191-513A-11
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Query Match 18.8%;
Best Local Similarity 26.7%;
Matches 64; Conservative 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Abbott Laboratories APPLICANT: Mukerji, Pardip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,6
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WCLQSILFVLPNGQAHKPSGARVPISLVEQLSLAMHWTWYLATM-FLFIKDPVNMLVYFL 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YDPDLQHMPVFAVSS---RFFNSITSHXYGRKXEFDXIAXFLICYQHFTFYPVMCVARVN 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLFWQQCGWLAHDFLHHQVFQDRFWGDLFGAFLGGVCQGFSSSWWKDKHNTHHAAPNVHG 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EDPDIDTHPLLTWSEHALEMFSDVPDEELTRMW-----SRFMVLNQTWFYFPILSFARLS 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GFLWIQSGWIGHDSGHYNVMLSRRLNRAIQILSGNILAGISIGWWKWNHNAHHIACNSLD 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 457 amino acids
TYPE: amino acid
STRANDEDNESS: No. US20030159164Å1 Relevant
TOPOLOGY: No. US20030159164A1 Relevant
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Leonard, Amanda E.
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  45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45; Mismatches
Score 247.5; DB 15; Length 458; Pred. No. 2.1e-17; 5; Mismatches 110; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32,837
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  21;
Gaps
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CURRENT APPLICATION NUMBER: US/10/191,513A
CURRENT FILING DATE: 2002-09-25
PRIOR APPLICATION NUMBER: US 09/227,613
PRIOR FILING DATE: 1999-01-08
PRIOR APPLICATION NUMBER: POT/US98/07422
PRIOR FILING DATE: 1998-04-10
PRIOR APPLICATION NUMBER: US 08/833,610
PRIOR APPLICATION NUMBER: US 08/833,610
PRIOR FILING DATE: 1997-04-11
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 4.0
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; OTHER INFORMATION: Xaa = Unknown or other at position US-10-191-513A-41
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                                                                                                                                                                                                                                                                                                                                                       Query Match 18.8%; Score 247.5; DB 15; Length Best Local Similarity 26.7%; Pred. No. 2.1e-17; Matches 64; Conservative 45; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 41, Application US/10191513A Publication No. US20030104596A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Abbott Laboratories APPLICANT: Mukerji, Pardip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF FILE REFERENCE: 6295.US.D3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens FEATURE: NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 458
TYPE: PRT
                                              194 LYLQTILLLF-----SRXKVQDRALNIMGILVFWTWFLFLLALLFV--PIQHIQFWL
                                                                                         221
                                                                                                                                     137
                                                                                                                                                                                 161
                                                                                                                                                                                                                                                                    101 AAEVRKLRTLFQSLGYYDSSKAYYAFKVSFNLCIWGLSTVIVAKWGQTSTLANVLSAALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 AAEVÄKLRTLFQSLGYYDSSKAYYAFKVSFNLCIWGLSTVIVAKWGQTSTLANVLSAALL 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     194 LYLQTILLEF-----
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WCLQSILFVLPNGQAHKPSGARVPISLVEQLSLAMHWTWYLATM-FLFIKDPVNMLVYFL
                                                                                                                                 YDPDLQHMPVFAVSS----RFFNSITSHXYGRKXEFDXIAXFLICYQHFTFYPVMCVARVN 193
                                                                                                                                                                               GLFWQQCGWLAHDFLHHQVFQDRFWGDLFGAFLGGVCQGFSSSWWKDKHNTHHAAPNVHG 220
                                                                                                                                                                                                                        GFLWIQSGWIGHDSGHYNVMLSRRLNRAIQILSGNILAGISIGWWKWNHNAHHIACNSLD 136
                                                                                                                                                                                                                                                                                                             SSDYRKLESDLSALNLENRKGHTTSILLSLILTLEPLS--VCGVLESDSTEVHVLSAALI 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WCLQSILFVLPNGQAHKPSGARVPISLVEQLSLAMHWTWYLATM-FLFIKDPVNMLVYFL 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EDPDIDTHPLLTWSEHALEMFSDVPDEELTRMW----SRFMVLNQTWFYFPILSFARLS
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                                                                                         EDPDIDTHPLLTWSEHALEMFSDVPDEELTRMW-----SRFMVLNQTWFYFPILSFARLS
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Leonard, Amanda E.
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RESULT 12 US-10-191-513A-17

Sequence 17, Application US/10191513A Publication No. US20030104596A1

GENERAL INFORMATION:

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: LOCATION: (323)...(323)

: OTHER INFORMATION: Xaa = Unknown or other at position

US-10-191-513A-17
                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-967-477B-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 323
TYPE: PRT
                                                            SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF FILE REFERENCE: 6295.US.D3
CURRENT APPLICATION NUMBER: US/10/191,513A
CURRENT FILING DATE: 2002-09-25
PRIOR APPLICATION NUMBER: US 09/227,613
PRIOR PILING DATE: 1999-01-08
PRIOR PILING DATE: 1999-01-08
PRIOR APPLICATION NUMBER: PCT/US98/07422
PRIOR FILING DATE: 1998-04-10
PRIOR FILING DATE: 1998-04-10
PRIOR FILING DATE: 1998-04-11
NUMBER OF SEQ ID NOS: 54
                                                                             PRIOR APPLICATION NUMBER: 60/297,562
PRIOR FILING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/967,477B
CURRENT FILING DATE: 2002-04-16
PRIOR APPLICATION NUMBER: 60/236,303
PRIOR FILING DATE: 2000-09-28
                                                                                                                                                                                                                                              APPLICANT: Xiao Qiu
APPLICANT: Haiping Hong
TITLE OF INVENTION: FAD4, FAD5, FAD5-2, AND FAD6, NOVEL
TITLE OF INVENTION: FATTY ACID DESATURASE FAMILY MEMBERS AND USES THEREOF
FILE REFERENCE: BNZ-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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APPLICANT: Mukerji, Pardip
ORGANISM: Thraustochytrium sp
                       LENGTH: 459
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188 IKDPVNMLVYFL 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234 V--PIQHIQFWL 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 TFYPVMCVARVNLYLQTILLLF-----SRXKVQDRALNIMGILVFWTWFLFLLALLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 HNAHHIACNSLDYDPDLQHMPVFAVSS---RFFNSITSHXYGRKXEFDXIAXFLICYQHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 STFVHVLSAALIGFLWIQSGWIGHDSGHYNVMLSRRLNRAIQILSGNILAGISIGWWKWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 HNTHHAAPNVHGEDPDIDTHPLLTWSEHALEMFSDVPDEELTRMW-----SRFMVLNQTW 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 STLANVLSAALLGLFWOOCGWLAHDFLHHOVFQDRFWGDLFGAFLGGVCQGFSSSWWKDK 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56;
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Tapas, Das
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Leonard, Amanda E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          323;
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APPLICANT: Napier, Johnathan A.
APPLICANT: Michaelson, Louise
APPLICANT: Michaelson, Louise
APPLICANT: Stobart, Keith
TITLE OF INVENTION: Desaturase
FILE REFERENCE: 005407.00004
CURRENT APPLICATION NUMBER: US/10/340,779A
CURRENT FILING DATE: 2003-03-24
PRIOR APPLICATION NUMBER: US 99/582,034
PRIOR APPLICATION NUMBER: US 99/582,034
PRIOR PILING DATE: 2000-12-19
PRIOR FILING DATE: 1998-12-23
PRIOR FILING DATE: 1998-12-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: C. elegans
US-10-340-779A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-340-779A-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 20 LENGTH: 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20, Application US/10340779A Publication No. US20030152983A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local
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PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: UK 9814034.6 PRIOR FILING DATE: 1998-06-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: UK 9727256.1 FILING DATE: 1997-12-23
179 QHFTFYPVMCVARVNLYLQTILLLFSRXKVQDRA------LNIMGILVFWTWFLFLLL
                                                                                                                                                                                                        147 G-----WYITSACLLALAWQQFGWLTHEFCHQQPFKNRPLNDTISLFFGNFLQGFSR 198
                                                                                          199 DWWKDKHNTHHAATNVIDHDGDIDLAPLFAF----
                                                                                                                                           119 GWWKWNHNAHHIACNSLDYDPDLQHMPVFAVSSRFFNSITSHXYGRKXEFDXIAXFLICY 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261 PFFIRNQAFLYFPLLLLARLSWLAQSFFYVFTEFSFGIFDKVEFDGPEKAGLIVHYIWQL
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                                                                                                                                                                                                                                                                 59 GVLFSDSTFVHVLSAALIGFLWIQSGWIGHDSGHYNVMLSRRLNRAIQILSGNILAGISI 118
                                                                                                                                                                                                                                                                                                                           89 VSAYDVSVAQEKKMVESFEKLRQKLHDDGLM--KANETYFLFKAISTLSIMAFAFYLQYL 146
                                                                                                                                                                                                                                                                                                                                                                                     10 LSDHTVSAAS-----SDYRKLFSDLSALNLFNRKGHTTSILLSLILTL-----FPLSVC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                        17.1%; Score 225.5; DB 12; Length 443; 26.7%; Pred. No. 4e-15; ative 36; Mismatches 115; Indels 41;
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                                                                                          ---IPGDLCKYKASFEKAILKIVPY
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT FILING DATE: 2003-02-28
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 6108
LENGTH: 473
TYPE: PAT
CORGANISM: Caenorhabditis elegans
US-10-369-493-6108
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US-10-369-493-6108
; Sequence 6108, Application US/10369493
; Publication No. US20030233675A1
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Search completed: January 1, 2004, 06:58:36 Job time: 49.1975 secs
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                                                                                                            339
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                                                                                                                                                           230 ALLFV-PIQHIQFWLNHLAENL 250
                                                                                                                                                                                                                                                                    179 QHFTFYPVMCVARVNLYLQTILLLFSRXKVQDRA-----LNIMGILVFWTWFLFLL 229
                                                                                                                                                                                                                                                                                                                                                                  119 GWWKWHNAHHIACNSLDYDPDLQHMPVFAVSSRFFNSITSHXYGRKXBFDXIAXFLICY 178
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SUMMARIES

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## ALIGNMENTS

REFERENCE AUTHORS TITLE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AX007239	RESULT 1
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                                                                                                                                                                 ACTATGTGGTTATGACAACCAATGGTTTCAACAAGGTTGCACAGATCCTCTCTGGGAACT
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369 c 375 g 468 t
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Pred. No. 1.5e-140;
0; Mismatches 405;
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RESULT 2 BNAJ4160 LOCUS REFERENCE AUTHORS TITLE REFERENCE AUTHORS TITLE ACCESSION VERSION KEYWORDS SOURCE DEFINITION JOURNAL MEDLINE ORGANISM JOURNAL PUBMED Submitted (13-FEB-1998) Sperling P., Physiola Allgemeine Botanik der Universitaet Hamburg, D-22609 Hamburg, GERMANY AJ224160 AJ224160.1 GI:3819707 delta-8 sphingolipid d Sperling, P.
Direct Submission Sperling, P., Zahringer, U. and Heinz, E.
A sphingolipid desaturase from higher plants.
new cytochrome b5 fusion protein
J. Biol. Chem. 273 (44), 28590-28596 (1998) Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica. Brassica napus Brassica napus 9786850 Brassica napus (rape) (bases 1 to 1610) mRNA 1610 bp for delta-8 desaturase; fusion mRNA linear sphingolipid desa Physiologie, Institut fuer Hamburg, Ohnhorststrasse 18 protein; sld1 inear PLN 24-FEB-2003 desaturase. Identification

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Best Local Similarity
Matches 933; Conserv
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RRYVDDRALNIAGILVEWTWFPLLVSFLPNWQDRIIFVENMAVTAIGHVQFCLMHFA
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/gene="sld1"
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PVVQELCKKINLPYRSLSWWEANVWTLRTLRKAAVQARDVTNPVLENLLWEALNTHG"
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dev_stage="18 to 35 DAF"
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No. 1.5e-140;
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Boraginaceae; Borago.
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Sperling, P., Libisch, B., 2
Functional identification
Borago officinalis
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Libisch, B., Sperling, P., Heinz, E., Say
Direct Submission
Submitted (08-MAR-1999) Cell Biology,
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                                            TTTGACACCAAAGGGCATGTCACTTCATGCACCCTTGCATCTGTTGCTGCTTATGTTCCTC
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/product="delta 8-sphingolipid desaturase"
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UPINNLAGQDATDAFIAYHPGTAWKNLENLFTGYHLEDYLVSEISKDYRKLASEFSKA
GLFEKKGHTVIYCLSFIALLLCGCYYGVLGSNSLWYHMLSGAMLGMCFIQAAYLGHDS
GHYTWMSSKGYNKFAQVLUNGNCLTGISIAWMKYTHNAHIACNSLDYDDEDQHLPFSG
GHYTWMSSKGYNKFAQVLUNGNCLTGISIAWMKYTHNAHIACNSLDYDDEDQHLPFST
VPSSFFKSLTSRFYGRELTFDGLSRFLVSYQHFTIYLVMIFGRINLYVQTFLLLFSTR
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VYVGPPTGTNWFEKQAAGTIJSCSSWMDWFTGGLQFQLEHHLFPRMPRCQLRNISFI
VQDYCKKHNLPYRSLSFFDANVATIKTLRTAALQARDLTVVPQNLLWEAFNTHG"
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/db_xref="taxon:13363"
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Pred. No. 9.5e-138;
0; Mismatches 403;
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AC005397 110149 bp DNA linear PLN 11-MAR-2002 Arabidopsis thaliana chromosome 2 clone T3F17 map CIC02E07, complete sequence.

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ACCESSION
VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (27-FEB-2002) The Institute for Genomic Research, Medical Center Dr. Rockville, MD 20850, USA, cdtown@tigr.or. On Apr 18, 2002 this sequence version replaced gi:6598465.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (09-MAR-2000) The Institute for Medical Center Dr., Rockville, MD 20850, U 3 (Dases 1 to 110149)
Town,C.D. and Kaul,S.
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1 (bases 1 to 110149)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="overlap with BAC clone F11C10 (AC006526:1. .7273)."
complement (3801. .3849)
/rpt_family="AT_rich"
4314. .5025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="synonym: T3F17.46; supported gi 15294169_gb AF410276 1 AF410276" join(4314. .4574,4732. .5025) /gene="At2946330"
                                              /translation="mvebaqldpksks!pnenlkfgeralsaggaaf!savivnpldv
vktrlqaqaagvpyqgscrlgcfdtnstlvhdlrsnsapgmcritgsasvcsdnqykg
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plvagtiarslaciscypvelartrmqafkgtqrnvklpgvmktludvvnpvkgsnng
                                                                                                                                                                                                                                                                                                    complement(join(5548. .5677,5751. .5809,5945. .6094,6186. .6362,6458. .6628,6761. .6811,7054. .7176,7264.
                                                                                                                                                                                                                                                                                                                                                                                                    complement(join(<5548. .5677,5751. .5809,5945. .6094, 6186. .6362,6458. .6628,6761. .6811,7054. .7176,7264. .7341,
                                                                                                                                                                                                                                                                                                                                                                                                                              /note="synonym: T3F17.3" complement(join(<5548. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (5548. .7570)
/gene="At2g46320"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="expressed protein"
/protein_id="AAM15047.1"
/db_xref="GI:20197373"
/translation="MASRNSVTGFALFSFVFAVILSLAGAQSLAPAPAPTSDGTSIDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(1. .7273)
  avaaaatcpldvaktrrqiekntdramtmttrqtlaeiwrdggmrgmfsgagarvgra
                            YRMLWTGLGAQLARDVPFSAICWSILEPTRRSIQSAMGEEPRAGSIIGANFAAGFVAG
                                                                                                                                                   /product="hypothetical protein"
/protein_id="AAM15049.1"
/db_xref="GI:20197376"
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                                                                                                                                                                                                                                                      'gene="At2g46320"
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ement(SEAO
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                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="mrpilmkgherpltflrynrngdllfscakdhtptvwfadnger
lgtvrghsgavwccoisrdssrlitgsadqtaklwdyksgkelfffkrgaparsvdps
vgdhlavitdhfvgfssalihvkrieddpedpvgdvulvlgspdgkklinravwgpln
Qtivsggedaairiwdatakosdeevchkeaitslckaaddshfltgshdktak
Lwdmrtltiktyttvpvnavamspllnhvvlgggqdasavtttdhragkfeaakfyd
Tilgeeiggykghfgpinalafspdgksfssggedgyvrlhhfdsnyfniki"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MADYQMNPVLQKPPGYRDPNMSSPPPPPPIQQQPMRKAVPMPT SYRPKKKRRSCCRFCCCICITLVLFIFLLVGTAVFYLWFDPKLPTFSLASFRLDGF KLADDPDGASLSATAVARVEMKNPNSKLVFYYGNTAVDLSVGSGNDETGMGETTMNGF RQGPKNSTSVKVETTVKNQLVERGLAKRLAAKRQSKDLVINVVAKTKVGLGVGGIKIG MLAVNLRCGGVSLNKLDTDSPKCILNTLKWYKIISN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(<14412..>15176)
/gene="At2g46300"

complement":
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                                                                                                                                                                                                                                           /note="Bynonym: T3F17.7; supported by cDNA:
gi 1036802 gb U36765 1 ATU36765"
joIn(18170. . 18358,18507. . 18722,18818. .18951,19049. .1
19279. .19368,19462. .19548,19649. .19728,19837. .20058)
/gene="Ac2946280"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Join(15955..16138,16274..16489,16586..16719,16820..16939,
17042..17131,17227..17313,17401..17480,17583..17658)
/gene="Rt2g46290"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="synonym: T3F17.6"
join(15933. .16138,16274. .16489,16586. .16719,16820. .16939,
17042. .17131,17227. .17313,17401. .17480,17583. .17768)
/gene="At2946290"
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/gene="At 2g46310"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="hypothetical protein"
/protein_id="AAC62876.1"
/db_xref="GI:3702319"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="putative AP2 domain transcription
/protein_id="AAC62875.1"
/db_xref="GI:3702318"
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JGTYRGHNGAVWCCDVSRDSSRLITGSADQTAKLWDVKSGKELFTFKFNAPTRSVDFA
                                                                                                                         product="eukaryotic translation initiation
                                                                                                                                                                        gene="At2g46280"
                                                                                                                                                                                                                                                                                                                                                                             gene="At2g46280"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     product="eukaryotic translation initiation factor 3 delta
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                         translation="MRPILMKGHERPLTFLRYNREGDLLFSCAKDHTPTLWFADNGER
                                                   db xref="GI:3702321"
                                                                           protein_id="AAC62878.1"
                                                                                                                                                      codon start=1
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Best Local Similarity
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     CCTCAGTGACTTCAAGGTCTCTGAGGTGTCCAAAGACTACAGAAAGCTTGCATCTGAGTT
                                                                                                                                            GCACCCTGGTGGTGATGTTCCAATCTCAAACCTTGCTGGCCAGGATGTCACTGATGCATT
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                                                                                                                                                                                                                                                                       GGCGGATCAAACGAAGAAGAGATACGTTACAAGCGAGGATTTGAAAAAAACACAACAAACC
                                         CATCGCTTACCATCCCGGAACCGCATGGCACCACTTAGAAAAGCTTCACAATGGCTATCA
                                                               CATAGCATACCATCCTGGCACAGCATGGTCACACCTTGAAAAATTCTTCACTGGCTACCA
                                                                                                                      TCATCCCGGAGGCGAAGCAGTCTCTCAATCTCGCCGGCCAAGACGTCACCGACGCGTT
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/gene="At2946260"
/codon_start=1
/product="expressed protein"
/protein_id="AAA62880.2"
/translation="Marcolar"
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21338. .21513,21600. .21648,21737. .21943,22008. .22069,
22157. .22240,22334. .22429,22512. .22556,22644. .22709))
/gene="At2g46270"
/codon_start=1
/product="G-box binding bZIP transcription factor"
/protein_id="AAC62879.1"
/db_xref="G1:3702322"
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AMPPYYNSAMAASGHPPPTKSTGMTMSFYGAPYAAVYPHGGVYAHPGIPMGSLPQ
GQKDPPLTTPGTLLSIDTPTKSTGNTDKJEMKKLKEFDGLAMSLGNGMPENGADEHK
SRNSSETDGSTDGSDGNTTGADBFKLKBSREGTPTKDGKQLVQASSFHSVSPSSGDTG
VKLIQGSGAILSPGVSANSNPFMSQSLAMVPPETWLQNERELKKERRKQSNRESARRS
RLRKQAETEELARKVEALTAENMALRSELNQLNEKSDKLRGANATLLDKLKCSEPEKR
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QTIVSGGEDKVIRIWDAETGKLLKQSDEEVGHKKDITSLCKAADDSHFLTGSLDKTAK
LWDMRTLTLLKTYTTVVPVNAVSLSPLLNHVVLGGGQDASAVTTTDHRAGKFEAKFYD
KILQEEIGGVKCHFGPINALAFNPDGKSFSSGGEDGYVRLHHFDSDYFNIKI"
20201 21488
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LRIEILGGPSDSRSDAEGCTSIADWARHRKRRREDNKKDNGVAISDIVACAEEQILTD
NNQPDMDDAPGGDNLDDEGEAMVEEALSGDDDASSEPNWGIDCSTVVRVKELHISSPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(join(<24966. .25936,26015. .26294,26522. .26686. .26804,26942. .27076,27202. .>27557))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (24966. .27557)
/gene="At2g46260"
/note="synonym: T3F17.9; supported by
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                                                                                                                                                                                                                                                                                                                                                                    34.8%;
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_family="(GA)n"
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                                                                                                                                                                                                                                                                                                                                                  0,
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Pred. No. 1.1e-136;
0; Mismatches 422;
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                                                               TTTGAAGAACGCGGCGATTCAAGCTAGAGATGCGACTAATCCTGTGTTGAAGAACTTGCT
                                                                                           CCTCAGGACTGCTGCCCTACAAGCTAGGGACTTAACAAACCCTGCCCCCTAAGAATTTGTT
                                                                                                                                      GCATAATCTACCGTATAGGAGTCTTTCGTGGTGGGAAGCTAATGTGTGGACGATTAGGAC
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Expression of a borage desaturase cDhataining an N-terminal cytochrome b5 domain results in the accumulation of high levels delta6-desaturated fatty acids in transgenic tobacco proc. Natl. Acad. Sci. U.S.A. 94 (8), 4211-4216 (1997)
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/db_xref="GI:4101266"
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/yvwmsgrfnklwQilsgnClagislawwkwninthhiakonslapedpluchhpepfx
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X87143.1 GI:1040728
Cytochrome B5 domain; delta-8 sphingolipid
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Helianthus annuus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; campanulids; Asterales; Asteraceae; Asteroideae;
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Direct Submission
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/translation="MyspsievlnsiaGkkyitskelkkhnnendlwisilgkyynv
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WMQIAYLGHDAGHYQMMATRGWNKFAGIFIGNCITGISIAWWKTHNAHHIACNSLDY
DPDLQHLPMLAVSSKLENSITSFYGRQLTFDDLARFFYSHYLYYSFUTVGSFCYTGIQH
LQTTLMHFSGDYYGPPKGDNWFEKQTRGTIDIACSSWMDWFFGGLQFQLEHHLFPRL
                                                                                                                                                                                                                                   /gene="sld1"
/note="stereo-unselective
N-terminal cytochrome b5
                                                                                                                                                /evidence=experimental
/product="delta-8 sphingolipid
/protein id="CA#00621.1"
/db_xref="GI:1040729"
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73. .1449
PRCHLRSISPICRELCKKYNLPYVSLSFYDANVTTLKTLRTAALQARDLTNPAPQNLA
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                                                                                                                                                                                                                                                                        RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAS (RAFL cDNA : 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Southwick, A., Nguyen, M., Tripp, M., Palm, C.J., Jones, T., Wu, T., Carninci, P., Chen, H., Cheuk, R., Chan, M.M., Chang, C.H., Dale, J.M., Deng, J.M., Hayashizaki, Y., Hsuan, V.W., Lee, J.M., Ishida, J., Kamiya, A., Kawai, J., Kim, C.J., Narusaka, M., Omodera, C.S., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Shinn, P., Tang, C.C., Toroumi, M., Wong, C., Wu, H.C., Yamada, K., Yu, G., Yuan, S., Shinozaki, K., Ecker, J., Theologis, A. and Davis, R.W., Direct Submission
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Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
Nguyen,M., (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W. (SSP/Stanford) contributed equally to this work as PIs.
                                                                                       The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Nguyen, M., Tripp, M., Southwick, A., Palm, C.J., Jones, T., Wu, T., Cheu, H., Cheuk, R., Chan, M.M., Chang, C.H., Dale, J.M., Deng, J.M., Hsuan, V.W., Lee, J.M., Kim, C.J., Quach, H.L., Onodera, C.S., Shinn, P., Tang, C.C., Toroumi, M., Wong, C., Wu, H.C., Yamada, K., Yu, G., Yuan, S., Ecker, J., Theologis, A. and Davis, R.W.
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GDTVLINIVGQDVTDARTAFHPGTAWHLDHLFTGYHIRDFQVESEDYRWAAEFR
KLGLPENKGHVTLYTLAFVAAMFLGVLYGVLACTSVPAHGIAAALGLLHGUSAYIGH
DSGHYVIMSNKSYNREADLASGNCITGISIAWKWTHNAHHLACNSLDYDDDLQHIPV
FAVSTKFFSSLTSRFYDRKLTFDPVARFLVSYQHFTYYPWCFGRINLFIQTFLLLFS
KREVPDRALNFAGILVEWTWFPLLVSCLPNWEERFFYTSFYVTALCHIGFTLNHFA
ADVYVGPPTGSDWFEKQAAGTIDISCRSYMDWFFGGLOFQLEHHLFPRLPRCHLRKVS
PVVQELCKKHNLPYRSMSWFEANVLTINTLKTAAYQARDVANPVVKNLVWEALNTHG"
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/mol_type="mRNA"
/db_xref="taxon:3702"
/chromosome="3"
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/protein_id="AAO30042.1"
/db_xref="GI:28059272"
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0; Mismatches 479;
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                                                                                                                                                                                                         Arabidopsis thaliana clone 34427 mRNA,
AY087345
                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; cosida; eurosida II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                      FLI CDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Haas, B.J., Volfovsky, N., Town, C.D., Tr
Feldmann, K.A., Flavell, R.B., White, O.
                                                                                                                                                                                        AY087345.1 GI:21406069
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                                                                                                                                                                                                                                                                                                                                                                                   TCAAGGTCTTTTTTTTTTTTTTTTCTCT 1718
                                                                                                                                                                                                                                                                                                                                                                                                                                         TTGGGAAGCTTTGAATACTCATGGCTAAATGATTTTAATCAAAAACAAAATATGCTTTTGT 1382
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Troukhan, M., Alexandrov, N., on Salzberg, S.L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               may contain polymorphisms when compared to sequences from Col-0. Genset carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (11-MAR-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brover, V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Biol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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                                                                                                                                                                                                                   GGGAGATTTATGGATCTCAATTCAAGGTAAGGTGTACAATGTCTCAGATTTGGGTCAAGGA 429
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CATAGCATACCATCCTGGCACAGCATGGTCACACCTTGAAAAATTCTTCACTGGCTACCA
                                                                TCATCCCGGAGGCGACACGGTGATTCTCAATCTCGTTGGTCAAGACGTCACCGATGCTTT
                                                                                                                    GCACCCTGGTGGTGATGTTCCAATCTCAAACCTTGCTGGCCAGGATGTCACTGATGCATT
                                                                                                                                                                                 TGGAGATCTATGGATCGCGATTCAAGGCAAGGTCTACAACGTCTCCGATTGGATTAAAAC 328
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GDTVILNILVGQDVTDAR IAFHFGTAWHLDHLFTGYHITDFQVSEVSRDYRWAAEFR
KLGLFENKGHVTLYTLAFVAAMFLRVLYGVLACTSVFAHGIAAALLGLHGANYIGH
DSGHYVIMSNKSYNRFAQLLSGNCITGISIAWWKWTINAHHLACNSLDYDPDLQHIPV
FAVSTKFFSSLTSRFYDRKLTFDPVARFLVSYQHFTYYPVMCFGRINLFIQTFLLLFS
KREVPDRALNFAGILVEWTWFPLLVSCLPHWPERFFVYFTYFVTALQHIQFTLNHFA
ADVYVGFPTGSDWFEKQAAGTIDISCRSYMDWFFGGLQFQLEHHLFPRLPRCHLRKVS
PVVQELCKKHNLFYRSWSWFEANVLTINTLKTAAYQARDVANPVVKNLVWEALNTHG"
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/product="delta-8 sphingolipid desaturase"
/protein id="AAM64895.1"
/db_xref="GI:21592945"
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Patent: WO 0000593-A 3 06-JAN-2000;
ZAEHRINGER ULRICH (DE); HEINZ ERNST (DE); SCHMIDT HERMANN SPERLING PETRA (DE); GYS GES FUER ERWERB UND VERWER (DE)
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                                                                                                               CCTCAGTGACTTCAAGGTCTCTGAGGTGTCCAAAGACTACAGAAAGCTTGCATCTGAGTT
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                                                               CATCAGAGATTTCCAAGTCTCCGAAGTCTCACGCGATTACCGTCGTATGGCTGCCGAGTT
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Direct Submission
Submitted (05-OCT-2001) Salk Institute Genomic Analysis Laboratory (SIGnAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, The Salk Institute for Pines Road, La Jolla, CA 92037, The Salk Institute for Pines Road, La Jolla, CA 92037, The Salk Institute for Pines Road, La Jolla, CA 92037, The Salk Institute for Pines Road, La Jolla, CA 92037, The Salk Institute for Pines Road, La Jolla, CA 92037, The Salk Institute for Pines Road, La Jolla, CA 92037, The Salk Institute for Pines Road, La Jolla, CA 92037, The Salk Institute for Pines Road, La Jolla, CA 92037, The Salk Institute for Pines Road, La Jolla, CA 92037, The Salk Institute for Pines Road, La Jolla, CA 92037, The Salk Institute for Pines Road, La Jolla, CA 92037, The Salk Institute for Pines Road, La Jolla, CA 92037, The Salk Institute for Pines Road, La Jolla, CA 92037, The Salk Institute for Pines Road, La Jolla, CA 92037, The Salk Institute for Pines Road, La Jolla, CA 92037, The Salk Institute for Pines Road, La Jolla, CA 92037, The Salk Institute for Pines Road, La Jolla, CA 92037, The Salk Institute for Pines Road, La Jolla, CA 92037, The Salk Institute for Pines Road, La Jolla, CA 92037, The Salk Institute for Pines Road, La Jolla, CA 92037, The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs. Cheuk, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Shinn, P., Bahh, J. Bowser, L., Dale, J.M., Goldsmith, A.D., Jiang, P.X., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Nguyen, M., Onodera, C.S., Palm, C.J., Pham, P.K., Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Davis, R.W., Theologis, A., and Ecker, J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 collection and clustering of RAFL CDNAs (RAFL CDNA; 'KIKEN Arabidopsis Full-Length CDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contributed equally to this work Location/Qualifiers
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/note="ecotype: Columbia"
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TGGAAGAATCAATCTCTTCATTCAAACGTTTCTCTTGCTCTTCTCCAAACGTGAAGTACC
                                            TGCCAGGGTCAACTTGTATCTGCAGACAATTCTGCTATTGTTTTCGAGGCGAAAAAGTGCA
                                                                                            TCCAGTCGCGAGATTCTTAGTCAGCTATCAACACTTTACTTATTATCCAGTTATGTGCTT
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PVVQBLCKKHNLPYRSMSWFEANVLTINTLKTAAYQARDVANPVVKNLVWBALNTHG"
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ADVYVGPPTGSDWFEKQAAGTIDISCRSYMDWFFGGLQFQLEHHLFPRLHRCHLRKVS
PVVQELCKKHNLPYRSMSWFBANVLTINTLKTAAYQARDVANPVVKNLVWBALNTHG"
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/clone_lib="lambda ZAP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Southwick, A., Tripp, M., Nguyen, M., Palm, C.J., Jones, T., Wu, T., Chen, H., Cheuk, R. Chan, M.M., Chang, C.H., Dale, J.M., Deng, J.M., Hsuan, V.W., Lee, J.M., Kim, C.J., Quach, H.L., Shinn, P., Tang, C.C., Toroumi, M., Wallender, E.K., Wong, C., Wu, H.C., Yamada, K., Yu, G., Yuan, S., Ecker, J., Theologis, A. and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'; Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Sh inozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (24-SEP-2002) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94
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Direct Submission
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GCACCCTGGTGGTGATGTTCCAATCTCAAACCTTGCTGGCCAGGATGTCACTGATGCATT
                                                             TGGAGATCTATGGATCGCGATTCAAGGCAAGGTCTACAACGTCTCCGATTGGATTAAAAC
                                                                                    GGGAGATTTATGGATCTCAAGTTCAAGGTAAGGTGTACAATGTCTCAGATTGGGTCAAGGA
                                                                                                                                            GGCGGAAGAGACGGAGAAAAGTACATTACGAACGAAGATCTTAAAAAACACAACAAATC
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                                                                                                                                                                                                                        Conservative
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EAVSTKEFESSLTSRFYDRKLTTDDVARFLVSYOHFTYYPVMCFGRINLFIQTFILLES
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ADVYVGPPTGSDWFEKQAAGTIDISCRSYMDWFFGGLQFQLEHHLFPRLPRCHLRKVS
PVVQBLCKKHNLPYRGMWFEANVLTINTLKTAAYQARDVANPVVKNLVWEALNTHG"
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/db_xref="taxon:3702"
/chromosome="3"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mlps.biochem.mpg.de/proj/thal/.
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Gaston Cremieux, BP191, 91006 Evry Cedex, France;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lemcke@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project Coordinator: Marcel Salanoubat and Francis Quetier, Groupement d'Interet Public, Centre National de Sequencage - GENOSCOPE; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (31-JAN-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:
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Direct Submission
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                                                                            /translation="MEEKEEAGVMDERIYVALGREIANNKSNLAWVLDNCQGNKICIV
LVHRPPQMIPVLGTKFDAATVDEELVRAYREKQKAKTDKILEVELRICLRKGVQAEKL
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                                                                                                                                                                                                                                                                         Arabidopsis thaliana,
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                                                                                                                                                                                                                                                                                                                                                                                                                       analysis
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BAC clone F2A19.
                                                                                                                                                                                                                                                                                                                                                                                                                                             please refer this BAC
                                                                                                                                                                                                                                                                                                                                                          .15842,15935.
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Search completed: December 31, 2003, 21:04:31 Job time : 4857.01 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polynucleotide encoding delta-6 desaturase enzyme useful for producing transgenic plants and for producing antibodies specific to which is useful for screening cDNA expression libraries -
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           This invention describes a novel sphingolipid desaturase that selectively C introduces a double bond into the sphingobase of the ceramide residue of sphingolipids and capnoids. A DNA sequence encoding the sphingolipid CC desaturase, or a vector containing the DNA sequence, can be used to produce transgenic plants, especially crop plants, with an increased or decreased delta-8 unsaturated long-chain base content or an altered delta-8 unsaturated long-chain base cis/trans ratio, especially to compensate for a delta-8-unsaturated long-chain base deficiency, to compensate for a delta-8-unsaturated long-chain base deficiency, to compensate for a delta-8-unsaturated bases, to increase tolerance corresistance to soil salinity, ion stress or toxicity, drought, wet conditions, cold or frost and/or phytopathogenic microorganisms or caller size growth and flowering time. Cells, transgenic organisms or plants containing the DNA sequence can be used to produce sphingolipids and capnoids with unsaturated sphingobases. The sphingolipids or capnoids can be used in cosmetics, pharmaceuticals and foods and as chemical raw materials. This sequence encodes the Brassica napus sphingolipid
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                         TGCCAGGGTCAACTTGTATCTGCAGACAATTCTGCTATTGTTTTCGAGGCGAAAAGTGCA
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0; Mismatches 422;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sphingolipid desaturase; sld1; sphingobase; ceramide; capnoid; transgenic plant; crop plant; delta-8-unsaturated long-chain base; tolerance; resistance; soil salinity; ion stress; toxicity; drought; cold; frost; phytopathogenic microorganism; flowering time; cosmetic; pharmaceutical; food; chemical raw material; ds.
New sphingolipid desaturase that selectively introduces double
                                                                                         WPI; 2000-127549/12
                                                                                                                                                                                                                                                                 27-JUN-1998;
                                                                                                                                                                                                                                                                                                                         27-JUN-1998;
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CC This invention describes a novel sphingolipid desaturase that selectively CC introduces a double bond into the sphingobase of the ceramide residue of csphingolipids and capnoids. A DNA sequence encoding the sphingolipid CC desaturase, or a vector containing the DNA sequence, can be used to CC produce transgenic plants, especially crop plants, with an increased or CC decreased delta-8-unsaturated long-chain base content or an altered CC delta-8-unsaturated long-chain base content or an altered CC compensate for a delta-8-unsaturated long-chain base deficiency, to CC exclude production of delta-8-unsaturated long-chain base deficiency, to CC conditions, cold or frost and/or phytopathogenic microase tolerance CC calter size growth and flowering time. Cells, transgenic organisms, or to CC alter size growth and flowering time. Cells, transgenic organisms or CC cand capnoids with unsaturated sphingolabases. The sphingolipids or capnoids can be used in cosmetics, pharmaceuticals and foods and as chemical raw CC materials. This sequence encodes a sphingolipid desaturase protein contentials. This sequence encodes a sphingolipid desaturase protein contentials.
Sequence 1606 BP; 412 A; 338 C; 370 G; 486 T; 0 other;
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Query Match Best Local

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DB 21;

Length

1606;

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AAC33846 standard; DNA; 1650 BP.  AAC33846;  17-OCT-2000 (first entry)  Arabidopsis thaliana DNA fragment SEQ ID NO: 4526.  Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.  Arabidopsis thaliana.  EP1033405-A2.  06-SEP-2000.  25-FEB-2000; 2000EP-0301439.	1303 ĠAACTCTĠCAAĠAATATAĠACTTAĆCCTTATGTĠAGTTTĠTĠAGTTTATGATĠCGAATGTA 1362  1556 TGGACAATTAGGACCCTCAGGACTGCCCTACAAGCTTAAGGAACCTTAACAAACCCTGCC 1615	16 AAGTTGGAGTTTGATTTCATTGCTAGGTTCTTGATCTGCTACCAGGACATTTACTTTTAC 10	763 CCGAIGTTAGCCGITTCTICCAAGCTTTTTAACTCAATAACTTCTGTTTTCTATGGGAQA 822
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                                                     TGCTGTTATGTTCCTCATTGTACTCTATGGTGTTCTGAGGTGCACTAGTGTGTGGGCTCA
TTCTGGCCACTATGTGGTTATGACAACCAATGGTTTCAACAAGGTTGCACAGATCCTCTC
               CCAAATCGCCGCCGCGCTTCTCGGTCTCCTCTGGATCCAGAGCGCTTACATAGGTCACGA
                       TTTGGGTTCAGGCATGCTCTTAGGGTTGCTTTTGGATGCAAAGTGCTTATGTGGGCCATGA
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GTGGGAAGCTGTTAATACCCCATGGCTGAGGCATTTGGAGTTTTAGAGTTTTAGGATTTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGATAGAGCCTTGAACATAATGGGGATCCTTGTGTTTTGGACTTGGTTCCCCTCTTTTAGT
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                                                                                  TTGGGAAGCTTTGAATACTCATGGCTAAATGATTTTAATCAAAACAAAATATGCTTTTGT
                                                                                                                                                                                                                                      CCTCAGGACTGCCTACCAAGCTAGGGACTTAACAAACCCTGCCCCTAAGAATTTGTT
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GGTTGTAGAAGGAGAAGAAGTACATAACCTCAGAGGACCTGAACGGTCACAACAAGA 369

Query Match Best Local ( Matches 93)

Local Similarity

33.2%;

Score 642.6; DB 21; Pred. No. 2e-116;

Length

0;

Gaps

0

Conservative

<u>,</u>

Mismatches

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                            This invention describes a novel sphingolipid desaturase that selectively CC introduces a double bond into the sphingolase of the ceramide residue of sphingolipids and capnoids. A DNA sequence encoding the sphingolipid CC desaturase, or a vector containing the DNA sequence, can be used to CC produce transgenic plants, especially crop plants, with an increased or CC decreased delta-8-unsaturated long-chain base content or an altered CC delta-8-unsaturated long-chain base content or an altered CC compensate for a delta-8-unsaturated long-chain base deficiency, to CC exclude production of delta-8-unsaturated bases, to increase tolerance CC or resistance to soil salinity, ion stress or toxicity, drought, wet conditions, cold or frost and/or phytopathogenic microorganisms, or to CC alter size growth and flowering time. Cells, transgenic organisms or CC plants containing the DNA sequence can be used to produce sphingolipids and as chemical raw can be used in cosmetics, pharmaceuticals and foods and as chemical raw can be used in cosmetics, pharmaceuticals and foods and as chemical raw can be used in cosmetics, pharmaceuticals and foods and as chemical raw can be used in cosmetics, pharmaceuticals and sphingolipid can be used in cosmetics.
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   Sequence 1678
                                                                                                                                                                                                                                                                                                                                                      Claim 11;
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                      CTCTTCGATGGATTGGTTTTTCGGTGGCTTGCAGTTTCAGCATCATTTGTTTCC
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                                                          The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising:

(a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and

(b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that with increased transpendence is stress regulated gene (ABZ12196-ABZ17574) used
                                                                                                                                                                                                                                                                                                                                                                         24-AUG-2000;
26-JAN-2001;
22-JUN-2001;
           Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office.
                                                   of an Arabidopsis thaliana stress regulated in methods of the invention.
                                                                                                                                                                                                          Claim
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This sequence is the gene encoding the borage (Borago officinalis) delta-6 desaturase enzyme. The lipid metabolism gene is an example of a heterologous gene which can be expressed at high levels in a
                                                                                                                                                                             New sunflower albumin 5' altered lipid metabolism
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P-PSDB; AAW67471.
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lipid metabolism; delta-6 desaturase; transgenic plant;
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                                                                                                                                                                                                                                                                                                                         Li Z,
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gamma-linolenic acid; or
                                                                                                                                               Nucleic acid containing oleosin 5'-regulatory region - useful modulating fatty acid synthesis and lipid metabolism in plants particularly to increase content of gamma-linolenic acid
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The present sequence encodes borage delta-6 desaturase (see AAW98130), an enzyme that catalyses the conversion of linoleic to gamma-linolenic acid (GLA). Delta-6 desaturase cDNA was

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  TATGTACAATCTCTCATAATGTTGTTGACCAAGAGAAATGTGTCCTATCGAGCTCAGGAA
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                                                                         TTGATCTGCTACCAGCACTTTACCTTTTTACCCCGGTAATGTGTGTTTGCCAGGGTCAACTTG
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              WPI; 1996-333997/33.
P-PSDB; AAR98455.
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                                                        Freyssinet GL,
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                                                                                                                                            28-DEC-1995;
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                                                                                    RHONE
                                                      Nuccio M,
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Delta-6-desaturase; gamma-linolenic acid; transgenic plant; polyunsaturated fatty acid; octadecatetraeonic acid;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    delta-6-desaturase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                   resistance; oilseed; ss;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A DNA clone (AAT30395) codes for borage delta-6-desaturase (AAR98455), which catalyses the conversion of linoleic acid to gamma-linolenic acid (GLA). It was isolated from a borage membrane-bound polysomal library using probes based on abundantly expressed seed storage protein cDNAs and with an isolated partial cDNA clone. The gene can be incorporated into a vector, pref. incorporating a tissue-specific promoter, for the expression of delta-6-desaturase in transgenic plants, esp. sunflower, soybean, maize, tobacco, peanut, carrot or oilseed rape, resulting in increased GLA prodn. Alteration of plant lipids may also lead to improved chilling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transgenic plants comprising the borage delta-6-desaturase gene show increased production of gamma linolenic acid and having increased resistance to chilling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1685 BP; 431 A;
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Similarity 66.5%;
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  TTGATCTGCTACCAGCACTTTACTTTTTACCCGGTAATGTGTGTTGCCAGGGTCAACTTG
                                                 GGTTCACTCACCTCTCATTTCTATGAGAAAAGGTTGACTTTTGACTCTTTATCAAGATTC
                                                                           AATTCCATAACCTCTCATTTCTATGGGAGGAAGTTTGGAGTTTGATTTCATTGCTAGGTTC
                                                                                                                                                      CTTGAATATGACCCTGATTTACAATATATACCATTCCTTGTTGTGTCTTCCAAGTTTTTT
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Pred. No. 1.1e-111;
0; Mismatches 446;
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  92US-0959952
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delta6-desaturase; sunflower; soybean; maize; tobacco; peanut; carrot; oil seed rape; gamma linolenic acid; G chilling tolerance; gene; ds; borage.
                                                                                                                                                                                                                                                                        Borago officinalis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTACAAGCTAGGGACTTAACAAACCCTGCCCCTAAGAATTTTGTTGTGGGGAAGCTGTTAAT 1645
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                                                                                                                                                                                                                                                                                                                                                                                                         Borago officinalis delta6-desaturase
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first
97US-0934254
                                                                                                                  /*tag= a
/product= "delta6-desaturase"
/transl_except= (pos:1151..11)
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Best Local S
Matches 886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention describes an isolated nucleic acid encoding an evening primrose Delta6-desaturase. The nucleic acid and a vector expressing the nucleic acid are useful for producing a plant such as sunflower, soybean, maize, tobacco, peanut, carrot or oil seed rape plant, with increased gamma linolenic acid (GLA) content, and also for inducing or increasing production of GLA in a bacteria or plant deficient, lacking in or producing low levels of GLA. The nucleic acid is also useful for inducing chilling tolerance in plants. This sequence encodes the borage delta6 desaturase involved in the production of gamma linoleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-OCT-1991;
08-JAN-1992;
14-SEP-1994;
28-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid encoding evening primrose delta6-desaturase which rts linoleic acid to gamma linolenic acid useful for producing linolenic acid in transgenic plant or bacteria
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                   GGGATAAGCATTGCTTGGTGGAAGTGGACTCACAATGCTCACCACAATTGCGTGCAACAGC
                                                                                                                                                                                                                                                                                                             GTCTCTGAGGTGTCCAAAGACTACAGAAAGCTTGCATCTGAGTTCTCAAAATTGGGTCTT
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                                                                                                                                                                                                                                                             TTTGACACCAAAGGGCATGTCACTTCATGCACCCTTGCATCTGTTGCTGTTATGTTCCTC
                                                                                                                                                                                                                                                                                             GTTTCTGAGGTTTCTAAAGATTATAGGAAGCTTGTGTTTTGAGTTTTCTAAAATGGGTTTG
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   GGAATAAGTATTGGTTGGTGGAAATGGAACCATAATGCACATCACATTGCCTGTAATAGC
                                                         GTAGTGTCTGATTCAAGGCTTAATAAGTTTATGGGTATTTTTGCTGCAAATTGTCTTTCA
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                                                                                      GTTATGACAACCAATGGTTTCAACAAGGTTGCACAGATCCTCTCTGGGAACTGCTTGACC
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92US-0817919.
94US-0307382.
97US-0789936.
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                                                                                   Delta-6-desaturase; gene; ss; delta-12-desaturase; sunflower; soybe maize; tobacco; peanut; carrot; oil seed rape; gamma-linolenic acid octadecatetraenoic acid; alpha-linolenic acid; delta-15-desaturase;
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                                                                                                                                              delta-6-desaturase
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                                                                                                                                                                                                                                                                                                                                                                                            CTACAAGCTAGGGACTTAACAAACCCTGCCCCTAAGAATTTGTTGTGGGAAGCTGTTAAT 1645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AACCTTAGGAAAATCTCGCCCTACGTGATCGAGTTATGCAAGAAACATAATTTGCCTTAC
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14-SEP-1994;
28-JAN-1997;
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19-SEP-1997;
10-OCT-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a nucleic acid encoding an evening primrose delta-6-desaturase polypeptide. The nucleic acid, a vector comprising the nucleic acid or a nucleic acid encoding delta-12-desaturase, is useful for producing a plant (such as sunflower, soybean, maize, tobacco, peanut, carrot or oil seed rape plant) with increased gamma-linolenic acid (GLA) content by transforming a plant cell with the nucleic acid or vector and regenerating a plant with increased GLA content from the plant cell, for inducing or increasing production of GLA in an organism lacking in or producing low levels of GLA and for inducing production of octadecatetraenoic acid in at least one of a plant deficient or lacking in or producing low levels of GLA and for inducing production of octadecatetraenoic acid, a bacterium which produces alpha-linolenic acid or a bacterium which established acid or a bacterium which exhibits a delta-15-desaturase activity on a GLA substrate. This sequence represents cDNA encoding a borage delta-6-desaturase polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel nucleic acid encoding evening primrose delta-6-desaturase, for producing plant with increased gamma linolenic acid content, for inducing octadecatetraenoic acid production in plant
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TTTGACACCAAAGGGCATGTCACTTCATGCACCCTTGCATCTGTTGCTGTTATGTTCCTC
                                                GTTTCTGAGGTTTCTAAAGATTATAGGAAGCTTGTGTTTTGAGTTTTCTAAAATGGGTTTTG
                                                                    GTCTCTGAGGTGTCCAAAGACTACAGAAAGCTTGCATCTGAGTTCTCAAAATTGGGTCTT
                                                                                                           GCCTCTACATGGAAGAATCTTGATAAGTTTTTCACTGGGTATTATCTTAAAGATTACTCT
                                                                                                                                        GGCACAGCATGGTCACACCTTGAAAAATTCTTCACTGGCTACCACCTCAGTGACTTCAAG
                                                                                                                                                                                        GTTCCAATCTCAAACCTTGCCTGGCCAGGATGTCACTGATGCATTCATAGCATACCATCCT
                                                                                                                                                                                                                                     TCGATTCAAGGGAAAGCCTATGATGTTTCGGATTGGGTGAAAGACCATCCAGGTGGCAGC
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/product= "Borage delta-6-desaturase #1"
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                                                                                                                                                                                                                                                                                             The invention describes an isolated nucleic acid encoding an evening primrose Delta6-desaturase. The nucleic acid and a vector expressing the nucleic acid are useful for producing a plant such as sunflower, soybean, maize, tobacco, peanut, carrot or oil seed rape plant, with increased gamma linolenic acid (GLA) content, and also for inducing or increasing production of GLA in a bacteria or plant deficient, lacking in or producing low levels of GLA. The nucleic acid is also useful for inducing chilling tolerance in plants. This sequence encodes the evening primrose delta6 desaturase involved in the production of gamma linoleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           delta6-desaturase; sunflower; soybean; maize; tobacco; peanut; carrot; oil seed rape; gamma linolenic acid; GLA; chilling tolerance; gene; ds; evening primrose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Column 41-46; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-OCT-1992;
10-OCT-1991;
                                                                                                                                                                                                                                                                       Sequence 1702 BP; 358 A; 471 C; 446 G; 427 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid encoding evening primrose delta6-desaturase which rts linoleic acid to gamma linolenic acid useful for producing linolenic acid in transgenic plant or bacteria -
                                                                                                                                                                                                                , 688
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                                                                                                                                                                                                                              Similarity
                                                                                                                GGATCTCAATTCAAGGTAAGGTGTACAATGTCTCAGATTGGGTCAAGGAGCACCCTGGTG
                                                                                                                                                                              AGGAGAAGAAGTACATAACCTCAGAGGAGCTGAAGGGTCACAACAAGGAGGAGATTTAT
    ATCCTGGCACAGCATGGTCACACCTTGAAAAATTCTTCACTGG----CTACCACCTCAGTG
                                                             GTGATGTTCCAATCTCAAACCTTGCTGGCCAGGATGTCACTGATGCATTCATAGCATACC
                                                                                            GGATCTCCATCCAGGGCAAGGTCTACGACTGCTCTCGGTGGGCGCGGAGCACCCCGGCG
                                                                                                                                                      AAGCTAAGAAGTATATCACGGCGGAGGACCTCCGCCGCCACAACAAGTCCGGCGATCTCT
                                GCGAGGTCCCGCTCAGTCTGGCCGGCCAGGACGTCACCGACGCCTTCATTGCGTACC
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/product= "delta6-desaturase"
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Pred. No. 2.8e-99;
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GGACTGCCCTACAAGCTAGGGACTTAA---CAAACCCTGCCCCTAAGAA---TTTGT
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                                              TGCCGTATAGGAGCTTCGGGTTTTTGGGACGACGCTAATGTCAGGACAATTCGGACGCTGA
                                                                         TGCCTTATAGGAGCTTGTCATTTTGG----GAGGCCAATCAGTGGACAATTAGGACCCTCA
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  Query Match
                                                                                                           The invention relates to a nucleic acid encoding an evening primrose delta-6-desaturase polypeptide. The nucleic acid, a vector comprising the nucleic acid or a nucleic acid encoding delta-12-desaturase, is useful for producing a plant (such as sunflower, soybean, maize, tobacco, peanut, carrot or oil seed rape plant) with increased gamma-linolenic acid (GLA) content by transforming a plant cell with the nucleic acid or vector and regenerating a plant with increased GLA content from the plant cell, for inducing or increasing production of GLA in an organism lacking in or producing low levels of GLA and for inducing production of octadecatetraenoic acid in at least one of a plant deficient or lacking in or producing low levels of octadecatetraenoic acid, a bacterium which produces alpha-linolenic acid or a bacterium which exhibits a delta-15-desaturase activity on a GLA substrate. This sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-OCT-1991;
08-JAN-1992;
14-SEP-1994;
28-JAN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel nucleic acid encoding evening primrose delta-6-desaturase, useful for producing plant with increased gamma linolenic acid content, and for inducing octadecatetraenoic acid production in plant -
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                                               Sequence 1702
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19-SEP-1997;
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	TGTGGGAAGCTGTTAATACCCATGGCTGAGGCATTTGGAGTTTTTAGAGTT 1679	1629	Ş
1377	GGGATGCGGCGGTTCAGGCGCGTGACCTTAATTCGGCCCCGTGCCCTAAGAAACTTGGGT 1377	1318	8
1628	1575 GGACTGCTGCCCTACAAGCTAGGGACTTAACAAACCCTGCCCCTAAGAATTTGT 1628	1575	5
1317	TGCCGTATAGGAGCTTCGGGTTTTGGGACGACGCTAATGTCAGGACAATTCGGACGCTGA 1317	1258	용
1574	TGCCTTATAGGAGCTTGTCATTTTGGGAGGCCAATCAGTGGACAATTAGGACCCTCA 1574	1518	5
1257	GCGTGGGCAGCTTAGGAAGATTGCGCCCTTGGCTCGGGACTTGTGTAAGAAGCACGGGA 1257	1198	용
1517	CTCGGTGCCAATTGAGGAAGATTTCGCCTTTTGGTAAGTGACCTTTTGCAAGAAGCATAATT 1517	1458	Ş
1197	TGGACTGGTTCTTTGGTGGGCTGCAGTTCCAGTTGGAGCACCACTTGTTCCCTAGGCTGC 1197	1138	8
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15947.709 Million cell updates/sec
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976973 QHI23	8 13 BQ9769	7.5		5
005403 VVB04	2 14 CD00540	7.7	43.	44
36433 AUJC	9 28 BH23643	7.8	344	43
24529 QHF41	6 13 BU02452	7.9	45.	42
3904 QHF14	4 13 BU02390	7.9	45.	41
829321 LjNES	1 14 CB82932	7.9	45.	0
26179 gael:	5 10 BG72617	7.9	346.2	39
024179 QHF16	5 13 BU02417	8.0	47.	38
53475 NP039	6 13 BQ15347	8.1	49.	37
002410	3 14 CB00241	8.1	49.	36
Q281359	4 13 BQ2813	8.1	S	35
02504	4 14 CB0025	8.1	50.	34
025175	2 13 BU0251	8.2		3
27841	5 28 BH9278	8.3	54.	32
H687867	3 28 BH6878	8.4	ū	31
D037696	7 14 CD0376	8.6	58.	30
B972811	6 14 CB9728	8.6	59.	9
68631	7 10 BF2686	8.6	60.	8
810	7 13 800280	8.7	61.	27
29088	5 14 CB8290	9.2	72.	6
25281	2 13 BU0252	9.3		25
U811579	5 13 BU8115	9.3	72.	24
U0252	7 13 800252	9.3	73.	23
U025380	5 13 BU0253	9.5	37	22
U024653	2 13 BU0246	9.7	81.	21
988466	3 9 AI98	9.7	381.4	0
B972537	1 14 CB97253	9.8	83.	6
U025987	6 13 BU0259	19.9 73	84	8
F003445	3 10 BF00344	9.9	œ	17
25031	2 13 BU02503	0.0	38	6
Q402431	6 13 BQ40243	0.0	87.	5
028011	1 13 BU02801	0.1		14
38317	5 14 CA9383	0.1	89.	3
87611	1 12 BI78761	0.1	89.	12
3768	8 12 BM143	0.3	91.	Ξ
93839	7 14 CB89383	0.4	39	0
094	8 14 CB2910	2.4		9
B291093	2 14 CB29109	2.9	43.	ω
935212	9 14 CA93521	3.2	4	7
7198	3 10 BG6	4.4		ð
311411	2 12 BI31141	4.7	8	5

## ALIGNMENTS

REFERENCE AUTHORS TITLE JOURNAL COMMENT RESULT 1 BE658198/c LOCUS SOURCE ORGANISM ACCESSION VERSION KEYWORDS DEFINITION Other EST8: AI748200 corresponding to Gm-c1011-238 (5')
Contact: Vodkin, L.O., PI, A Functional Genomics Program
Soybean (NSF 9872565)
Lewin, H. A., Director, Keck Center for Comparative and F Vodkin,L., Keim,P., Shoemaker,R., Retzel,E., Khanna,A., Erpelding,J., Raph,C., Shoop,E., Pardinas,J., Liu,L. and Functional Genomics Program for Soybean (NSF 9872565) Glycine max (soybean)
Glycine max BE658198 776 bp mRNA linear EST 24-MAY-2001 GM700005A20G6 Gm-r1070 Glycine max cDNA clone Gm-r1070-1836 3', University of Illinois Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA Tel: (217) 244-6147 Unpublished Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Genomics BE658198.1 GI:9984146 mRNA sequence Glycine. (bases 1 to 776) Keck Center for Comparative and Functional and Coryell, V., for

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BASE COUNT
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AAGGCTACCTCGGTGCCAATTGAGGAAGATTTCGCCTTTGGTTAGTGACCTTTGCAAGAA 1509
                                                                                                                                           CTCTTCGATGGATTGGTTTTTCCGGTGGCTTGCAGTTTTCAGCTTGAGCATCATTTGTTTTCC
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/clone="The library Gm-r1070 is a sequence-driven, reracked set of 9,216 clones selected from cDNA libraries from various tissues and stages of development of soybean that represent 2,639 sequences from immature cotyledons, 1,770 from immature seed coats, 3,338 from flowers, and 869 from young pods. The 5' ESTs of the source clones from the different libraries was used to select singletons, or a representative of each contig, which were reracked corntig analysis to select unique genes was performed by the laboratory of Ernest Retzel, Center for Computational Genomics and Bioinformatics, University of Minnesota, http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html
Reracking was performed by Genome Systems, St. Louis, http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html
Reracking was performed by Genome Systems, St. Louis, http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html
Reracking was performed by Genome Systems, St. Louis, http://www.life.uiuc.edu/biotech/keck.html Note: The Keck Center for Comparative and Functional Genomics, University of Illinois,
http://www.life.uiuc.edu/biotech/keck.html Note: The corresponding 5' EST from each clone in the Gm-r1070 library is listed in the 'OTHER EST' field. The detailed information on the source library for each clone can also be obtained by referring to the Genome Systems clone ID of the original cDNA library that is also listed under 'OTHER EST'."

110 close '180 close '180 close '180 close '180 close '180 close '180 close '180 close '180 close '180 close '180 close '180 close '180 close '180 close '180 close '180 close '180 close '180 close '180 close '180 close '180 close '180 close '180 close '180 close '180 close '180 close '180 close '180 close '180 close '180 close '180 close '180 close '180 close '180 close '180 close '180 close '180 close '180 close '180 close '180 close '180 close '180 close '180 close '180 close '180 close '180 close '180 close '180 close '180 close '180 close '180 close '180 close '180 close
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FEATURES BOUICE	AUTHORS AUTHORS TITLE JOURNAL COMMENT	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	1 SULT 2 748200 CUS	Oy 1.  Db 1.  Oy 1.	9 9 9 9 9	מם
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Email: est@watson.wustl.edu Possible reversed clone: similarity on wrong strand This clone is available through: Resdeen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800 )-533-4363 or contact via email: ccu@resgen.com Insert Length: 1134 Std Error: 0.00 High quality sequence stop: 412. Location/Qualifiers 1579 /organism="Glycine max" /mol type="maRNA" /db xref="taxon:3847" /clone="GENOME SYSTEMS CLONE ID: Gm-c1011-238" /tissue_type="immature cotyledons of greenhouse grown plants" /lab_host="DH10B"	Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R. Public Soybean EST Project Unpublished Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project Washington University School of Medicine	Gm-Cl011-238 5' similar to TR:082348 O82348 PUTATIVE CYTOCHROME , mRNA sequence. AI748200 AI748200.1 GI:5126464 EST. Glycine max (soybean) Glycine max Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyt Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; ros ; eurosids I; Fabales; Fabaceae; Papillonoideae; Phaseoleae; Glycine.	310 CAAATGGATGGTGATCCA-GATGTTACTGCAGTTCATGTGCTTTTGCATCAAT 1860	.690 TCAAGGTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAAAAAAA	510 GCATAATTTGCCTTATAGGAGCTTGTCATTTTGGGAGGCCAATCAGTGGACAATTAGGAC 1569	415 AAGGCTACCTCGGTGCCAATTGAGGAAGATTTCGCCTTTGGTTAGTGACCTTTGCAAGAA 356

BASE COUNT

63108,

USA

, Khanna Beck,C.,

Matches

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Query Match
Best Local Similarity
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                                                                                   SP2 bp mRNA linear EST 04-DEC-2001 sp06h07.y1 Gm-c1041 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1041-2102 5' similar to TR:O82348 O82348 PUTATIVE CYTOCHROME B5. ', mRNA sequence.
BE347857.1 GI:925971
EST.
Glycine max (soybean)
                                                                         BE347857
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//note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: XhoI; This cDNA library was constructed_from mRNA isolated from immature cocyledons (100-200mgs) of greenhouse grown plants. The cDNA library was prepared using the Life Technologies pSuperScript cDNA library construction kit. Complementary DNA was synthesized from mRNA using a poly (dT) sequence with a Not I restrictions site. Sal I linkers adapters were ligated to the blunt-ended cDNA fragments followed by NotI digestion. The cDNA fragments were directionally cloned into the NotI-Sal I restriction site of the pSPORT I vector. The ligated cDNA fragments were transformed into E. coli ElectroMax DH10B host cells. This library was constructed by Dr. Lila Vodkin and Dr. Anu Khanna."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Materston, R., and Wilson, R.
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/clone="GENOME SYSTEMS CLONE ID:
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                 Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA

If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.lastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of t maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V. Maize Mapping Project/DuPont Consensus Sequences for Design
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                                                                      contigs to seed DuPont contigs, this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

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                                                                                                                                                                /note="this sequence is part of a project of EST assemblies resulting from the application of public
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/mol_type="mRNA"
/db_xref="MaizeDB:634923"
/db_xref="taxon:4577"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid;
; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Michael A. Grusak
USDA/ARS Children's Nutrition Research
Baylor College of Medicine
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EST5313161 GESD Medicago
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/note=TVector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Immature seeds, collected from pods ranging in age from 11 to 19 days after pollination, were harvested from greenhouse-grown plants. Seeds were removed and separated from pod walls and were immediately frozen in liquid nitrogen. Seeds throughout the age range were poolled for mRNA extraction. CDNA was prepared from polyA+enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing
                                                                                                                                                      pollination"
                                                                                                                                                                  /tissue_type="immature seeds"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                902 GCTCACCACATTGCGTGCAACAGCCCTTGACCATGACCCTGATCTGCAGCACATGCCCGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 TTCGCTGTCTCATCGCGATTCTTTGGTTCGATTAAATCTTATTTTCTATGATAGACAGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 GCTCATCATATTGCTTGCAATAGTCTTGATTATGATCCTGATTTGCAGCATATCCCTGTT
                                                                                                                        ACAATTAGGACCCTCAGGACTGCTGCCCTACAAGCTAGGGACTTAACAAACCCTGCCCCT 1618
                                                                                                                                                                                                             CTTTGCAAGAAGCATAATTTGCCTTATAGGAGCTTGTCATTTTGGGAGGCCAATCAGTGG
                                                                                                                                                                                                                                                                                                    CATTTGTTTCCAAGGCTACCTCGGTGCCAATTGAGGAAGATTTCGCCTTTTGGTTAGTGAC
                                                                                                                                                                                                                                                                                                                                                                                              ATCTCTTGTGCCTCTTCGATGGATTGGTTTTTCGGTGGCTTGCAGTTTCAGCTTGAGCAT
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Pred. No. 2.2e-36;
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Seq primer: SKmod (CTA gAA CTA
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Medicago.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone lib="HOGA"
//clone lib="HOGA"
//note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
XhoI; cDNA was prepared into the Unizap XR vector from
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in SOLR cells."

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/tissue_type="3 day old seedling roots"
/tissue_erype="3 hours after treatment in
with 0.5 mg/ml oligogalacturonides (DP of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control
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/cultivar="A17"
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Pred. No. 1e-35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycine max (soybean)
Glycine max
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449 bp mRNA linear EST 30-DEC-2002 sau50d04.yl Gm-c1071 Glycine max cDNA clone SOYBEAN CLONE ID: Gm-c1071-4376 5' similar to TR:082348 082348 PUTATIVE CYTOCHROME
                                                                                                                                                                                                                                                                                              Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project Washington University School of Medicine
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                                                                                                                                                                            This clone is available through: ResGen, Invitrogen Corp. South Memorial Parkway Huntsville, AL 35801 For further in
                                                                                                                                                                                                                                     Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                         call: (800)-533-4363 or contact:
                                                                                                                                                                                                                     Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                              4444 Forest Park Parkway,
                                                                                                                                                                                                                                                                                                                                                                              Public Soybean EST Project
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/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID:
                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                              Box 8501,
                                                                                                                                                         ccu@resgen.com
  Gm-c1071-4376"
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Citrus elensis
Citrus elensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids II; Sapindales; Rutaceae; Citrus.
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0CRCS01_02bd10_b1 Washington Navel orange cold acclimated flavedo & albedo cDNA library Citrus sinensis cDNA clone UCRCS01_02bd10, mRNA
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// Notes "Vector: pSPORTI; Site 1: NotI; Site 2: SalI; The cDNA library was constructed from mRNA isoTated from immature pods (approximately 2cm long) of greenhouse grown plants. The library was prepared using the Life Technologies pSuperScript cDNA library construction kit. Complementary DNA was synthesized from mRNA using a poly(dT) sequence with a NotI restrictions site. SalI linkers adapters were ligated to the blunt-ended cDNA fragments followed by NotI digestion. The cDNA fragments were directionally cloned into the NotI-SalI restriction site of the pSPORTI vector. The ligated cDNA fragments were transformed into E.coli ElectroMax DH10B host cells. This library was constructed in the laboratory of Dr. Lila Vodkin by Anu Khanna at the University of Illinios at Urbana-Champaign. email: 1-vodkin@uiuc.edu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="immature pods (~2cm long) of greenhouse
grown plants"
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Pred. No. 1.9e-33;
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Department of Botany & Plant Sciences, University of California
Riverside, CA, 92521-0124
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Close, T.J., Collura, K., Fenton, R.D.,
Kudrna, D., Wanamaker, S., Wing, R. and
Development of EST Resources and New
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TGGTTCCCTCTTTTAGTGTCTTGCCTGCCAAATTGGCCTGAGAGGGTTATGTTTGTGCTT 1252
                                                                                                                                                                                                                    TACCCGGTAATGTGTGTGCCAGGGTCAACTTGTATCTGCAGACAATTCTGCTATTGTTT 1132
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                                                                                                                                                                                                                                                                                                                                        AGGAAGTTGGAGTTTGATTTCATTGCTAGGTTCTTGATCTGCTACCAGCACTTTACTTTT
                                                                                              TCGAGGCGAAAAGTGCAGGATAGAGCCTTGAACATAATGGGGGATCCTTGTGTTTTTGGACT 1192
                                                                                                                                                                          TACCCTGTTATGTGTGGCCAGAGTAAATTTATATTTACAGACACTTTTGTTATTGTTT
                                                         TCAAAGCGTAAGGTCCCAGATAGAGCCTTGAACATCATGGGTACTCTTGTCTTTTGGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone lib="Washington Navel orange cold acclimated flavedo & albedo cDNA library"

/note="Vector: Lambda Uni-ZaP XR, excised phagemid; Site 1: ECORE, Site 2: XhoI, Plants were grown in the field at University of California, Riverside Agricultural Operations since 1983. The scion was Mashington Navel orange and the rootstock Carizzo Citrange. Tissue from mature fruit was harvested at mid-day in January 2002 during a cold spell, when pre-dawn temperatures were approximately -2 to 2 degree C. Approximately 2 cm median sections of the rind were excised in the field from several fruits, then wrapped in aluminum foll and frozen quickly in dry ice. Total RNA was extracted using a phenol extraction procedure described in J. Japanaese Soc. Hort. Sci. (1996) 64:809-814. Poly(A) RNA was purified, a cDNA library was made, and 1 million primary lambda cDNA clones were in vivo excised to give a population of pBluescript SK(-) phagemids. All steps to this point were performed in the TJ Close lab at the University of California, Riverside (Fenton). Phagemids were plated, plasmid DNA purified, cDNA clones archived, and DNA sequences determined bi-directionally using an ABI350 at the Arizona Genomics Institute, University of Arizona (Collura Feuerbacher, Kim, Kudrna, Wing, Yu). Chromatogram files were transmitted to UC Riverside (by Yu), then processed at UC Riverside (by Wanamaker) using the HarvEST pipeline (http://harvest.ucr.edu) to remove vector and cloning oligo sequences and various contaminants, and to trim to a high quality region. Sequences that retained a phred 17 region of at least 100 bases were deposited to GenBank."
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/lab_host="E. coli TJC121"
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/db_xref="taxon:2711"
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Pred. No. 3.8e-33;
0; Mismatches 136;
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                                                                                                                                                                                                                            Unpublished Close Contact: Timothy Close Department of Botany & Plant Riverside, CA, 92521-0124 Tel: 9097873318
                                                                                                                                                                                                                                                                                                                                                                                                 Citrus sinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid; eurosids II; Sapindales; Rutaceae; Citrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CB291094 868 bp mRNA linear EST 28-FEB-2003 UCRCS01_02bd10_g1 Washington Navel orange cold acclimated flavedo & albedo cDNA library Citrus sinensis cDNA clone UCRCS01_02bd10, mRNA
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Close, T.J., Collura, K., Fenton, R.D., Kudrna, D., Wanamaker, S., Wing, R. and Development of EST Resources and New
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                                                                                                                                                                                            timothy.close@ucr.edu
/organism="Citrus sinensis"
/mol type="mRNA"
/cultivar="Washington Navel"
/db xref="taxon:2711"
/clone="UCRCSO1_02bd10"
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/dev stage="Mature fruit"
/lab_host="E. coli TJC121"
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BASE COUNT ORIGIN

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/clone_lib="Washington Navel orange cold acclimated flavedo & albedo cDNA library"
/note="Wector: Lambda Uni-ZAP XR, excised phagemid;
/note="Wector: Lambda Uni-ZAP XR, excised phagemid;
Site 1: EcoRI; Site 2: XhoI; plants were grown in the field at University—of California, Riverside Agricultural Operations since 1983. The scion was Washington Navel orange and the rootstock Carizzo Citrange. Tissue from mature fruit was harvested at mid-day in January 2002 during a cold spell, when pre-dawn temperatures were approximately—2 to 2 degree C. Approximately 2 cm median sections of the rind were excised in the field from several fruits, then wrapped in aluminum foil and frozen quickly in dry ice. Total RNA was extracted using a phenol extraction procedure described in J. Japanaese Soc. Hort. Sci. (1996) 64:809-814, Poly(A) RNA was purified, a cDNA library was made, and 1 million primary lambda cDNA clones were in vivo excised to give a population of pBluescript SK(-) phagemids. All steps to this point were performed in the TJ Close lab at the University of California, Riverside (Fenton). Phagemids were plated, plasmid DNA purified, cDNA clones archived, and DNA sequences determined bi-directionally using an ABIS30 at the Arizona Genomics Institute, University of Arizona (Collura, Feuerbacher, Kim, Kudrna, Wing, Yu). Chromatogram files were transmitted to UC Riverside (by Yu), then processed at UC Riverside (by Wanamaker) using the HarvEST pipeline (http://harvest.ucr.edu) to remove vector and cloning oligo sequences and various contaminants, and to trim to a high quality region. Sequences that retained a phred 17 region of at least 100 bases were deposited to GenBank."

22.4%; Score 432.4; DB 14; Length 868; Similarity 80.1%; Pred. No. 4.2e-32; B Conservative 0; Mismatches 186; Indels 0; Gaps 0; Mismatches 186; Indels 0; Gaps 0; Mismatches 186; Indels 0; Gaps 0; Mismatches 186; Indels 0; Gaps 0; Mismatches 186; Indels 0; Gaps 0; Mismatches 186; Indels 0; Gaps 0; Mismatches 186; Indels 0; Gaps 0; Mismatches 186; Inde
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á 맑 밁 á 밁 밁 5 밁 S 닭 á 밁 Ś В Ś 8 Ś Matches 508; Query Match Best Local Similarity 1400 1280 1100 1340 1220 508 628 808 889 CGGTGCCAATTGAGGAAGATTTCGCCTTTGGTTAGTGACCTTTGCAAGAAGCATAATTTG 1519 GATIGGITITITCGGIGGCITGCAGITITCAGCITGAGCATCATITGITITCCAAGGCIACCI 1459 CACATTCAGTTCTGTTTGAATCACTTTGCTGCAAATGTATATGTCGGGCCACCGAGTGGG TTGAACATAATGGGGATCCTTGTGTTTTTGGACTTGGTTTCCCCTCTTTTAGTGTCTTGCCTG AACTTGTATCTGCAGACAATTCTGCTATTGTTTTCGAGGCGAAAAGTGCAGGATAGAGCC 1159 CCTTATAGGAGCTTGTCATTTTGGGAGGCCAATCAGTGGACAATTAGGACCCTCAGGACT 1579 GATTGGTTTCATGGTTGCAGTTTCAGCTAGAGCATCATTTGTTTCCAAGGTTGCCA AATGACTGGTTTGAGAAGCAGACAAGTGGTACATTGGATATCTCTTGTGCCTCTTCGATG 1399 CACATTCAGTTTTGTTTAAACCACTTTGCTGCAAACGTGTATCTTGGTCCGCCTAAAGGG CCAAACTGGCCTGAAAGGGTGATGTTTGTGATGGCAAGTTTTTACTGTCACGGCCATCCAA 629 TTGAACATCATGGGTACTCTTGTCTTTTGGACTTGGTTCCCACTTCTAGTTTCATATCTA 689 AATTTATATTTACAGACACTTTTGTTATTGTTTTCAAAGCGTAAGGTCCCAGATAGAGCC AGGTGCCAATTGAGGAAGATTTCGCCGGTGGTGAGGGATCTTTGCAAGAAGCACAATATG 449 509 569 1219 749 389

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 165
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Complex Carbohydrate Research
University of Georgia
220 Riverbend Road, Athens, GA
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EST646631 HOGA Medicago truncatula cDNA clone HOGA-29M7, mRNA
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                                                                                                                                                                                              /tissue_type="3 day old seedling roots"
/dev stage="24 hours after treatment in the
with 0.5 mg/ml oligogalacturonides (DP 6-20)
presence of 100 ug/ml Gentamicin"
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BM143768
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Glycine max (soybean)
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid
; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                 1 (bases 1 to 588)
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanns Shoemaker,R., Keim,P., Vodkin,L., Kucaba,T., Martin,J., Beck,C.,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Bowers Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
                                             Contact: Shoemaker R/Public Soybean EST Public Soybean EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
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Gm-c1072-2921 5' similar to T
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                           CGGTTCTTCAATTCCATAACCTCTCTATTCTATGGGAGGAAGTTGGAGTTTGATTTCATT
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h Memorial Parkway Huntsville, AL 35801 For further information
: (800)-533-4363 or contact: ccu@resgen.com web site:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                library was prepared using the Stratagene phluescript II SK(+) library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with an XhoI restriction site. EcoRI adaptors were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA insert is protected from XhoI digestion via methylation during first strand synthesis. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the phluescript vector. The ligated cDNA fragments were transformed into E.coli ElectroMax DHIOB host cells. Plants were inoculated by Shuxian Li (clen Hartman lab, University of Illinois).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone lib="Gm-c1072"
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library wms constructed from mRNA isolated from 2-3 week old seedlings that were induced for symptoms of SDS (Sudden Death Syndrome) disease by the translocation of culture filtrate of Pusarium solani f. sp. glycines (Plant Cell Report 18:375-380). Cultivar PI 567374 is partially resistant to the disease SDS. Plant tissue (expanded leaves, folded leaves, and new shoots) were collected at 1, 6, 24, and 48 hrs. after inoculation and their mRNA pooled equally for cDNA construction. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Library was constructed by Steve Clough (Lila Vodkin lab, University of Illinois)."

120 c 138 g 205 t 1 others
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(Sudden Death Syndrome) disease"
/dev stage="2-3 weeks old"
/lab_host="DH10B"
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/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-c1072-2921"
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Pred. No. 3.5e-28;
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BI787611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccu@resgen.com Seq primer: -40RP from Gibco High quality sequence ston: 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycine.

1 (bases 1 to 571)

1 (bases 1 to 571)

Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,..., Beck,C., A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,A., Bolla,B., Marra,M., Hillier,D., Kucaba,T., Allen,M., Bowers Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers Wylie,T., Underwood,K., Steptoe,M., Pape,D., Harvey,N., Schurk Wylie,T., Underwood,K., Steptoe,M., Pape,D., Harvey,N., Schurk Wylie,T., Underwood,K., Steptoe,M., Packson,Y., Cardenas,M., McCann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y., Person,B., Swaller,T., Gibbons,M., Pape,I.,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y.,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BI787611 GI:15815336
BST.
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Glycine max
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid;
eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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ID: Gm-c1065-6425 5' similar to TR:082348 082348 PUTATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
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/clone_lib="Gm-c1065"
/note="Vector: pBluescript II Sk+; Site 1: EcoRI; Site_2:
/note="Vector: pBluescript II Sk+; Site_1: EcoRI; Site_2:
XhOI; The cDNA library was constructed from mRNA isolated
germinating shoots of the cultivar Williams. The seeds
were allowed to germinate for 24 hours prior to being
cold stressed for 2 days at 4C. Complementary DNA was
synthesized from mRNA using a primer consisting of a
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with a XhOI restriction site. EcoRI
adapters were ligated to the blunt-ended cDNA fragments
followed by XhOI digestion. The cDNA fragments were
directionally cloned into the EcoRI-XhOI restriction site
of the pBluescript vector. The ligated cDNA fragments were
transformed into DH10B host cells (GibcoBRL). This library
                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Glycine max"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                    tissue_type="germinating/lab_host="DH10B"
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Best Local Sim
Matches 456;
      TITLE
                                                                                                                                                                                            ORGANISM
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                                                                                                                                      CA938317.1 GI:27426797
EST.
Glycine max (soybean)
Glycine max
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                CA938317

575 bp mRNA linear EST 30-DEC-2002 gav30g08.yl Gm-c1048 Glycine max cDNA clone SOYBEAN CLONE ID: Gm-c1048-7215 5' similar to TR:082348 082348 PUTATIVE CYTOCHROME
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna, A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
                                                                                                                           Glycine.
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Fax: 314 286 1810
Email: est@watson.wustl.edu
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Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, I
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Arizona University."
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/dev_stage="1 week old"
/lab_host="DH10B"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 741)
Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Ellis, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
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BU028011.1 GI:22463531
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
belongs to contig QH_CA_Contig742, see http://cgpdb.ucdavis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
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      Conservative
                                                                              /Clone_lib="QH_EFGHJ sunflower RHA280"
//Clone_lib="QH_EFGHJ sunflower RHA280"
//note="Vector: pBRcDNASfiAB; The library was constructed from 11 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/TAG_ILB=CH_EFGHJ sunflower RHA280
TAG_SIZS_TCOCEGGG"
TAG_SIZS_TCOCEGGGGT"
180 c 157 g 223 t
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                                                                                                                                                                                                                                                                                                                                                                                                                G9 row: G column:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/cultivar="RHA280"
                                                                                                                                                                                                                                                                                                         /lab_host="E.coli"
                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:4232"
/clone="QHG9G05"
                                                                                                                                                                                                                                                                                                                                                                                     organism="Helianthus"
                   20.1%;
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QH EFGHJ sunflower RHA280 Helianthus annuus cDNA
mRNA sequence.
   Score 388.2; DB 13;
Pred. No. 6.5e-28;
0; Mismatches 218;
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827 AACAAGGTTGCACAGATCCTCTCTGGGAACTGCTTGACCGGGATAAGCATTGCTTGGTGG
1 (bases 1 to 676)
Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmo,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, development, of the cotton fiber
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                      BQ402431
GA_Ed0049E09f Gossypium
arboreum cDNA clone GA_E
                                                                                                                                                                      Gossypium arboreum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
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                                                                                                                                                                                                                                                                                                                                                                     GI:21090118
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m arboreum 7-10 dpa fiber library
_Ed0049E09f, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: rwing@clemson.edu
Total High Quality bases = 565
Total High Quality bases = 565
Seq primer: TAATACGACTCACTATAGGG
High Quality sequence start: 5
High quality sequence stop: 641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Wing RA
Clemson University
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 864 656 7288
Fax: 864 656 4293
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                                                                                                                                TTACAGACATTACTGCTATTGTTCTCAAACCGGAAAGTCCCAGATAGAGCATTTAACATA
                                                                                                                                                                  CTGCAGACAATTCTGCTATTGTTTTCGAGGCGAAAAGTGCAGGATAGAGCCTTGAACATA 1168
                                                                                                                                                                                                                                                                                                                                                     GATTATGACCCTGACCTCCAGCATATCCCCTTTTTTGCAGTCTCTTCACGTTTTTTCAAT
                                                                                                                                                                                                      ATCTGCTACCAGCACTTTACTTTTTACCCGGTAATGTGTGTTTGCCAGGGTCAACTTGTAT 1108
ATGGGGATCCTTGTGTTCTGGACTTGGTTCCCTCTCCTGCTTTCCTATCTACCCAATTGG
                                                                                   TCATTAACGTCTTGCTTTTACGGGAGGAAGTTGAATTTTGACCCTCTTGCAAGGTTTCTC
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/clone="GA_Ed0049E09f"
/clissue_type="Fibers isolated from bolls harvested 7-10
/clissue_type="Fibers isolated from bolls harvested 7-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Gossypium arboreum"
/mol_type="mRNA"
/strain="AKA"
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/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
149 c 150 g 226 t
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Query Match 32.0%; Score 618.4; DB 2; Length 1684; Best Local Similarity 66.5%; Pred. No. 2e-128; Matches 886; Conservative 0; Mismatches 446; Indels 0; Gaps	RESULT 1  US-08-831-570-1  US-08-831-570-1  Sequence 1, Application US/08831570  Patent No. 5959175  PARENT No. 5959175  PAPELICANT: Numberg, Andrew N. APPLICANT: Numberg Of SEQUENCES: COURSESPONDENCE ADDRESS:  DADRESSEE: SCOLLY, SCOCK, MUTCH, SCOCKESPONDENCE ADDRESS:  ADDRESSEE: SCOLLY, SCOCK, MUTCH, SCOCKES, COUNTRY: USA  COUNTRY: USA  COUNTRY: USA  COMPUTER: LBM PC Compatible OPERATION SYSTEM: PC-DOS/MS-DOS  SOUTWARE PATENTIALE FORM:  MEDIUM TYPE: Floppy disk COUNTRY: USA  COMPUTER: LBM PC Compatible OPERATION SYSTEM: PC-DOS/MS-DOS  SOUTWARE DATE: 09-AFR-197  APPLICATION NUMBER: US/08/831.570  FILING DATE: 09-AFR-197  ATTOREY/AGENT INFORMATION:  TELEPHONE: (516) 73-4343  TELEPHONE: (516) 73-4366  INFORMATION OF SEO ID NO: 1:  SEQUENCE CHARACTERISTICS:  SEQUENCE CHARACTERISTICS:  SEQUENCE CHARACTERISTICS:  SEQUENCE CHARACTERISTICS:  SEQUENCE CHARACTERISTICS:  SEQUENCE CHARACTERISTICS:  SEQUENCE CHARACTERISTICS:  SEQUENCE CHARACTERISTICS:  SEQUENCE CHARACTERISTICS:  SEQUENCE CHARACTERISTICS:  SEQUENCE CHARACTERISTICS:  SEQUENCE CHARACTERISTICS:  SEQUENCE CHARACTERISTICS:  SEQUENCE CHARACTERISTICS:  SEQUENCE CHARACTERISTICS:  SEQUENCE CHARACTERISTICS:  SEQUENCE CHARACTERISTICS:  SEQUENCE CHARACTERISTICS:  SEQUENCE CHARACTERISTICS:  SEQUENCE CHARACTERISTICS:  SEQUENCE CHARACTERISTICS:  SEQUENCE CHARACTERISTICS:  SEQUENCE CHARACTERISTICS:  SEQUENCE CHARACTERISTICS:  SEQUENCE CHARACTERISTICS:  SEQUENCE CHARACTERISTICS:  SEQUENCE CHARACTERISTICS:  SEQUENCE CHARACTERISTICS:  SEQUENCE CHARACTERISTICS:  SEQUENCE CHARACTERISTICS:  SEQUENCE CHARACTERISTICS:  SEQUENCE CHARACTERISTICS:  SEQUENCE CHARACTERISTICS:  SEQUENCE CHARACTERISTICS:  SEQUENCE CHARACTERISTICS:  SEQUENCE CHARACTERISTICS:  SEQUENCE CHARACTERISTICS:  SEQUENCE CHARACTERISTICS:  SEQUENCE CHARACTERISTICS:  SEQUENCE CHARACTERISTICS:  SEQUENCE CHARACTERISTICS:  SEQUENCE CHARACTERISTICS:  SEQUENCE CHARACTERISTIC	28 62 3.2 2634 4 US-09-463-238-3 Sequence 3, Appli 30 62 3.2 7724 4 US-09-463-245-1 Sequence 1, Appli 31 61.8 3.2 1166 5 PCT-US96-12129B-1 Sequence 1, Appli 32 61.2 3.2 2184 3 US-08-400-06B-6 Sequence 1, Appli 33 61.2 3.2 2184 3 US-08-90-06B-6 Sequence 1, Appli 34 61.2 3.2 2184 3 US-08-95-918C-1 Sequence 1, Appli 35 61.2 3.2 2184 3 US-08-97-705-1669 Sequence 1, Appli 36 61.2 3.2 221.4 US-09-77-05-1669 Sequence 1, Appli 36 61.2 3.2 2821 4 US-09-736-457-1669 Sequence 1669, Appli 36 61.2 3.2 2821 4 US-09-736-457-1669 Sequence 1669, Appli 37 61 3.1 570 1 US-09-865-970A-10 Sequence 10, Appli 39 60.8 3.1 570 1 US-09-865-970A-10 Sequence 10, Appli 60.8 3.1 570 1 US-08-298-687A-10 Sequence 10, Appli 60.8 3.1 570 1 US-08-298-829-10 Sequence 10, Appli 60.8 3.1 570 1 US-08-298-829-10 Sequence 10, Appli 60.8 3.1 609 2 US-08-797-355-9 Sequence 9, Appli 60.8 3.1 746 3 US-09-013-810-1 Sequence 9, Appli 60.8 3.1 888 3 US-09-13-810-1 Sequence 1, Appli 60.8 3.1 888 3 US-09-188-930-13 Sequence 1, Appli 60.8 3.1 888 3 US-09-188-930-13 Sequence 1, Appli 60.8 3.1 888 3 US-09-188-930-13 Sequence 13, Appli 60.8 3.1 888 3 US-09-188-930-13 Sequence 13, Appli 60.8 3.1 888 3 US-09-188-930-13
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                        TGGTTTGAGAAGCAGACAAGTGGTACATTGGATATCTCTTTGTGCCTCTTCGATGGATTGG
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                                                                                                                     ; LOCATION:
US-08-831-575-1
                                             Best Loc
Matches
                                               Query Match
Best Local Similarity
Matches 886; Conserv
                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vei
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/831,575
FILING DATE: 09-APR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGIO, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10203
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                             TELEFAX: (516) 742-436
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Li, Zhongsen
TITLE OF INVENTION: AN OLEOSIN 5'REGULATORY REGION FOR THE
TITLE OF INVENTION: MODIFICATION OF PLANT SEED LIPID COMPOSITION
                                                                                                                                                                      MOLECULE TYPE:
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
                                                                                                                                                                                                                          LENGTH: 1684 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                  TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
                                                                                                                                                        NAME/KEY:
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                                               Score 618.4; DB 2;
Pred. No. 2e-128;
0; Mismatches 446;
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                             TTTTTCGGTGGCTTGCAGTTTCAGCTTGAGCATCATTTGTTTCCAAGGCTACCTCGGTGC 1465
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                                                                                                                     TGGTTTGAGAAGCAGACAAGTGGTACATTGGATATCTCTTGTGCCTCTTCGATGGATTGG
                                                                                                                                                                                        CAGTTCTCCTTGAACCACTTCTCTTCAAGTGTTTATGTTGGAAAGCCCTAAAGGGAATAAT 1077
                                                                                                                                                                                                                                                                                     TGGGGTGAAAGAATTATGTTTGTTATTGCAAGTTTATCAGTGACTGGAATGCAACAAGTT
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US-08-366-779-4
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TELEPHONE: (516) 742-4343
TELEPAX: (516) 742-4346
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1685 base pairs
                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08366779 Patent No. 5614393
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FILING DATE: 30-DEC-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Presset, Leopold
REGISTRATION NUMBER: 19,8:
REFERENCE/DOCKET NUMBER: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Freyssinet, Georges L.
APPLICANT: Numberg, Andrew N.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID
TITLE OF INVENTION: DELTA 6-DESATURASE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: APPLICANT:
                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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CITY: Garden City
STATE: New York
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386 TCAATTCAAGGTAAGGTGTACAATGTCTCAGATTGGGTCAAGGAGCACCCTGGTGGTGAT
                                                                                 AAGAAGTACATAACCTCAGAGGAGCTGAAGGACGACAACAAGGAGGAGGATTTATGGATC
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                                                          AAGAAATACATTACCTCAGATGAACTCAAGAACCACGATAAACCCCGGAGATCTATGGATC
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400 Garden City Plaza
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Nuccio, Michael
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                                                                                                                                    Conservative
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                                                                                                                                Score 618.4; DB 1;
Pred. No. 2e-128;
0; Mismatches 446;
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                                             CAATTGAGGAAGATTTCGCCTTTGGTTAGTGACCTTTGCAAGAAGCATAATTTGCCTTAT 1525
                                                                                                                        TTTTTCGGTGGCTTGCAGTTTCAGCTTGAGCATCATTTGTTTCCAAGGCTACCTCGGTGC 1465
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AACCTTAGGAAAATCTCGCCCTACGTGATCGAGTTATGCAAGAAACATAATTTGCCTTAC
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MOLECULE TYPE:
US-08-789-936-4
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GENERAL INFORMATION:
                                                                                                                        Query Match 32.0%;
Best Local Similarity 66.5%;
Matches 886; Conservative
                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/366,779
FILING DATE: 30-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION UNMBER: 19,827
REFERENCE/DOCKET NUMBER: 8383ZXX
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEPAX: (516) 742-4343
                                                                                                                                                                                                                                                                                                     TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Thomas, Terry L.
APPLICANT: Reddy, Avutu S.
APPLICANT: Nuccio, Michael
APPLICANT: Freyssinet, Georges L.
APPLICANT: Nunberg, Andrew N.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC
TITLE OF INVENTION: DELTA 6-DESATURASE
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
CITY: Ga
STATE: N
COUNTRY:
                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/789,936 FILING DATE: 28-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                      LENGTH:
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Garden City
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TCAATTCAAGGTAAGGTGTACAATGTCTCAGATTGGGTCAAGGAGCACCCTGGTGGTGAT 445
                                                                                     AAGAAGTACATAACCTCAGAGGAGCTGAAGGGTCACAACAAGGAGGGGGAGATTTATGGATC 385
                                                         AAGAAATACATTACCTCAGATGAACTCAAGAACCACGATAAACCCGGAGATCTATGGATC
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                                                                                                                          Score 618.4; DB 1;
Pred. No. 2e-128;
0; Mismatches 446;
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                                      CAATTGAGGAAGATTTCGCCTTTGGTTAGTGACCTTTGCAAGAAGCATAATTTGCCTTAT 1525
                                                                                                                                                                                                                                                                                                                                                                CTCTTGGGATGCCTAGTGTTCTCGATTTGGTACCCGTTGCTTGTTTTCTTTGCCTAAT
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                                                                                                            TTTTTCGGTGGCTTGCAGTTTCAGCTTGAGCATCATTTGTTTCCAAGGCTACCTCGGTGC 1465
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Sequence 4, Application US/08934254
Patent No. 635861
GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLEN
TITLE OF INVENTION: DELTA 6-DESATURASE.
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: lir
; MOLECULE TYPE:
US-08-934-254-4
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEPAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 base pairs
                                                                                                                                                                                                                                                                                                                     Matches 886;
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM_PC_COMPatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,254
FILING DATB:
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: both
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                                                                                                                                                                                                                                                                      326 AAGAAGTACATAACCTCAGAGGAGCTGAAGGGTCACAACAAGGAGGAGATTTATGGATC
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GGCACAGCATGGTCACACCTTGAAAAATTCTTCACTGGCTACCACCTCAGTGACTTCAAG
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                                               TTTCCCTTGAAGAGTCTTGCTGGTCAAGAGGTAACTGATGCATTTGTTGCATTCCATCCT
                                                                                  GTTCCAATCTCAAACCTTGCTGGCCAGGATGTCACTGATGCATTCATAGCATACCATCCT
                                                                                                                                    TCGATTCAAGGGAAAGCCTATGATGTTTCGGATTGGGTGAAAGACCATCCAGGTGGCAGC
                                                                                                                                                                              TCAATTCAAGGTAAGGTGTACAATGTCTCAGATTGGGTCAAGGAGCACCCTGGTGGTGAT 445
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PRODUCTION OF GAMMA LINOLENIC
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Pred. No. 2e-128;
0; Mismatches 446;
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                                                                      AATTATGCATCTTTCTCCAAGGCCAATGAAATGACACTCAGAACATTGAGGAACACAGCA 1318
                                                                                                             AGGAGCTTGTCATTTTGGGAGGCCAATCAGTGGACAATTAGGACCCTCAGGACTGCTGCC
                                                                                                                                                            AACCTTAGGAAAATCTCGCCCTACGTGATCGAGTTATGCAAGAAACATAATTTGCCTTAC
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RESULT 6
US-08-934-254-26
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US-08-934-254-26
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Patent No. 6355861
GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
                                                                                                                                                                                                                                                                                  Query Match 28.7%;
Best Local Similarity 64.8%;
Matches 889; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (516) 742-4343
TELEPAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 26
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PLANT PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, V:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,254
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION UMMBER: 19,827
REFERENCE/DOCKET NUMBER: 8383
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: FEATURE: NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC TITLE OF INVENTION: DELTA 6-DESATURASE NUMBER OF SEQUENCES: 27
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NAME/KEY:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                               GGATCTCAAGTTCAAGGTAAAGGTGTACAATGTCTCAGATTGGGTCAAGGAGCACCCTGGTG 440
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GGGATGCGGCGGTTCAGGCGTGACCTTAATTCGGCCCCGTGCCCTAAGAAACTTGGGT
                        GGACTGCTGCCCTACAAGCTAGGGACTTAA---CAAACCCTGCCCCTAAGAA---TTTGT
                                                      TGCCGTATAGGAGCTTCGGGTTTTGGGACGACGCTAATGTCAGGACAATTCGGACGCTGA
                                                                                                              CGCGTGGGCAGCTTAGGAAGATTGCGCCCTTGGCTCGGGACTTGTGTAAGAAGCACGGGA
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                                                                                 TGCCTTATAGGAGCTTGTCATTTTGG---GAGGCCAATCAGTGGACAATTAGGACCCTCA
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GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLY
FILE REFERENCE: PL-0017 US
CURRENT APPLICATION UNMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEO ID NOS: 7600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:

NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6476212 700551823H1
NAME/KEY: unsure
LOCATION: 256
OTHER INFORMATION: a, t, c, g; or other
US-09-313-294A-1966
                                                                                                                                                                                                                                                                                                  RESULT 8
US-09-313-294A-3256
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US-09-313-294A-1966
; SOFTWARE: PER
; SEQ ID NO 3256
; LENGTH: 266
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Patent No. 6476212
GEMERRAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN.
FILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
SEQ ID NO 1966
LENGTH: 291
                                                                                                                                                                                                                                                        Sequence 3256, Application US/09313294A Patent No. 6476212
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Best Local Similarity
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                                              PERL Program
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Pred. No. 3e-25;
                                                                                                                                                     AND POLYPEPTIDES DERIVED FROM CORN
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US-09-904-615-21
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                                                                                                                                                                                                                                                         ; SEQ ID NO 21
; LENGTH: 1443
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-904-615-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 21, Application US/09904615 Patent No. 6566325
                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 142; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 09/511,554
PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 60/097,917
PRIOR FILING DATE: 1998-08-25
                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/098,634
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: PZ032P1
CURRENT APPLICATION NUMBER: US/09/904,615
CURRENT FILING DATE: 2001-07-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rosen et al.
TITLE OF INVENTION: 49 Human Secreted Proteins
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NAME/KEY: misc_feature
OTHER INFORMATION: Inc:
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LOCATION: 262
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AATTTAACTTTTTGTTAGGTGTGGTGTACAAATGGATGGTGATCCAGATGTTACTGCAGT 1841
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                                                     AGAAAATTACTTTTACTAAATTTTTTTGTGTGAATTTAAACAGCTAAATAGGGATCAGTA 1290
                                                                                    AAAAGAAAAAATTCTCATTGTGATTTTGCTAGCCCCCACTTTTCCAGATTGGGCTTTG 1781
                                                                                                                      TTTTAAATGTTGTTTGAAAAATGTTTTCCCAAGGAAAGTTTATTATTTGCTGCTGTTTCA
                                                                                                                                                        TGCAGGCCAGGAGCGCCACA
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Pred. No. 3.8e-16;
0; Mismatches 85
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                                                                                                                                                                                                       Score 67;
Pred. No.
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                                                                                                          Matches
                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: UBIQUITOUS NUCLITITLE OF INVENTION: METHODS NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Rela
SOFTWARE: #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                           TOPOLOGY: 1i MOLECULE TYPE:
                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1813 base pair
                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION: NAME: BARBARA S. KITCHELL
                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                               TELEFAX: 79-0924
                                                                                                                                                                                     STRANDEDNESS: 81.
                                                                                                                                                                                                                                                                          TELEPHONE: (516) 789-2679
                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 10-NO' CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: ARC
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US94/12883 FILING DATE: Concurrently Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
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                                                                                1836
                          1291 ACTTTATCTCTATCCTTAATGAACATTTGTTTTATTGGTGGCTGGAAATATTTCTATTGT
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                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                 (512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                  10-NOV-1993
                                                                                                                                                                           DNA (genomic)
                                                                                                                                                                                                      single
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                                                                                                                       78.8%;
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                                                                                                       Score 65.4; DB 5;
Pred. No. 1.5e-05;
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                                                                                                                                    Length 1813;
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RESULT 11 US-09-482-273-31 ; Sequence 31, Application US/09482273

PPLICANT: Rosen et al.
ITLE OF INVENTION: 71 Human Secreted Proteins

INFORMATION

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                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Brassica napus
US-08-821-994-59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-482-273-31
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Matches
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Sequence 59, App...
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Tocal Similarity
                                                                                                             Matches
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Best Local Similarity
                                                                                                                                                                                                                                                      SEQ ID NO 59
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                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Promoters
FILE REFERENCE: PPD 50108
CURRENT APPLICATION NUMBER: US/08/821,994A
CURRENT FILING DATE: 1997-03-22
EARLIER APPLICATION NUMBER: PCT/GB97/00729
EARLIER FILING DATE: 1997-03-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/482,273
CURRENT FILING DATE: 2000-01-13
EARLIER APPLICATION NUMBER: PCT/US99/15849
EARLIER FILING DATE: 1999-07-14
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 89
SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                          EARLIER APPLICATION NUMBER: GB 9606062.9 EARLIER FILING DATE: 1996-03-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Greenland, Andrew J
APPLICANT: Thomas, Didier RP
APPLICANT: Jepson, Ian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLIER APPLICATION NUMBER: 60/092,922
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/092,956
EARLIER FILING DATE: 1998-07-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: PZ030P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                   ENGTH: 1577
                                                                    1786 TAACTTTTTGTTAGGTGTGTGTACAAATGGATGGTGATCCAGATGTTACTGCAGTTCAT 1845
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INFORMATION:
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                                   TGATTACTTTATAGCTGTTGTTGTGATATGTATTATTAGTCTCTTATTTGGATGTATACA 1487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCGGGGGGGGGGGGTATCCAGAATTGGTTGTAAATACTTTGCATATTGTCTGATTAAA
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                                                                                                            Conservative
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                                                                                                                           64.4%;
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                                                                                                          0; Mismatches
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Pred. No. 1.
                                                                                                                           Score 64.2; DB 3;
Pred. No. 2.6e-05;
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US-09-360-545-66
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/360,545
CURRENT FILING DATE: 1999-07-26
EARLIER APPLICATION NUMBER: 60/052,249
EARLIER FILING DATE: 1997-11-07
EARLIER APPLICATION NUMBER: PCT/US98/14528
                                                                                                                                                                                                                                                                 GENERAL INFORMATION: APPLICANT: FASEL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JENERAL INFORMATION:
APPLICANT: Croteau, Rodney B
APPLICANT: Bohlmann, Jorg
APPLICANT: Bohlmann, Jorg
APPLICANT: Steele, Christopher L
APPLICANT: Phillips, Michael A
APPLICANT: Phillips, Michael A
TITLE OF INVENTION: MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)
FILE REFERENCE: weur13885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EARLIER FILING DATE: 1998-07-10 NUMBER OF SEQ ID NOS: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: (34)..(1923)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Abies grandis
                                                                                                                                                                                 APPLICANT: FASEL, NICOLAS JOSEPH
APPLICANT: REYMOND, CHRISTOPHE DOMINIQUE
TITLE OF INVENTION: DICTYOSTELID EXPRESSION VECTOR AND
TITLE OF INVENTION: METHOD FOR EXPRESSING A DESIRED PROTEIN
RUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK
COMPUTER: Midwest Micro 486-50
                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: THE WEBB
STREET: 700 KOPPERS
                                                                         COUNTRY:
                                                                                                                    CITY: PITTSBURGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1822 GATCCAGATGTTACTGCAGTTCATGTGCTTTGCATCAATACAAATTCATATCATGTATGC 1881
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1978 CATGTGCATGTCTCTCTATGTAACTAGTTGTATGCGTGGTATGATTATAAAATTGGAGGT 2037
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                                                                                               PENNSYLVANIA
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                                                                           UNITED STATES OF
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BUILDING,
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                                                                             AMERICA
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Pred. No. 2.9e-05;
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                                                                                                                                    SEVENTH AVENUE
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OPERATING SYSTEM:

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US-09-073-569-1
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Best Local Similarity 55.6%;
Matches 148; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Grossmann, Angelika
TITLE OF INVENTION: NOVEL TUMOR ANTIGENS
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 07/9
FILING DATE: 15-JAN-1993
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 1
FILING DATE: 26-MAY-:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,438
                                                                      PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                        STREET: 1201 E.
CITY: Seattle
STATE: WA
                                                                                                                          APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                    COUNTRY: US
ZIP: 98102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: NUCLEIC ACID STRANDEDNESS: SINGLE
                                                                                                           CLASSIFICATION:
                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1789 CTTTTTGTTAGGTGTGGTGTACAAATGGATGGTGATCCAGATGTTACTGCAGTTCATGTG 1848
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WORDPERFECT 6.1
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Pred. No. 2.3e-05;
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                                                                                                                                        LOCATION: 34...13
OTHER INFORMATION:
US-09-073-569-1
                                                                                         Query Match
Best Local Similarity
Matches 82; Conserv
                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 206-442-6672
                                                                                                                                                                                                                                                                                 TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                     LENGTH: 1733 base pairs
1823 ATCCAGATGTTACTGCAGTTCATGTGCTTTGCATCAAATTCATATCATATCATGTATGCC 1882
                                                                                           Conservative
                                                                                                                                                               Coding Sequence
                                                                                                                                                                                                    linear
                                                                                                                                                                                                           single
                                                                                                     3.3%;
73.2%;
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                                                                                                     Score 64; DB 3;
Pred. No. 3e-05;
                                                                                           Mismatches
                                                                                             30; Indels
                                                                                                                 Length 1733;
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Gaps

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Search completed: January 1, 2004, 00:05:29 Job time : 98.9683 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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seq length: 2000000000
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## SUMMARIES

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## ALIGNMENTS

US-09-938-842A-558

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Sequence 558, Application US/09938842A

Patent No. US20020160378A1

Patent No. US20020160378A1

Patent No. US20020160378A1

PAPLICANT: Harper, Jeff
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIPTION UMBER: US 60/227, 866

PILE REFERENCE: SCRIPTION UMBER: US 60/227, 866

PRIOR APPLICATION NUMBER: US 60/227, 866

PRIOR APPLICATION NUMBER: US 60/264,647

PRIOR APPLICATION NUMBER: US 60/264,647

PRIOR APPLICATION NUMBER: US 60/264,647

PRIOR APPLICATION NUMBER: US 60/300,111

PRIOR APPLICATION NUMBER: US 60/300,111

PRIOR FILLING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: 5379

SEQ ID NO 558

TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-558
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                                                                                                                                                                                                                                                    Query Match 33.1%;
Best Local Similarity 67.1%;
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                                                                                                                                           310 GGTTGTTGAGAAGGAGGAAGTACATAACCTCAGAGGAGGCTGAAGGGTCACAACAAGGA 369
                                                  370 GGGAGATTTATGGATCTCAATTCAAGGTAAGGTGTACAATGTCTCAGATTGGGTCAAGGA 429
63 TGGÁGATCTÁTGGATCGCGÁTTCAÁGGCAAGGTCTÁCAACGTCTCCGATTGGATTÁAAAC 122
                                                                                                              3 GGCGGAAGAGACGGAGAAAAGTACATTACGAACGAAGATCTTAAAAAACACAACAAATC
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                                                                                                                                                                                                                                                                                 DB 10; Length 1350;
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TCGCTTACCTCGTTGCCATCTCCGGAAAGTTTCTCCGGTGGTTCAAGAGCTTTGCAAGAA
                                     AAGGCTACCTCGGTGCCAATTGAGGAAGATTTCGCCTTTGGTTAGTGACCTTTGCAAGAA 1509
                                                                                                                         CTCTTCGATGGATTGGTTTTTCGGTGGCTTGCAGCTTTCAGCTTGAGCATCATTTGTTTCC
                                                                                                                                                                                                                           ACCGAGTGGGAATGACTGGTTTGAGAAGCAGACAAGTGGTACATTGGATATCTCTTGTGC
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MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID
US-10-029-756-4
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Best Local Similarity
Matches 886; Conserv
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Publication No. US20020108147A1
GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/934,254
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/029,756
FILING DATE: 21-Dec-2001
CLASSIFICATION: <Unknown>
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS: Scully, Scott, Murphy & Presser ADDRESSEE: Scully, Scott, Murphy & Presser STREET: 400 Garden City Plaza
CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Thomas, Terry L.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY
DELTA 6-DESATURASE
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446 GTTCCAATCTCAAACCTTGCTGGCCAGGATGTCACTGATGCATTCATAGCATACCATCCT
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                                                                                             TCAATTCAAGGTAAGGTGTACAATGTCTCAGATTGGGTCAAGGAGCACCCTGGTGGTGAT
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REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 8383ZYXWVU
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
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                                                            TCGATTCAAGGGAAAGCCTATGATGTTTCGGATTGGGTGAAAGACCATCCAGGTGGCAGC 178
                                                                                                                                         AAGAAATACATTACCTCAGATGAACTCAAGAACCACGATAAACCCGGAGATCTATGGATC
                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid STRANDEDNESS: both
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TELEFAX: (516) 742-4366
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                                                                                 ACCTTAGGAAAATCTCGCCCTACGTGATCGAGTTATGCAAGAAACATAATTTGCCTTAC 1258
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AATTATGCATCTTTCTCCAAGGCCAATGAAATGACACTCAGAACATTGAGGAACACAGCA 1318
                                       AGGAGCTTGTCATTTTGGGAGGCCAATCAGTGGACAATTAGGACCCTCAGGACTGCTGCC
                                                                                                              CAATTGAGGAAGATTTCGCCTTTGGTTAGTGACCTTTGCAAGAAGCATAATTTGCCTTAT 1525
                                                                                                                                                                     TTTCATGGTGGATTGCAATTCCAAATTGAGCATCATTTGTTTCCCAAGATGCCTAGATGC
                                                                                                                                                                                                             TITTTCGGTGGCTTGCAGTTTCAGCTTGAGCATCATTTGTTTCCAAGGCTACCTCGGTGC 1465
                                                                                                                                                                                                                                                                                                                                      CAGTTCTCCTTGAACCACTTCTCTTCAAGTGTTTATGTTGGAAAGCCTAAAGGGAATAAT 1078
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US-10-029-756-26
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Publication No. US20020108147A1
GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
APPLICANT: Thomas, Terry L.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID
                                                                                                                                                  Query Match 28.7%;
Best Local Similarity 64.8%;
Matches 889; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: 48..1406
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/934,254
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/029,756
FILING DATE: 21-Dec-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic) FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 83
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy &
STREET: 400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DELTA 6-DESATURASE
NUMBER OF SEQUENCES: 27
CORRESPONDENCES:
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                              GGATCTCAATTCAAGGTAAGGTGTACAATGTCTCAGATTGGGTCAAGGAGCACCCTGGTG 440
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                                                                          AAGCTAAGAAGTATATCACGGCGGAGGACCTCCGCCGCCACAACAAGTCCGGCGATCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTCATGGTTAA 1390
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                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Garden City
                                                                                                                                                                                                                                                                                                                             LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1702 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Presser, Leopold
                                                                                                                                                                                                                                                                                                                             CDS
48..1406
                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                    0;
                                                                                                                                                                      Score 555; DB 14;
Pred. No. 3.3e-121;
                                                                                                                                                      Mismatches 470;
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                                                                                                                                                                                      Length 1702;
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CTCGGTGCCAATTGAGGAAGATTTCGCCTTTGGTTAGTGACCTTTGCAAGAAGCATAATT
                                                                               TGGATTGGTTTTTCGGTGGCTTGCAGTTTCAGCTTTGAGCATCATTTTTTTCCAAGGCTAC
                                                                                                                                                                                   GGAATGACTGGTTTGAGAAGCAGACAAGTGGTACATTGGATATCTCTTTGTGCCTCTTCGA
                                                                                                                                                                                                                                                                                                   AGCACATTCAGTTCTGTTTGAATCACTTTGCTGCAAATGTATATGTCGGGCCACCGAGTG
                                                                                                                                                                                                                                                                                                                                                                                TGCCAAATTGGCCTGAGAGGGTTATGTTTGTGCTTGCTTAGCTTTTGCTGCTTTGCTTCCATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCTTGAACATAATGGGGATCCTTGTGTTTTGGACTTGGTTCCCCTCTTTTAGTGTCTTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GACTCTTCAACTCCATCACCTCGGTCTTCTATGGCCGAGTCCTGAAATTCGACGAAGTGG
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APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
APPLICANT: Hurban, Patrick
FIILE OF INVENTION: Expressed Sequences of Arabidopsis
FILE REFERENCE: 2024 (PARA-013PRV)
CURRENT APPLICATION NUMBER: US/09/770,149
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,506
PRIOR APPLICATION NUMBER: 60/178,506
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 494
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TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-149-494
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US-09-770-149-494/c
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Patent No. US20020059663A1
GENERAL INFORMATION:
APPLICANT: Gorlach, Jorn
APPLICANT: An, Yong-Qiang
                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 381; Conserv
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APPLICANT:
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                                                                                                                                                                                                                                                                                        1152 ATAGAGCCTTGAACATAATGGGGATCCTTGTGTTTTGGACTTGGTTCCCTCTTTTAGTGT
                                                                                                                                                                                                              1392 CTTCGATGGATTGGTTTTTCGGTGGCTTGCAGTTTCAGCTTGAGCATCATTTGTTTCCAA 1451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Garcia, Carlos A.
Kricker, Maja
Kricker, Ted
Slader, Ted
Davis, Keith R.
Allen, Keith
                                                                                                                                    CCATCCAGCACATTCAGTTCTGTTTGAATCACTTTGCTGCAAATGTATATGTCGGGCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       An, Yong-Qiang
Hamilton, Carol M.
Price, Jennifer L.
Raines, Tracy M.
Yu, Yang
Rameaka, Joshua G.
                                                              CGAGTGGGAATGACTGGTTTGAGAAGCAAGACAAGTGGTACATTGGGATATCTCTTGTGCCT 1391
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                                       CCACCGGTAGCGACTGGTTCGAGAAGCAAGCGGCGGGAACAATCGATATCTCTTGTAGAT
                                                                                                                 CGCTTCAACACATTCAATTCACGCTTAACCATTTCGCTGCTGATGTCTACGTTGGTCCAC
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                                                                                                                                                                                                                                                                                                                                       13.9%; Score 269.4; DB 9; 67.2%; Pred. No. 1.2e-53; ative 0; Mismatches 186;
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GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: LA ROSA, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 15653
LENGTH: 267
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; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID:
US-09-878-574-15653
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US-09-878-574-15653
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RESULT 6
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Best Local Similarity 99.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 267;
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                                                                                                                                                               TCTATTTATCTTCTTATTGTAGTTCTCATTGTGTCTGATTTCAGTGATTTGTGTTTTT
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                                                        TGGTTAACACAAGCAATGGAGGTTGTTG
                                                                                         TGGTTAACACAAGCAATGGAGGTTGTTG 317
                                                                                                                                                                                                                                                                                                                                                      GGGTAAAAAGGGTATTAGATCCTTGAACCAGATCAAATCATCAAAATCTCTGTCTATGGGG
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Pred. No. 1.1e-50;
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; LOCATION: (1)...(476)
; OTHER IMPORMATION: n = A,T,C or G
US-09-770-444-39
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SOFTWARE: FRATSEQ for Windows Version 4.0
SEQ ID NO 39
LENGTH: 476
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APPLICANT: Gorlach, Jorn
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Best Local Similarity
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APPLICANT: Hurban, Patrick
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thallana
FILE REFERENCE: 2027 (PARA-016PRV)
CURRENT APPLICATION NUMBER: US/09/770,444
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,502
PRIOR FILING DATE: 2000-01-27
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ORGANISM: Arabidopsis thaliana
FEATURE:
                                                                       318
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378
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                                                                                                                                                                                                                                                   638 GGGCATGTCACTTCATGCACCCTTGCATCTGTTGCTGTTATGTTCCTCATTGTACTCTAT
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AAATCTTATAACAGATTCGCTCAGCTTCTCTNNGGTAACTGTCTCACCGGAATCTCAATC
                                   AATGGTTTCAACAAGGTTGCACAGATCCTCTCTGGGAACTGCTTGACCGGGATAAGCATT
                                                                                                            CTTTGGATGCAAAGTGCTTATGTGGGCCATGATTCTGGCCACTATGTGGTTATGACAACC
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Kricker, Maja
Slader, Ted
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Rameaka, Joshua G
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Allen, Keith
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Indels Length

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Gaps

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637

577 77

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GCTTGGTGGAAGTGGACTCACAATGCTCACCACATTGC

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Sequence 370, Application US/09924035A
Patent No. US20020142319A1
GENERAL INFORMATION:
APPLICANT: Grlach, Jrn
TITLE OF INVENTION: Expressed Sequences of Ar
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2011US
CURRENT APPLICATION NUMBER: US/09/924,035A
CURRENT FILING DATE: 2000-08-11
CURRENT FILING DATE: 1990-08-13
NUMBER OF SEQ ID NOS: 900
SOFTWARE: FASTSEQ for Windows Version 3.0
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US-09-924-035A-370/c
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules an
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
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SEQ ID NO 3260
LENGTH: 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KRY: unsure
LOCATION: (1)..(287)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: LIB3028-013-Q1-B1-H6
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ORGANISM: Glycine max
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 78.4
mes 225; Conservative
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Pred. No. 1.3e-34;
0; Mismatches 62;
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)8
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 9255
LENGTH: 263
TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: 701102270H1
US-09-878-574-9255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-924-035A-370
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Best Local Similarity
Matches 234; Conserv
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                                                                                                                                                                                                                           199;
                                                                                             GGAAGTGGACTCACAATGCTCACCACATTGCGTGCAACAGCCTTGACCATGACCCTGATC
                                                                                                                                                                            TCAACAAGGTTGCACAGATCCTCTCTGGGAAACTGCTTGACCGGGATAAGCATTGCTTGGT
                   TGCAGCACATGCCGGTCTTTGCAGTTTCGTCGCGGTTCTTCAATTCCATAACCTCTCATT 1004
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GGAAGTGGACTCACAATGCTCACCACATCTCATGCAATAGTCTTGACTATGATCCTGAT- 130
                                                                                                                                                  TCGAGCGGCTCGAGCAAATCCTTTGTGGCAATTGCATGACTGGGATAAGCATTGCATGGT
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Pred. No. 5.4e-27
0; Mismatches 5:
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CURRENT APPLICATION NUMBER: US/09/923,876
CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/298,329
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/085,331
PRIOR FILING DATE: 1998-05-05
I PRIOR FILING DATE: 1998-05-05
I VIMBER OF SEQ ID NOS: 6332
SOFTWARE: PERL Program
SEQ ID NO 5116
LENGTH: 265
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US-09-923-876-5116
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Patent No. US20020013958A1
GENERAL INFORMATION:
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Best Local Similarity
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NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID
-09-923-876-5116
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APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Kamigaki, Laura Y. (Ito)
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLECTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: PL-0012-1 CON
CURRENT APPLICATION NUMBER: US/09/923,876
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APPLICANT: Kamigaki, Laura Y. (Ito)
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: PL-0012-1 CON
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ilarity 62.0%;
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Pred. No. 2e-12;
0; Mismatches 92; Indels
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CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/298,329
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/685,331
PRIOR FILING DATE: 1998-05-05
PRIOR FILING DATE: 1998-05-05
NUMBER OF SEQ ID NOS: 6332
SOFTWARE: PERL PROGRAM
SEQ ID NO 5116
LENGTH: 265
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                                                                                                                                                            ; ORGANISM: Neurospora crassa US-10-369-493-27824
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                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 27824
LENGTH: 1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 27824, Application US/10369493 Publication No. US20030233675A1 GENERAL INFORMATION:
                                                                               Matches
                                                                                                Query Match
Best Local :
                                                                                                                                                                                                                                                                                                           APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052) B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
CURRENT FILING DATE: 2003-02-28
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Best Local Similarity
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FEATURE:
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20030237110A9 700456385H1
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                                                                                                    Local Similarity
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TCGGCTCTTTCTGGCACCAGCTAGTCTTCACTGCCCATGACGCCGGACACATGGGCATCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCGTCGCGGTTCTTCAATTCCATAACCTCTCATTTCTATGGGAGGAAGTTGGAGTTTGAT 1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATCGCCTGCAACAGCCTGGACCATGACCCGGACCTCCAGCACATGCCGCTCTTCGTTGTC
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                                                                             Conservative
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                                                                                                4.6%;
53.1%;
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                                                                           Score 89.6; DB 12;
Pred. No. 7.9e-11;
0; Mismatches 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 94.8; DB 12;
Pred. No. 2e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92;
                                                                                                                Length 1098;
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APPLICANT: Lee, John
APPLICANT: Lille, James
APPLICANT: Thompson, Pamela
APPLICANT: Lille, James
APPLICANT: Lille, James
ITILE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
ITILE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
ITILE OF INVENTION: THERAPY OF OVARIAN CANCER
ILLE REFERENCE: MRI-006B
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: US 60/191,031
PRIOR APPLICATION NUMBER: US 60/207,124
PRIOR APPLICATION NUMBER: US 60/207,124
PRIOR APPLICATION NUMBER: US 60/211,940
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 60/216,820
PRIOR APPLICATION NUMBER: US 60/216,820
PRIOR APPLICATION NUMBER: US 60/220,661
PRIOR APPLICATION NUMBER: US 60/220,661
PRIOR APPLICATION NUMBER: US 60/220,661
PRIOR APPLICATION NUMBER: US 60/220,661
PRIOR APPLICATION NUMBER: US 60/257,672
PRIOR APPLICATION NUMBER: US 60/257,672
                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; CRANISM: Homo sapiens
; FEATURE:
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 225, 226, 227, 228
; OTHER INFORMATION: n = A,T,C oz.
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US-09-814-353-17782/c
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Best Local Similarity
Matches 144; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 17782, Application US/09814353 Publication No. US20030165831A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 17782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 200
PRIOR FILING DATE: 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 22037
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH:
1798 AGGTGTGGTGTACAAATGGATGGTGATCCAGATGTTACTGCAGTTCATGTGCTTTGCATC 1857
                                                                                                  1738 TCATTGTGATTTTGCTAGCCCCCACTTTTCCAGATTGGGCTTTGAATTTAACTTTTTGTT
                                                                                                                                                                                   1050 TCTGCTACCAGCACTTTACTTTTACCCGGTAATGTGTGTTGCCAGGGTCAACTTGTATC
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Pred. No. 1.8e
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4844
LENGTH: 299
                                                                                                                                                                                                                                    Matches 119;
                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lee, John
APPLICANT: Thompson, Pamela
APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REFERENCE: MRI-006B
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                    FEATURE: FEATURE: NAME/KEY: misc_feature
LOCATION: 146, 163, 175, 190, 191,
LOCATION: 206, 213, 214, 217, 222,
LOCATION: 246, 247, 249, 254, 255,
LOCATION: 246, 247, 249, 254, 255,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/191,031 PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 2000-12-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/216,820 PRIOR FILING DATE: 2000-07-07 PRIOR APPLICATION NUMBER: US 60/220,661
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PRIOR APPLICATION NUMBER: US 60/211,940
PRIOR FILING DATE: 2000-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/207,124
                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
                                                                                     1827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 2000-07-25
                                                                                                                                              1918 ААЛАЛАЛАЛАЛАЛАЛА 1934
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                                                                                                                  TTTGTTTTCTCTTTAAAAAGAAAAAATTCTCATTGTGATTTTGCTAGCCCCCACTTTT
                                                        AGATGTTACTGCAGTTCATGTGCTTTGCATCAATACAAATTCATATCATGTATGCCAAAA 1886
                                                                                                                                                                           TTTTTTTTTTTNANAAAAAAANTTTTTNCCCNTTTTTTNNNTTTTNANNGATTTT
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                                                                                                                                                                                                                                                 3.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60/257,672
                                                                                                                                                                                                                                     Score 74.6; DI
Pred. No. 1.4e
0; Mismatches
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224,
256,
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No. 1.
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225,
264,
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226,
268,
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229,
274,
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232,
284,
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FILE REFERENCE: MRI-006B

CURRENT APPLICATION NUMBER: US/09/814,353

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: US 60/191,031

PRIOR APPLICATION NUMBER: US 60/207,124

PRIOR FILING DATE: 2000-05-25

PRIOR FILING DATE: 2000-05-25

PRIOR APPLICATION NUMBER: US 60/211,940

PRIOR FILING DATE: 2000-07-07

PRIOR APPLICATION NUMBER: US 60/216,820

PRIOR FILING DATE: 2000-07-07

PRIOR APPLICATION NUMBER: US 60/220,661

PRIOR FILING DATE: 2000-07-25

PRIOR APPLICATION NUMBER: US 60/257,672

PRIOR APPLICATION NUMBER: US 60/257,672

PRIOR APPLICATION NUMBER: US 60/257,672

PRIOR APPLICATION NUMBER: US 60/257,672

PRIOR APPLICATION NUMBER: US 60/257,672

PRIOR APPLICATION NUMBER: US 60/257,672

PRIOR APPLICATION NUMBER: US 60/257,672

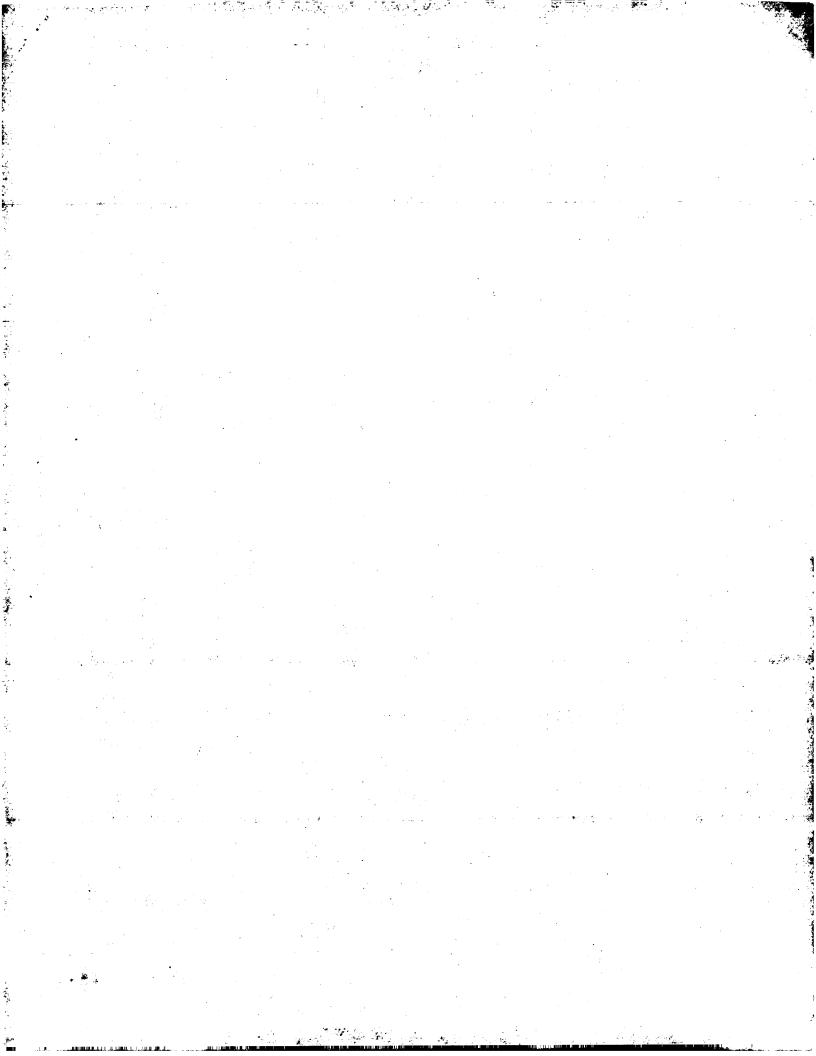
PRIOR TILING DATE: 2000-12-21

NUMBER OF SEQ ID NOS: 22037

SECONDAME: FASESEQ for Windows Version 4.0

SEQ ID NO 11141

LENGTH: 299
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FEATURE:
FEATURE:
NAME/KEY: misc_feature
LOCATION: 146, 163, 175, 190, 191, 192, 195, 198, 199, 201, 202, 203, 100CATION: 206, 213, 214, 217, 222, 224, 225, 226, 229, 232, 233, 239, 100CATION: 246, 247, 249, 254, 255, 256, 264, 268, 274, 284, 286
COTHER INFORMATION: n = A,T,C or G
US-09-814-353-11141
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Search completed: January 1, 2004, 05:19:34
Job time : 484.374 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 3.9%;
Best Local Similarity 52.2%;
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APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1707 TTTGTTTTCTCTTTAAAAAGAAAAAAATTCTCATTGTGATTTTGCTAGCCCCCCACTTTT 1766
                                                                                                                                                        1827 AGATGTTACTGCAGTTCATGTGCTTTGCATCAATACAAATTCATATCATGTATGCCAAAA 1886
                                                                                                                                                                                                                                                                                                                                                                                                                           299 TTTTTTTTTTTTNANAAAAAAAANTTTTTNCCCCVTTTTTTTNNNTTTTNANNGATTTT
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Match
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1: pir1:*
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1 MEVVEKEKKYITSE
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     \begin{array}{c} 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\ 5.5 \\
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       \begin{array}{c} 4449 \\ 4449 \\ 4440 \\ 4444 \\ 4444 \\ 4444 \\ 33454 \\ 4447 \\ 33454 \\ 4447 \\ 33454 \\ 4477 \\ 13568 \\ 9677 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 13347 \\ 1
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A; Residues: 1-449 < STO>
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Matches 346; Conserv
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  MDWFFGGLQFQLEHHLFPRLPRCHLRTVSPVVKELCKKHNLPYRSLSWWEANVWTIRTLK
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
131	132.5	133	133	133.5	134	136	136	136.5	136.5	137	137	139	140	140.5	142.5
5.3	5.4	5.4	5.4	5.5	5.5	5.6	5.6	5.6	5.6	5.6	5.6	5.7	5.7	5.7	5.8
134	135	211	134	134	864	894	384	129	98	926	112	141	370	140	135
μ	<u>ب</u>	N	۳	μ.	<u>ب</u>	2	ب	N	_	<u>س</u>	N	N	N	N	N
CBRT5	CBRTSM	T49930	CBPG5	CBBO5	JC1422	S52857	S54484	T41083	JN0316	RDSPNH	S71324	T15210	B83034	T52468	S49200
•	cytochrome b5, out	hypothetical prote	cytochrome b5, mic	cytochrome b5, mic	nitrate reductase	nitrate reductase	probable fatty aci	probable cytochrom	cytochrome b5, ery	nitrate reductase	cytochrome b5 - pi	probable cytochrom	conserved hypothet	cytochrome b5 [imp	cytochrome b5 - co

## ALIGNMENTS

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.: euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: A84900 RESULT 1
A84900
AB4900
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: A84900 MDWFFGGLQFQLEHHLFPRLPRCQLRKISPLVSDLCKKHNLPYRSLSFWEANQWTIRTLR LPNWPERVMFVLASFAVCSIQHIQFCLNHFAANVYVGPPSGNDWFEKQTSGTLDISCASS CLTGISIAWWKWTHNAHHIACNSLDHDPDLQHIPIPAVSTKFFNSMTSRFYGRKLTFDPL CLTGISIAWWKWTHNAHHIACNSLDHDPDLQHMPVFAVSSRFFNSITSHFYGRKLEFDFI.244 MLAAVLYGVLACTSIWAHLISAVLLGLLWIQSAYVGHDSGHYTVTSTKPCNKLIQLLSGN MFLIVLYGVLRCTSVWAHLGSGMLLGLLWMQSAYVGHDSGHYVVWTTNGFNKVAQILSGN Conservative GB:AE002093; NID:g3702328; PIDN:AAC62885.1; GSPDB:GN00139 79.3%; Score 1943; DB 2; 77.6%; Pred. No. 1.1e-160; 7ative 41; Mismatches 59; Length 449; Indels 0, Gaps 184 123 424 363 364 304 243 183 124 63 303 0

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A;Experimental source: cultivar Columbia; BAC clone F2A1
R;Sperling, P.; Zaehringer, U.; Heinz, E.
J. Biol. Chem. 273, 28590-28596, 1998
A;Title: A sphingolipid desaturase from higher plants. 1
A;Reference number: Z22986; MUID:99003197; PMID:9786850
A;Accession: T51848
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A; Accession: T47950
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                                                                                                            LPNWPERVMFVLASFAVCSIQHIQFCLNHFAANVYVGPPSGNDWFEKQTSGTLDISCASS
                                                                                                                                                                       ARFLICYQHFTFYPVMCVARVNLYLQTILLLFSRRKVQDRALNIMGILVFWTWFPLLVSC
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                                                                                                                                                                                                                                                                                MFLGVLYGVLACTSVFAHQIAAALLGLLWIQSAYIGHDSGHYVIMSNKSYNRFAQLLSGN
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                                                                                                                                                                                                                                                                                                                                               FHPGTAWHHLDHLFTGYHIRDFQVSEVSRDYRRMAAEFRKLGLFENKGHVTLYTLAFVAA
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 TAALQARDLTNPAPKNLLWEAVNTHG
                                                                                                                                                                                                                     CLTGISIAWWKWTHNAHHLACNSLDYDPDLQHIPVFAVSTKFFSSLTSRFYDRKLTFDPV
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                                                                                          LENWPERFFEVFTSFTVTALQHIQFTLNHFAADVYVGPPTGSDWFEKQAAGTIDISCRSY
                                                                                                                                                       ARFLVSYQHFTYYPVMCFGRINLFIQTFLLLFSKREVPDRALNFAGILVFWTWFPLLVSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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ce: cultivar Columbia; mainly green parts,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77.7%; Score 1902; DB 2; 74.9%; Pred. No. 3.9e-157; tive 54; Mismatches 58;
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January 2000
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delta-8 sphingolipid desaturase [imported] - rape
C;Species: Brassica napus (rape)
C;Ate: 21-Uil-2000 #sequence_revision 21-Jul-2000 #text_change 15-Sep-2000
C;Accession: T50555
R;Sperling, P.; Zaehringer, U.; Heinz, E.
J. Biol. Chem. 273, 28590-28596, 1998
A;Title: A sphingolipid desaturase from higher plants. Identification of a naparate number: Z22986; MUID:99003197; PMID:9786850
A;Accession: T50555
A; Reference number: $68358;
A; Accession: $68358
A; Status: preliminary
                                           Eur. J. Biochem. 232, 798-805, 1995
A;Title: A cytochrome-b(5)-containing fusion
A;Reference number: S68358; MUID:96028121; PM
                                                                                  Delta8 sphingolipid desaturase (EC 1.14.99.-) [similarity] - C;Species: Helianthus annuus (common sunflower) C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_chan C;Accession: S68358 C;Accession: S68358 R;Sperling, P.; Schmidt, H.; Heinz, E. Eur. J. Blochem. 232, 798-805, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-449 <SPE>
A;Crose-references: EMBL:AJ224160; PIDN:CAA11857.1
A;Experimental source: cultivar Drakkar
                                                                                                                                                                                                                                      RESULT 4
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLTGISIAWWKWTHNAHHIACNSLDHDPDLQHMPVFAVSSRFFNSITSHFYGRKLEFDFI 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LPNWPERVMFVLASFAVCSIQHIQFCLNHFAANVYVGPPSGNDWFEKQTSGTLDISCASS
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                                                                                                                                                                                                                                                                                                                                                                                        MDWFFGGLQFQLEHHLFPRLPRCHLRGVSPVVQELCKKHNLPYRSLSWWEANVWTLRTLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LPNWQERIIFVFLSMAVTAIQHVQFCLNHFAADVYTGPPNGNDWFEKQTAGTLDISCRSY 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITGISIAWWKWTHNAHHISCNSLDHDPDLQHIPVLAVSNKFFKSMTSRFYGRKLTFDPL
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74.7%;
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                                                  on protein similar
PMID:7588718
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                                                                                                                                                 #text_change
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C;Species:
C;Date: 30-
C;Accession
R;Laoteng,
                                                                                                                                                               A;Cross-references: GB:AP290983
A;Experimental source: strain ATCC 24905
C;Comment: This enzyme, a membrane-bound key enzyme,
C;Keywords: oxidoreductase; transformation
                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-523 < LAO >
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;51,74/Binding site: heme iron (His) (axia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;Cross-references: EMBL:X87143; NID:g1040728; PIDN:CAA60621.1; PID:g1040729; Superfamily: cytochrome b5 core homology; Keywords: heme; iron; metalloprotein; oxidoreductase
                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                     Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 03-Jun-2002
Accession: JC7556
                                                                                                                                                                                                                                                                                                                                                                   Species: Mucor rouxii
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Best Local :
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mes 317; Conserv
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                                                                                                                       Similarity
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   HPGTAWSHLEKFFTGYHLSDF---
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                                               RSSNIVTEEKFOELIKOGDSVFIYEOKVYRVNNFMAKHPGGEAALRSALGRDVTDEIRTM
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                                                                         KEKKYITSEELKGHNKEGDLWISIQGKVYNVSDWVKEHPGGDVPISNLAGQDVTDAFIAY
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                                                                                                                       28.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         iron (His) (axial ligands)
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Pred. No. 2.3e
55; Mismatches
                                                                                                       Score 684.5; DB 2
Pred. No. 2.1e-51;
6; Mismatches 200
                                                                                                                                                                                                                                                                                                                                                                                                 Mucor rouxii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.3e-148;
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                                                                                                                                     DB 2;
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A; Residues: 1-444 < AKI>
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                                                                                                                                                                                                                                                       14 BELKGHNKEGDLWISIQGKVYNVSDWVKEHPGGDVPISNLAGQDVTDAFIAYHPGTAWSH
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                                                                                                                                                                                                                                                                                                    Similarity
TSHFYGRK----LEFDFIARFLICYQHFTFYFVMCVARVNLYL--QTILLLFSRRKVQDR
                                                                                                                                     LASVAVMFLIVLYGVLRCTSVWAHLGSG------MLLGLLWMQSAYVGHDSGHYVVMT
                                                                                                                                                                                                LEKFFTGYHLSDF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WTWFPLLVSCLPNWPBRVMFVLASFAVCSIQHIQFCLNHFAANVYVGPPSGNDWFEKQTS
                                             KSIWNHIVHKFVIGHLKGASANWWNHRHFQHHAKPNIFHKDPDIKSLHVFVLGE--WQPL
                                                                                                                                                                  LDLDFVGKFLKPLLIGELAPEEPSLDRGKSSQITEDFRALKKTAEDMNLFKTNHLFFFLL
                                                                                                                                                                                                                            EEIQKHNLRTDRWLVIDRKVYNVTKWSQRHPGGHRVIGHYSGEDATDAFRAF-----H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANOWTIRTLRTAALQARDLTNPAPKNL-LWEAVNTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTLDISCASSMDWFFGGLQFQLEHHLFPRLPRCQLRKISPLVSDLCKKHNLPYRSLSFWE 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YGRKLEFDFIARFLICYOHFTFYPVMCVARVNLYLQTILLLFSRRKVODRALNIMGILVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DHVIGVIIANFIGGLSLGWWKDNHNVHHIVTNHPEHDPDIQHVPFMAITTKFFNNIYSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NKVAQILSGNCLTGISIAWWKWTHNAHHIACNSLDHDPDLQHMPVFAVSSRFFNSITSHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YAREGCRYTLLIFLSLWFTLKGTETWHYMAGAAFMAMFWHQLVFTAHDAGHNEITGKSEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DDAIQDLHKHHSHDLIKDAVLQKDLNGDQIRNAYRKLBAELYAKGLF-----KCNYWK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HPPQVY---EKLINLYCIGDYMPDVIRPASMKQQHTFTKPKEDKPVLTATWEGGFTVQAY 133
                                                                         TNGFNKVAQILSGNCLTGISIAWWKWTHNAHHIACNSLDHDPDLQHMPVFAVSSRFFNSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTMDVDCPEWHDWFHGGLQYQAVHHLFPRLPRHNLRQCVPLVKKFCDEVGLHYYMYNFST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FVWFGSLLSTLPTWNIRIAYIMVSYMLTFPLHVQITLSHFGMSTEDRGPD-EPFPAKMLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YKRVLPFDAASRFFVRHOHYLYYLILSFGRFNLHRLSFAYLLTCKNVRTRTLELVGITFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VA-----VMFLIVLYGVLRCTSVWAHLGSGMLLGLLWMQSAYVGHDSGHYVVMTTNGF
                                                                                                                                                                                                                                                                                                                                                site: heme iron (His) (axial ligands)
                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                    18.4%;
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                                                                                                                                                                                                                                                                                        62;
                                                                                                       --ILSYFGNGWIPTVITAFVLATSQAQAGWLQHDYGHLSVYK 189
                                                                                                                                                                                                                                                                                                    Score 451.5; DB 2
Pred. No. 2.9e-31;
                                                                                                                                                                                                                                                                                      Pred. No. 2.90
2; Mismatches
                                                                                                                                                                                               ----KVSEVSKDYRKLASEFSKLGLFDTKGHVTSCT 118
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dest <u>~</u>

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A;Note: DKPZp586C201.1
C;Superfamily: cytochrome b5 core homology
C;Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase; unsaturated
C;Keywords: chromoprotein b5 core homology <CB5>
F;18-94/Domain: cytochrome b5 core homology <CB5>
F;53,76/Binding site: heme iron (His) (axial ligands) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Cho, H.P.; Nakamura, M.T.; Clarke, S.D. Biol. Chem. 274, 471-477, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linoleoyl-CoA desaturase (EC 1.14.19.3) [validated] -
N;Alternate names: Delta6 fatty acid desaturase; prot
C;Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;Gene: GDB:FADSD6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 03-Jun-2002;
Accession: T13155; T08765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cross-references: GDB:9956652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecule type: mRNA; Residues: 'RTRG',138-428,'D',430,'M',432-444 <WAM; Cross references: EMBL:AL050118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cross-references: EMBL:AF126799; NID:g4406527; PID:g4406528; PIDN:AAD20018.1; Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. ibmitted to the Protein Sequence Database, March 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecule type: mRNA
Residues: 1-444 <CHO>
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Best Local
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                                                                                                                                                                                                                                                                                                                                                           LEKFFTGYHLSDF------KVSEVSKDYRKLASEFSKLGLFDTKGHVTSCTLASVA 123
                                                                                                                                                                                                                                                                    VMFLIVLYGVLRCTSV-W---AHLGSG------MLLGLLWMQSAYVGHDSGHYVVMTT 171
                                                                                                                                                                                                                                                                                                                                                                                                    EEIQKHNLRTDRWLVIDRKVYNITKWSIQHPGGQRVIGHYAGEDATDAFRAFHPDLEF--
                                                                                                                                                                               NGENKVAQILSGNCLTGISIAWWKWTHNAHHIACNSLDHDPDLQHMPVFAVSSRFFNSIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E---YGKKKLKYLPYN----HQHEYFFLIGPPLLIPMYFQYQIIMTMIRRRDWVDL
                                                                                         SHFYGRK----LEFDFIARFLICYQHFTFYPVMCVARVNLYL--QTILLLFSRRKVQDRA
                                                                                                                                                                                                                                                                                                                  VGKFLKPLLIGELAPEEPSQDHGKNSKITEDFRALRKTAEDMNLFKTN------H
                                                                                                                                                                                                                                                                                                                                                                                                                                           EELKGHNKEGDLWISIQGKVYNVSDWVKEHPGGDVPISNLAGQDVTDAFIAYHPGTAWSH
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                                             ---YGKKKLKYLPYN-----HQHEYFFLIGPPLLIPMYFQYQIIMTMIVHKNWVDLA
                                                                                                                                      PKWNHLVHKFVIGHLKGASANWWNHRHFQHHAKPNIFHKDPDVNMLHVFVLGE--WQPIE
                                                                                                                                                                                                                         VFFLLLLAHIIALESIAWFTVFYFGNGWIPTLITAFVLATSQAQAGWLQHDYGHLSVYRK 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18.0%;
28.1%;
    ---LNIMGILVFWTWFPLLVSCLPNWPERVMFVLASFAVCSIQHIQF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 441.5; DB 2;
Pred. No. 2.2e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 171;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linoleoyl-CoA desaturase (EC 1.14.19.3) W08D2.4 - N_iAlternate names: Delta6 fatty acid desaturase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
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A;Residues: 1-38,69-430,'V',432-473 <NAP>
A;Cross-references: EMBL:AF031477; NID:g3088519; PIDN:AAC15586.1; PID:g3088520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Identification of a caenorhabditis elegans Delta6-fatty-acid-desaturase A;Reference number: Z21637; MUID:98149727; PMID:9480865 A;Accession: T37238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Experimental source: clone W08D2
R;Napier, J.A.; Hey, S.J.; Lacey, D.J.; Shewry, P.R.
Biochem. J. 330, 611-614, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: translated from GB/EMBL/DDBJA;Molecule type: DNA
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A; Accession: T26280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Date: 09-Jun-2000 #sequence_revision;Accession: T26280; T37238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cross-references: EMBL:Z70271; PIDN:CAA94233.1; GSPDB:GN00022; CESP:W08D2
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                                                                                                                                                               HNAHHIACNSLDHDPDLQHMPVFAVSSRFFNSITSHFYGRKLEFDFIARFLICYQHFTFY 257
                                                                                                                                                                                                                                                                                                                                                                                                      LYFYRNSDATHIFHAFHEGSSQAYKQLDLLKKHGEHDEFLEKQLEKRLDKVDINVSAYDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RKISPLVSDLCKKHNLPYRSLSFWEANQWTIRTLR 424
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    PERVMFVLAS--FAVCSIQHIQFCLNHFAANVYVGPPSG---NDWFEKQTSGTLDISCAS 363
                                             AMLPMLRESWTGQSVQWVFKENQMEYKVYQRNAFWEQATIVG---HWAWVFYQLFLLPTW
                                                                                         PVMCVARVNLYLQTILLLFSRRKVQDRA-----LNIMGILVFWTWFPLLVSCLPNW 308
                                                                                                                                                                                                                           --W-YITSACLLALAWQQFGWLTHEFCHQQPTKNRPLNDTISLFFGNFLQGFSRDWWKDK
                                                                                                                                                                                                                                                                      SVWAHLGSGMLLGLLWMQSAYVGHDSGHYVVMTTNGFNKVAQILSGNCLTGISIAWWKWT 197
                                                                                                                                                                                                                                                                                                               SVAQEKKMVESFEKLRQKLHDDGLM--KANETYFLFKAISTLSIMAFAFYLQYLG----
                                                                                                                                                                                                                                                                                                                                                           SDFKVSEVSKDYRKLASEFSKLGLFDTKGHVT----SCTLASVAVMFLIVLYGVLRCT 137
                                                                                                                                                                                                                                                                                                                                                                                                                                             ---LAGODVTDAFIAYHPGTAWSH------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NASG-LRMKVDGKWLYLSEELVKKHPGGAVIEQYSIPPLNKNIETRGIITTRGSSNALDI 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HKIAPLVKSLCAKHGIEYQEKPLLRALLDIIRSLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.4%; Score 401; DB 1; Length 473; 25.3%; Pred. No. 7.6e-27;
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A;Map position: 4
A;Map position: 4
A;Introns: 43/3; 80/3; 197/3; 295/3; 318/2; 349/1; 384/3
C;Superfamily: Caenorhabditis elegans Delta6 fatty acid of C;Keywords: oxidoreductase; unsaturated fatty acid biosy.
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A;Residues: 1-197,'VSHIFNN',198-447 <WIL>
A;Cross-references: EMBL:Z81122; PIDN:CAB03352.1; GSPDB:GN00022; CESP:T13F2.1
A;Experimental source: clone T13F2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data A; Reference number: Z19947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-447 <MIC>
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                                                                                                                                                                                                                                                                                                                                      YIRKILETIFTILFAFYLQYHTY--YLPSAILMGVAWQQLGWLIHEFAHHQLFKNRYYND 186
                                                                                                                                                                                                                                                                                                                                                                                CTLASVAVMFLIVLYGVLRCTSVWAHLGSGMLLGLLWMQSAYVGHDSGHYVVMTTNGFNK 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WISIQGKVYNVSDWV-KEHPGGDVPISNLAGQDVTDAFIAYHPGT----AW-SHLEK---
      GN---DWFEKQTSGTLDISCASSMDWFFGGGLQFQLEHHLFPRLPRCQLRKISPLVSDLCK 401
                                                                         --VGLSLHWAWSLGQLYFLPDWSTRIMFFLVSHLVGGFLLSHV-VTFNHYSVEKFA--LS
                                                                                                                  NIMGILVFWTWFPLLVSCLPNWPERVMFVLASFAVCS--IQHIQFCLNHFAANVYVGPPS
                                                                                                                                                                                                         RKLEFDFIARFLICYQHFTFYPVMCVARVNLYLQTILLL-----FSRRKVQDRAL
                                                                                                                                                                                                                                                    LASYFVGNFLQGFSSGGWKEQHNVHHAATNVVGRDGDLDLVPFYATVAEHLNNYSQ----
                                                                                                                                                                                                                                                                                             VAQILSGNCLTGISIAWWKWTHNAHHIACNSLDHDPDLQHMPVFAVSSRFFNSITSHFYG 236
                                                                                                                                                                                                                                                                                                                                                                                                                             TQEPEIPDIKDDPIKGIDDVNMGTFNISEKRSAQINKSFTDLRMRVRAEGLMD--GSPLF 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FIKIDGKWCQIDDAVLRSHPGGSA-ITTYKNMDATTVFHTFHTGSKEAYQWLTELKKECP
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                                                                                                                                                             ----DSWVMTLFRWQHVHWTFMLPFLRLSWLLQSIIFVSQMPTHYYDYYRNTAIYEQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.3%; Score 373.5; DB 1; 24.7%; Pred. No. 1.7e-24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78; Mismatches 198; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 1.7e-24;
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probable Delta6 fatty acid desaturase (EC 1.14.99.-) SCH35.42c [similarity] C;Speciles: Streptomyces coelicolor C;Deate: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 20-Jun-2000 C;Accession: T36617 R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology A;Reference number: A75000; MUID:99069613; PMID:9851916 A;Roterence number: A75000; MUID:99069613; PMID:9851916 A;Roter see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_elegans/A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;anonymous, The C. elegans Sequencing Consortium Science 282, 2012-2018, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein T13F2.1 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001
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411 LVKEFAAANGLPYMVDDYFTGFWLEIEQFRNIANVAAKLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   YIRKILETIFILFAFYLQYHTY--YLPSAILMGVAWQQLGWLIHEFAHHQLFKNRYYND 186
                                                                                                                  VYVGPPSGN---DWFEKQTSGTLDISCASSMDWFFGGLQFQLEHHLFPRLPRCQLRKISP
                                                                                                                                                                              AIYEQ----VGLSLHWAWSLGQLYFLPDWSTRIMFFLVSHLVGGFLLSHV-VTFNHYSVE 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTLASVAVMFLIVLYGVLRCTSVWAHLGSGMLLGLLWMQSAYVGHDSGHYVVMTTNGFNK 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FIKIDGKWCQIDDAVLRSHPGGSA-ITTYKNMDATTVFHTFHTGSKEAYQWLTELKKECP
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                                         LVSDLCKKHNLPYRSLSFWEANQWTIRTLRTAALQARDLT
                                                                                        KFA--LSSNIMSNYACLQIMTTRNMRPGRFIDWLWGGLNYQIEHHLFPTMPRHNLNTVMP
                                                                                                                                                                                                                      KVQDRALNIMGILVFWTWFPLLVSCLPNWPERVMFVLASFAVCS--IQHIQFCLNHFAAN 337
                                                                                                                                                                                                                                                                                                              ITSHFYGRKLEFDFIARFLICYQHFTFYPVMCVARVNLYLQTILLL-----FSRR
                                                                                                                                                                                                                                                                                                                                                             LASYFVGNFLQVSHIFNNGFSSGGWKEQHNVHHAATNVVGRDGDLDLVPFYATVAEHLNN 246
                                                                                                                                                                                                                                                                                                                                                                                                      VAQILSGNCL-----TGISIAWWKWTHNAHHIACNSLDHDPDLQHMPVFAVSSRFFNS 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TQEPEIPDIKDDPIKGIDDVNMGTFNISEKRSAQINKSFTDLRMRVRAEGLMD--GSPLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----FFTGYHLSDFKVSEVSKDYRKLASEFSKLGLFDTKGHVTS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNIMSNYACLQIMTTRNMRPGRFIDWLWGGLNYQIEHHLFPTMPRHNLNTVMPLVKEFAA 410
                                                                                                                                                                                                                                                                    YSQ------DSWVMTLERWQHVHWTFMLPELRLSWLLQSIIFVSQMPTHYYDYYRNT
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24.3%;
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B.G.; Rajandream,

M. A.

Streptomyce

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A; Molecule type: DNA
A; Residues: 1-359 < KAN>
A; Cross - references: EMBL;
A; Cross - the nucleotide se
C; Keywords: oxidoreducta:
                                                                                                                                                                                                                                                                                                                                                                                                                                       Delta6 fatty acid desaturase (EC 1.14.99.-) [imported] - Synechocystis Sp. C;Species: Synechocystis Sp. C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-C;Accession: $35.157; $76243 R;Reddy, A.S.; Nuccio, M.L.; Gross, L.M.; Thomas, T.L. Plant Mol. Biol. 22, 293-300, 1993 Plant Mol. Biol. 22, 293-300, 1993 A;Title: Isolation of a Delta(6)-desaturase gene from the cyanobacteriu A;Reference number: $35157; MUID:93283633; PMID:8389613 A;Accession: $35157 AUID:93283633; PMID:8389613 A;Accession: $35157 AUID:93283633; PMID:8389613 A;Status: preliminary
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C;Genetics:
C;Keywords: oxidoreductase; ur
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A;Accession: T36617
A;Status: preliminary; translated
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                                                                                                                                                                                          A; Accession: $76243
A; Status: preliminary
                                                                                                                                                                                                                                                                    DNA Res. 3, 109-136, 1995
A;Title: Sequence analysis of the genome of the unicellular
                                                                                                                                                                                                                                                                                                             A;Croos-references: GB:L11421; NID:g349562; PIDN:AAA27286.1; PID:g349563; R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, B.; Nakamura, Y.; Miyo, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, DNA Res. 3, 109-136, 1996
                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-359 <RI
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                                                                                                                                                                                                                                               A;Reference number: S74322; MUID:97061201; PMID:8905231
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Best Local S
Matches 89
  Query Match
Best Local Similarity
                                                                                  Cross-references: EMBL:D90914; GB:AB001339; NID:g1653477; PIDN:BAA18502.1; Experimental source: PCC 6803; Experimental source: PCC 6803; Note: the nucleotide sequence was submitted to the EMBL Data Library, June
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             377
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                                                                  oxidoreductase; unsaturated fatty
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAVMYGQVALVAHDMAHRQVFRRRRASELSGRIAGASI-GMSYGWWQDKHTRHHANPNTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGLLWMQSAYVGHDSGHYVVMTTNGFNKVAQILSGNCLTGISIAWWKWTHNAHHIACNSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DFARLSKKVADAGLLGRRPGYYTLRITAVTGLYAAGWAAFVLVG-----ASWWTLAIAAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EHHLFPRLPRCQLRKISPLVSDLCKKHNLPYRSLSFWEANQWTIRTLRTAALQARDLTNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HQCLFGVYLGSAFAPN-HKGMPILTADDRPDFLRRQVLTSRNVNGGLFTDLALGGLNHQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HVASGRAMANRR-LKRRALD--GAL-----LLAHCAV-YLTALFWVLPPGMAIAFLAV
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ilarity 24.7%;
Conservative 5
8.3%;
23.6%;
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Score 202.5; DB 2
Pred. No. 9.2e-10;
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linoleoyl-CoA desaturase (EC 1.14.19.3) - W,Alternate names: Delta6-desaturase C;Species: Spirulina platensis C;Date: 08-U1-1995 #sequence_revision 21-C;Accession: S54809
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S54809
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Best Local Similarity
Matches 80; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                  TSCTLASVAVMELIVLYGVLRCTSVWAHLGSGMLLGLLWMQSAY-VGHDSGHYVVMTTNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y----RF-----QFYIWGL--------YLFIPFY------WFLYDVYLVLNKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MYLKTLIIVLWLFSAWAFVLFAPVIFPVRLLGCMVLAIALAAFSFNVGHDANHNAYSSNP
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VHHLFPHICHIHYPKIAPILAEVCEEFGVNY
                              EHHLEPRLPRCQLRKISPLVSDLCKKHNLPY
                                                                 GLVACVVFMLAHVIBPABFLDPDNLHIDDEWAIAQVKTTVDFAPNNPIINWYVGGLNYQT
                                                                                                   HIOFCLNHFAANV-----YVGPPS---GNDWFEKOTSGTLDISCASS-MDWFFGGLOFOL 376
                                                                                                                                        QYHDHEIPSPTWVDIATLLAFKAFGVAVFLI-IPIAVGYSP-----LEAVIGASIVYMTH
                                                                                                                                                                          KVQDR-----
                                                                                                                                                                                                                                           FNSITSHFYGRKLEFDFIARFLICYQHFTF---YPVM----CVARVNLYLQTILLLFSRR 279
                                                                                                                                                                                                                                                                                                                FNKVAQI--LSGNCLT----GISIAWWKWTHNA-HHIACNSLDHDPDLQHMPVFAVSSRF
                                                                                                                                                                                                                                                                                                                                                 TAIILAWVVSAWTFVVFGP---DVLWMKLLGCIVLGFGVSAVGFNISHDGNH-----GG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KYHDHKIPPFQPLELASLLGIKLLWLGY---VFGLPLALGFSIPEVLIGASVTYMTYGIV
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                                                                                                                                                                                                           -SMEYRWYHR-----QTMLF---KR
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                                                                                                                                                                          ALNIMGILVFWTWFPLLVSCLPNWPERVMFVLASFAVCSIQ 325
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Search completed: January 1, 2004, 06:39:43 Job time: 18.9369 secs

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Copyright (c) 1993 - 2  ein - protein search, using sw me  January 1, 2004, 06:29:  US-09-857-524B-8  BCOOTE: 2449  e: 1 MEVVEKEKKYITSEELKGHN.  table: BLOSUM62 Gapop 10.0, Gapext 0.5  d: 127863 seqs, 47026705 re  umber of hits satisfying chosen p  DB seq length: 0  DB seq length: 200000000  OCCESSING: Minimum Match 0% Maximum Match 100%  Listing first 45 summax  red. No. is the number of resulte  Core greater than or equal to the  Match Length DB ID  137 5.6 2 134 1 CYB5_BR  148 5.9 133 1 CYB5_RR  149.5 6.1 137 1 CYB5_BR  149.5 6.2 134 1 CYB5_BR  149.5 6.3 134 1 CYB5_BR  149.5 6.3 134 1 CYB5_BR  140 5.7 132 1 CYB5_BR  141.5 5.8 136 1 CYB5_BR  142.5 5.8 136 1 CYB5_BR  144 5.9 133 1 CYB5_BR  145 5.6 2 134 1 CYB5_BR  146 5.6 2 134 1 CYB5_BR  147 1 VDAA-SC  148 5.9 133 1 CYB5_BR  149.5 5.6 2 1 NIA_BBR  131 5.3 133 1 CYB5_BR  132 5.4 133 1 CYB5_BR  133 5.4 133 1 CYB5_BR  134 5.5 133 1 CYB5_BR  135 5.5 1 134 1 CYB5_BR  136 5.6 2 1 NIA_BBR  137 5.6 2 1 NIA_BBR  138 5.3 133 1 CYB5_BR  139 5.3 133 1 CYB5_BR  139 5.3 133 1 CYB5_BR  139 5.3 133 1 CYB5_BR  139 5.3 133 1 CYB5_BR  139 5.3 133 1 CYB5_BR  139 5.3 133 1 CYB5_BR  139 5.3 133 1 CYB5_BR  139 5.3 133 1 CYB5_BR  139 5.3 133 1 CYB5_BR  139 5.3 133 1 CYB5_BR  139 5.3 133 1 CYB5_BR  139 5.3 133 1 CYB5_BR  139 5.3 133 1 CYB5_BR  139 5.3 133 1 CYB5_BR  139 5.3 133 1 CYB5_BR  139 5.3 133 1 CYB5_BR  139 5.3 133 1 CYB5_BR  139 5.3 133 1 CYB5_BR  139 5.3 133 1 CYB5_BR  139 5.3 133 1 CYB5_BR  139 5.3 133 1 CYB5_BR  139 5.3 133 1 CYB5_BR  139 5.3 133 1 CYB5_BR  139 5.3 133 1 CYB5_BR  139 5.3 133 1 CYB5_BR  139 5.3 133 1 CYB5_BR  139 5.3 133 1 CYB5_BR  139 5.3 133 1 CYB5_BR  139 5.3 133 1 CYB5_BR  139 5.3 133 1 CYB5_BR  139 5.3 133 1 CYB5_BR  139 5.3 133 1 CYB5_BR  139 5.3 133 1 CYB5_BR  139 5.3 133 1 CYB5_BR  139 5.3 133 1 CYB5_BR  139 5.3 133 1 CYB5_BR  139 5.3 139 1 CYB5_BR  139 5.3 139 1 CYB5_BR  130 5.3 139 1 CYB5_BR  130 5.3 139 1 CYB5_BR  130 5.3 139 1 CYB5_BR  130 5.3 139 1 CYB5_BR  130 5.3 139 1 CYB5_BR  130 5.3 139 1 CYB5_BR  130 5.3 139 1 CYB5_BR  130 5.3 139 1 CYB5_	11111111111111111111111111111111111111	Result	Databas P	Post-pr	Minimum Minimum	arch	Scoring	Title: Perfect Sequenc	Run on:	OM prote	
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  This
                                                                                                                                                                                                                                                                                                                                                                              Reddy A.S., Nuccio M.L., Gross L.M., Thomas T.L.;
"Isolation of a delta 6-desaturase gene from the cyanobacterium Synachocystis sp. strain PCC 6803 by gain-of-function expression Anabaena sp. strain PCC 7120.";
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=93283633; PubMed=8389613;
Reddy A.S., Nuccio M.L., Gross L.
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CATALYTIC ACTIVITY: Linoleoyl-CoA +
linolenoyl-CoA + A + 2 H(2)0.
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EMBL; D90914; BAA18502.1; -.
EMBL; D90914; BAA18502.1; -.
InterPro; IPR005804; FA_desat_fam.
Pfam; PF00487; FA_desat_tams; 1.
ProDom; PD001081; FA_desat_fam; 1.
ProDom; PD001081; FA_desat_fam; 1.
Prodom; PD001081; FA_desat_fam; 1.
Prodom; PD001081; FA_desat_fam; 33FB165AEB98C05F
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P08619;
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=74-OR23-1A / FGSC 987;
MEDLINE=91287699; PubMed=1829499;
                                                                                                                                                                                                                                                                                                                                                          Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Sordariomycetidae; Sordariales; Sordariaceae;
                                                                                                                                                                                        crassa: nucleotide sequence and regulation
                                                                                                                                                                                                             Okamoto P.M., Fu Y.-H., Marzluf G.A.; "Nit-3, the structural gene of nitrate reductase
                                      "On the presence of a heme-binding domain homologous tin Neurospora crassa assimilatory nitrate reductase.";
                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                         NIT-3
                                                                                                                                                                                                                                                                                                                                                                                                                                            Nitrate reductase
                                                                                  Le K.H.D.,
                                                                                                     PRELIMINARY PARTIAL
                                                                                                                                                                    turnover."
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Neurospora.
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InterPro; IPR000572; Euk_Mb_oxred.
InterPro; IPR005066; Mo-co dimer.
InterPro; IPR005066; Mo-co dimer.
InterPro; IPR005066; Mo-co dimer; 1.
Pfam; PF00970; FAD binding_6; 1.
Pfam; PF00173; Name 1; 1.
Pfam; PF00174; Mo-co dimer; 1.
Pfam; PF00174; Oxidored_molyb; 1.
                                                                                                                                                                                                                                                                                                                              PRODOM; PD000612; Cyt B5; 1.

PROSITE; PS00191; CYTOCHROME B5 1; 1.

PROSITE; PS50255; CYTOCHROME B5-2; 1.

PROSITE; PS00559; MOLYBDOPTERIN EUK; 1.

PROSITE; PS00559; Plavoprotein; PAD; NADP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Okamoto P.M., Marzluf G.A.;
"Nitrate reductase of Neurospora crassa: the functional role of individual amino acids in the heme domain as examined by site-directed mutagenesis.";
Mol. Gen. Genet. 240.222
DOMAIN
NP_BIND
MUTAGEN
MUTAGEN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                     Nitrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00406; CYTBSRDTASE.
PRINTS; PR00363; CYTOCHROMEBS.
PRINTS; PR00407; EUMOPTERIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001834; Cyt_B5_reductase.
InterPro; IPR000572; Euk_Mb_oxred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P00171; 1F03.
InterPro; IPR001199; Cyt_B5.
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MEDLINE=9324176; PubMed=8479443;
Okamoto P.M., Garrett R.H., Marzluf G.A.;
"Molecular characterization of conventional and new repeat-induced "Molecular characterization of conventional and new repeat-induced mutants of nit-3, the structural gene that encodes nitrate reductase
                                                                                                                                                METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mol. Gen. Genet.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: Nitrate reductase is a key enzyme involved in the first step of nitrate assimilation in plants, fund and bacteria. CATALYTIC ACTIVITY: Nitrite + NADP(+) + H(2)O = nitrate + NADPH. COFACTOR: EACH SUBUNIT CONTAINS 1 EQUIVALENT OF FAD, HEME IRON, AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS. THE HEME GROUP IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-TERMINAL DOMAIN.
SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INDUCTION: ITS EXPRESSION IS HIGHLY REGULATED AND RESPONDS RAPIDLY TO NITRATE INDUCTION AND TO NITROGEN REPRESSION.
SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PATHWAY: Nitrate assimilation (denitrification). SUBUNIT: Homodimer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C-TERMINAL DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CALLED CYTOCHROME B-557.
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                                                                                                                                                                                                                                                                                                                     assimilation
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675
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   108432
                                                                              MOLYBDENUM-PTERIN (POTENTIAL).

MOLYBDENUM-PTERIN (POTENTIAL).

INTERCHAIN (POTENTIAL).

HEME-BINDING (BY SIMILARITY).

IRON (HEME AXIAL LIGAND) (BY SIMILARITY).

IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
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   IRÓN (HEME AXIAL LIGAND) (BY SIMILARI
IRÓN (HEME AXIAL LIGAND) (BY SIMILARI
FLAVIN-BINDING DOMAIN (BY SIMILARITY)
NADP (BY SIMILARITY).
H->A: LITTLE LOSS OF ENZYME ACTIVITY.
H->A: LOSS OF ENZYME ACTIVITY.
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METAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001199; Cyt B5.

Pfam; PP00173; heme_1; 1.

ProDom; PD000612; Cyt B5; 1.

PROSITE; P800191; CYTOCHROME B5_1; 1.

PROSITE; P850255; CYTOCHROME B5_2; 1.

PROSITE; P850255; CYTOCHROME B5_2; 1.

Electron transport; Transmembrane; Heme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYB5 ORYSA
P49100;
01-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytochrome b5.
Oryza sativa (Rice).
Oryza sativa (Rice).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORYSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -I- FUNCTION: Membrane bound hemoprotein which function as an electron carrier for several membrane bound oxygenases (By similarity).
-i- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Smith M.A., Stobart A.K., Shewry P.R., Napier J.A.; "Tobacco cytochrome b5: CDNA isolation, expression analysis vitro protein targeting."; Plant Mol. Biol. 25:527-537(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; S46307; S46307.
HSSP; P00171; 1EHB.
Gramene; P49100; -.
                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
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(Rel. 33, Last sequence update)
(Rel. 41, Last annotation updat
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15296 MW;
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                                                                                                                                                                           Score 156.5;
Pred. No. 3.3e
L6; Mismatches
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IRON (HEME AXIAL LIGAND)
; 4260C9D633E60FDA CRC64;
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Pred. No. 2e-05;
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            CY51 ARATH STANDARD; PRT; 134 AA Q42342; Q9SB05; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update)
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Kearns E.V., Keck P., Somerville C.R.;
"Nucleotide sequence of cDNA for cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochrome of the cytochr
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Pfam; PF00173; heme 1; 1.

PRINTS; PR00363; CYTOCHROMEB5.

ProDom; PD000612; Cyt B5; 1.

PROSITE; PS00191; CYTOCHROME B5 1; 1.

PROSITE; PS50255; CYTOCHROME B5 2; 1.

Electron transport; Transmembrane; Heme; Iron; Microsome.
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01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plant
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764DC24A4CDDD591 CRC64;
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Pred. No. 4.8e-06;
5; Mismatches 28;
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STRAIN=cv. Columbia;
STRAIN=cv. Columbia;
MEDLINE=99097071; PubMed=9880378;
MEDLINE=99097071; PubMed=9880378;
Fukuchi-Mizutani M., Mizutani M., Tanaka Y., Kusumi T.,
Fukuchi-Mizutani M., Mizutani M., Tanaka Y., Kusumi T.,
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Fukuchi-Mizutani M., Mizutani                                                                                                                                                                                                      METAL
CONFLICT
SEQUENCE
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Pfam; PF00173; heme 1; 1.

PRINTS; PR00363; CYTOCHROMEB5.

ProDom; PD000612; Cyt_B5; 1.

PROSITE; PS00191; CYTOCHROME B5 1; 1.

PROSITE; PS50255; CYTOCHROME B5 2; 1.

Electron transport; Transmembrane; Heme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- FUNCTION: Membrane bound hemoprotein which function as an electron carrier for several membrane bound oxygenases (By similarity).
-!- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                             METAL
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EMBL; AB015476; BAB09732.1; -.
EMBL; F20001; CAA23377.1; -.
EMBL; F252469; T52469.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There by non-profit institutions as long modified and this statement is not removed. I entities requires a license agreement (See httentities requires a license agreement (See
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Multigene family.
TRANSMEM 107
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Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
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P09437;
01-MAR-1989
PEAM; PF01070; FMN_dh; 1.

PEAM; PF00173; heme 1; 1.

PRINTS; PR00363; CYTOCHROMEB5.

ProDom; PD000612; CYT B5; 1.

PROSITE; PS00191; CYTOCHROME_B5_1; 1.
                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
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MEDLINE-90088451; PubMed=2688640;

Black M.T., Gunn F.J., Chapman S.K., Reid G.A.;

"Structural basis for the kinetic differences by
flavocytochromes b2 from the yeasts Hansenula as
Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE=90045973; PubMed=2813072;

Risler Y., Tegoni M., Gervais M.;

"Nucleotide sequence of the Hansenula anomala
flavocytochrome b2 (L-lactate:cytochrome c oxi

Nucleic Acids Res. 17:8381-8381(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-1989 (Rel. 10, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
101-JAN-1990 (Rel. 14, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cytochrome B2, mitochondrial precursor (EC 1.1.2.3) (L-lactate dehydrogenase [Cytochrome]) (L-lactate ferricytochrome C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hansenula anomala (Yeast) (Candida pelliculosa).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Pichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HANAN
                                                                                                                                            InterPro; IPR001199; Cyt_B5.
InterPro; IPR003009; PMN_enzyme.
InterPro; IPR002062; PMN_hydxyac_dh.
                                                                                                                                                                                                                                             PIR; S06600; S06600.
HSSP; P00175; 1LCO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haumont P.-Y., Thomas M.-A., Labeyrie F., Lederer F.; "Amino-acid sequence of the cytochrome-b5-like heme-binding from Hansenula anomala flavocytochrome b2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=88082787; PubMed=3319613; Haumont P.-Y., Thomas M.-A., Labe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 80-163.
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                                                                                                                                                                                                                  InterPro; IPR001199;
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SUBUNIT: Homotetramer.
SUBCELLULAR LOCATION: Mitochondrial intermembrane s
SUBCELLANEOUS: THIS ENZYME BINDS FMN AND PROTOHEME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: TO SPINACH GLYCOLATE OX P. PUTIDA S-MANDELATE DEHYDROGENASE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . J. Biochem. 169:539-546(1987).
CATALYTIC ACTIVITY: (S)-lactate + 2 ferricytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY:
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                                                                                                                                                                                                                                                                                                       X16051; CAA34183.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TO SPINACH GLYCOLATE OXIDASE (33% IDENTITY), TO MANDELATE DEHYDROGENASE, AND TO M.SMEGMATIS LACTATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ä
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E IX PROSTHETIC
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Best Local :
                                                                                                                                                                                                                                                                                                                     MEDLINE=20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V
Buell C.R., Ketchum K.A., Lee.J.J., Ronning C.M., Koo H.L.,
Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
Goodman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACT_SITE
SEQUENCE
                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the St the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                               -i- FUNCTION: Membrane bound hemoprotein which function as an electrarier for several membrane bound oxygenases (By similarity).
-i- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
Probable cytochrome b5 isoform 2.
AT2G32720 OR F24L7.14
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARATH
            EMBL; AC003974; AAC04491.1; -. PIR; T00796; T00796.
                                                        entities requires a license agreement (s or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                           "Sequence and analysis thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CV.
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                                                                                                                                                                                                                                                              Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                                           Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          METAL
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PROSITE; PS00557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EQUENCE FROM N.A.
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e; Mitochondrion;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Columbia;
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Respiratory chain; Oxid
drion; Transit peptide.
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CYTOCHROME DOMAIN (CORE).

CYTOCHROME DOMAIN (CORE).

IRON (HEME AXIAL LIGAND) (BY SIMILARITY).

IRON (HEME AXIAL LIGAND) (BY SIMILARITY).

REMOVES THE SUBSTRATE ALPHA-PROTON AS THE FIRST STEP IN CATALYSIS (BY SIMILARITY).

SUBSTRATE BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85
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                                                  RX. MEDILINE-21848401; PubMed=11859360;

RX MEDILINE-21848401; PubMed=11859360;

RA Sgouros J., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

RA Sgouros J., Peat N., Hayles J., Bakker S., Basham D., Bowman S.,

RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

RA HOlroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

RA Mooney P., Moule S., Mangall K., Murphy L., Niblett D., Odell C.,

RA Moliver K., O'Neil S., Pearson D., Quail M.A., Sharp S.,

RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

RA Woodward J., Volckaert G., Squares R., Squares S., Stevens K.,

RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

RA Woodward J., Volckaert G., Holzer E., Mosefer M., Milbert H.,

RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

RA Woodward J., Volckaert G., Helter F., Meller Auer S.,

RA Woodward J., Volckaert G., Helter F., Mosefer M., Meller-Auer S.,

RA Gabel C., Fuchs M., Fritzc C., Holzer E., Mosefer M., Hilbert H.,

RA Geffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

RA Geffeau A., Cadieu E., Jimenez J., Sanchez M., Garzon A., Thode G.,

RA Lucas M., Rochet M., Galilardin C., Tallada V.A., Garzon A., Thode G.,

RA Locas M., Rochet M., Combie W.R., Paulsen I., Potashkin J.,

"The genome sequence of Schizosaccharomyces pombe.";

RA Shakovski G.V., User C., Warse S.,

RA Shakovski G.V., User G., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YDAA SCHPO STANDARD; PRT; 147 AA. Q10352; O1-OCT-1996 (Rel. 34, Created) O1-OCT-1996 (Rel. 34, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Hypothetical protein CIF12.10c in chromosome SPACIF12.10C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001199; Cyt_B5.
Pfam; PF00173; heme_1; 1.
PRINTS; PR00363; CYTOCHROMEB5.
PRODOM; PD000612; CYt_B5; 1.
PROSITE; PS00191; CYTOCHROME B5_1; 1.
PROSITE; PS00191; CYTOCHROME B5_2; 1.
PROSITE; PS50255; CYTOCHROME B5_2; 1.
Electron transport; Transmembrane; Heme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schizosaccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=4896;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                    SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
SWISS-PROT entry
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HSESAREMMEQYYVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EKKYITSEELKGHNKEGDLWISIQGKVYNVSDWVKEHPGGDVPISNLAGQDVTDAF-IAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64
134 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107
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40 II
64 II
; 15016 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pombe (Fission yeast).
scomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.1%;
is copyright.
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IRON (HEME AXIAL LIGAND)
IRON (HEME AXIAL LIGAND)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 149.5; DB 1
Pred. No. 1.2e-05;
5; Mismatches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B405F5430F5716C1 CRC64;
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  18
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produced through
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78)
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  collaboration
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RESULT 10
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Best Local S
Matches 31
                                                                                                                                                                                                                                                                                                                                                       MEDININ=10/10/27; PubMed=8370541; MEDININ=3380674; PubMed=8370541; Diolez A., Langin T., Gerlinger C., Brygoo Y., Daboussi M.-J.; Diolez A., Langin T., Gerlinger C., Brygoo Y., Daboussi M.-J.; Withen in gene of Fusarium oxysporum: isolation, sequence and development of a homologous transformation system."; Gene 131:61-67(193).

Gene 131:61-67(193).

-i- FUNCTION: Nitrate reductase is a key enzyme involved in the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of
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P39863;
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                                                                                                                                  step of nitrate assimilation in plants, fungi and bacter il CATALYTIC ACTIVITY: Nitrite + NADP(+) + H(2)O = nitrate cOFACTOR: REQUIRES FAD, A HEME GROUP (CALLED CYTOCHROME AND ONE MOLYBDENUM ATOM.

-!- SUBUNIT: Homodimer (By similarity).

-!- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES

-!- SIMILARITY: CONTAINS 1 CYTOCHROME BEDUCTASES IN C-TERMINAL DOMAIN.

-!- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN C-TERMINAL DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P00175; 1LTD.
GeneDB SPombe; SPACIF12.10c; -
InterPro; IPR001199; Cyt_B5.
Pfam; PP00173; heme_1; 1.
PRINTS; PR00363; CYTOCHROMEB5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions
use by non-profit institutions as long as its content is in
modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=FOM24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Fungi; ... Hypocreomycetidae; NCBI_TaxID=5507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fusarium oxysporum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nitrate reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1995 (Rel.
01-FEB-1995 (Rel.
28-FEB-2003 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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PROSITE; PS00191; CYTOCHROME B5_1;
PROSITE; PS0255; CYTOCHROME_B5_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z69944; CAA93814.1; -. PIR; S67453; S67453.
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METAL
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106 106 IR
129 129 IR
147 AA; 16667 MW;
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31, Last sequence update)
41, Last annotation update)
[NADPH] (EC 1.7.1.3) (NR).
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IRON (HEME AXIAL LIGAND)
; E874859F52E1AF1D CRC64;
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Pred. No. 2.5e-05;
3; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --
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ХВ)
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SIMILARITY).
                                                                        a collaboration -
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B-557)
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Matches
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PRINTS; PR00406; CYTBSRDTRASE.
PRINTS; PR004063; CYTCCHROMEB5.
PRINTS; PR00407; EUNOPTERIN.
PRINTS; PR00371; FPNCR.
PRODOM; PD000612; CYC_HOME_B5; 1.
PROSITE; PS00151; CYTCCHROME_B5_2; 1.
PROSITE; PS00559; MOLYBODPTERIN_EUK; 1.
                                                                                                                                                                         CYB5_RABIT STANDARD;
P00169; Q28726;
21-JUL-1986 (Rel. 01, Created)
01-NOV-1990 (Rel. 16, Last seq
15-SEP-2003 (Rel. 42, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
NP_BIND
                                           SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE-89128816; PubMed=3222252;
Dariush N., Fisher C.W., Steggles A.W.;
"The nucleotide sequence of rabbit liver cytochrome
                                                                                                                Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam;
Pfam;
Pfam;
Pfam;
                                                                                                                                                                                                                                       RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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InterPro; IPR001834; Cyt B5 reductase.
InterPro; IPR000572; Euk Mb_oxred.
InterPro; IPR001709; FPN_cyt redctse.
InterPro; IPR005066; Mo-co_dimer.
InterPro; IPR001433; Oxred_FAD/NAD(P).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
SEQUENCE FROM N.A. STRAIN=New Zealand
                                                                                                                                                                  Cytochrome b5.
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                                   Procein
                                                                                                                                                                                                                                                                                                                                                                                            Local
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n; PF03404; Mo-co dimer; 1.
n; PF00175; NAD binding 1; 1.
n; PF00174; oxidored molyb; 1.
NTS; PR00406; CYTB5RDTASB.
NTS; PR00363; CYTOCHROMEB5.
                                                                                                                                                                                                                                                                                      885
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                                                                                                                                                                                                                                                                                                           ISNLAGODVTDAFIAYHPGTAWSHLEKFFTG
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428
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884
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36.3%;
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                                  1:351-353(1988).
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Pred. No. 0.00022;
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IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FLAVIN-BINDING DOMAIN (BY SIMILARITY).
NADP (BY SIMILARITY)
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MOLYBDENUM-PTERIN (PO:
INTERCHAIN (POTENTIAL)
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                                                                                                                                                                                                                                                                            MEDLINE=20117684; PubMed=10651812;
Banci L., Bertini I., Rosato A., Scacchieri S.;
Banci L., Bertini II., Rosato A., Scacchieri S.;
"Solution structure of oxidized microsomal rabbit cytochrome "Solutions determining the heterogeneous binding of the heme.";
Eur. J. Biochem. 267:755-766(2000).
-1- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Takagaki Y., Gerber G.E., Nihei K., Khorana H.G.; "Amino acid sequence of the membranous segment of rabbit liver cytochrome b5. Methodology for separation of hydrophobic peptides."; J. Biol. Chem. 255:1536-1541(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Takamatsu H., Kozutsumi Y., Suzuki A., Kawasaki T., "Molecular cloning of rabbit cytochrome b5 genes: evidence occurrence of two separate genes encoding the soluble and forms.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-10. MEDLINE=89323209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=80115672; PubMed=7354043;
Takagaki Y., Gerber G.E., Nihei K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tsugita A., Kobayashi M., Tani
Kajihara T., Hagihara B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 6-7 AND 46-48.
MEDLINE=70289989; PubMed=5272324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tsugita A., Kobayashi M., Kajihara "Primary structure of rabbit liver J. Biochem. 64:727-730(1968).
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                                                                                                                                                                                                                                                                                                                                                                                                                       membrane
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"Primary structure of the
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MEDLINE=69108767; PubMed=5709273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. Biophys. Res. Commun. 185:845-851(1992).
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                                                                                                      Name=1; Synonyms=Liver, Membrane-bound;
IsoId=P00169-1; Sequence=D1splayed;
Name=2; Synonyms=Erythrocyte, Cytoplasmic;
IsoId=P00169-2; Sequence=VSP_001244, VSP_00124;
SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
                                                                                                                                                                   OXYGENASES.
SUBCELULIAR LOCATION: MICROSOWAL MEMBRANE. BO CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2; Name=1; Synonyms=Liver, Membrane-bound;
                                                                                                                                                                                                                                                              FUNCTION AS AN ELECTRON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86:1119-1128(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence
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245:4863-4874(1970)
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3., Sato R., Narita K.;
e of the membrane-binding
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Best Local S
Matches 36
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=97245296; PubMed=9090055;
de Antoni A., D'Angelo M., Dal Pero F., Sartorello f
de Antoni A., Lanfranchi G., Valle G.;
Pallavicini A., Lanfranchi G., Valle G.;
                                                                                                                                                                            CYB5 YEAST
P40312;
01-FEB-1995
01-OCT-1996
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D10901; BAAVI.
PIR; JN0316; JN0316.
PIR; S03373; CBRB5.
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EMBL; D10901;
                                                                                                                                      CYB5 OR YNLlic OR N1949.

Saccharomyces cerevisiae (Baker's yeast).

Bukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                    YEAST
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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Pfam; PF00173; heme_1; 1.
ProDom; PD0000312; Cyt_B5; 1.
PROSITE; PS00191; CYTOCHROME_B5_1; 1.
PROSITE; PS50255; CYTOCHROME_B5_2; 1.
Electron transport; Transmembrane; Heme;
                                                         MEDLINE=94237477; PubMed=8181746;
Truan G., Epinat J.-C., Rougeulle C., Cullin C., Pompon D.;
"Cloning and characterization of a yeast cytochrome b5-encoding
which suppresses ketoconazole hypersensitivity in a NADPH-P-450
reductase-deficient strain.";
Gene 142:123-127(1994).
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STRAIN=FL100;
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103
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annotation
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T -> P (in isoform 2).
/FTId=VSP_001244.
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/FTId=VSP 001245.
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HEME-BINDING.
MEMBRANE-BINDING.
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RESULT
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CYS5 TOBAC
P49099;
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01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2093 (Rel. 41, Last annotation update)
Cytochrome b5, seed isoform.
Nicotiana tabacum (Common tobacco).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheospermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the Buropean Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con entitles requires a license agreement (See http://www.isb-sib.ch/ar or send an email to license@isb-sib.ch).
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CONFLICT
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Prodom; PRO00612; CYT B5; 1.

PROSITE; P800191; CYTOCHROME B5 1; 1.

PROSITE; P850255; CYTOCHROME B5 2; 1.

PROSITE; P850255; CYTOCHROME B5 1; 1.

PROSITE; P850255; CYTOCHROME POTENTIAL.

TRANSMEM 98 118 POTENTIAL.

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EMBL; Z69382; CAA93396.1; -.
EMBL; Z71387; CAA95990.1; -.
EMBL; S63052; S63052.
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                                NCBI_TaxID=4097;
SEQUENCE FROM N.A.
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GO; GO:0016126; P:sterol biosynth
InterPro; IPR001199; Cyt_B5.
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S0005055; CYB5.
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29.9%;
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IRON (HEME AXIAL LIGAND)
E -> Q (IN REF. 1).
; 598EF2A6730CAD19 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 143; DB 1;
Pred. No. 3.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                       DVDKTSERVSVE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                     135
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YB)
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RESULT 14
CYB5_TOBAC
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Best Local
                                                                                                                                                                                      CYB5 TOBAC
P49098;
01-FEB-1996
01-FEB-1996
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Napier J.A., Smith M.A., Stobart A.K., Shewry P.R.;
"Isolation of a cDNA encoding a cytochrome b5 specifically expressed in developing tobacco seeds.";
planta 197:200-202(1955)
-I- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND OXYGENASES. WAY PLAY A KEY ROLE IN THE MODIFICATION BY DESATURATION OF PARTY ACIDS IN THE ENDOPLASMIC RETICULUM, WHICH ITHE DEVELOPING SEED IS UTILIZED FOR MEMBRANE SYNTHESIS AND IN THE DEVELOPMENTALLY REGULATED PRODUCTION OF LARGE AMOUNTS OF STORAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                         Nicotiana tabacum (Common tobacco).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledona; core eudicots;
Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METAL
METAL
MEDLINE=94325476; PubMed=8049375;
Smith M.A., Stobart A.K., Shewry P.R., 
"Tobacco cytochrome b5: cDNA isolation,
                                                                                                                                                                           Cytochrome b5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Electron transport; Transmembrane; Heme; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00173; heme 1; 1.

ProDom; PD000612; Cyt B5; 1.

PROSITE; PS00191; CYTOCHROME B5 1; 1.

PROSITE; PS50255; CYTOCHROME B5 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=cv. Samsun;
MEDLINE=96009039; F
                                                                                             NCBI_TaxID=4097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P00171; 1CYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X80008; CAA56318.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro
                                                               EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIPIDS.
SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULM (BY SIMILARITY). TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN DEVELOPING SEEDS. SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S49200; S49200.
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                                                                                                                                                                                                                                                                                                                                 HSSSARAMLDEYYVG
                                                                                                                                                                                                                                                                                                                                                              HPGTAWSHLEKFFTG
                                                                                                                                                                                                                                                                                                                                                                                             QSKVFTLAEVSNHNNAKDCWLIISGKVYNVTKFLEDHPGGGEVLLSATGKDATDDFEDIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR001199; Cyt_B5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64
135 AA;
                                                                                                                                                                                   (Rel. 33, Created)
(Rel. 33, Last seq
(Rel. 41, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                     STANDARD;
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h M.A., Stobart A.K.,
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14869 MW;
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36.0%;
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                                                                                                                                                                                     sequence update) annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 142.5; DB 1
Pred. No. 4.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IRON (HEME AXIAL LIGAND) (BY IRON (HEME AXIAL LIGAND) (BY A36CCA081A72ECBC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                    136
                Napier J
   expression
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CYM5_HUMAN
RRR RNX
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Best Local
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043169;
16-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plant Mol. Biol. 25:527-537(1994).

-I- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND OXYGENASES. MAY PLAY A KEY ROLE IN THE MODIFICATION BY DESATURATION OF FATTY ACIDS IN THE ENDEPLASMIC RETICULUM, WHICH IN THE DEVELOPMENTALLY REGULATED PRODUCTION OF LARGE AMOUNTS OF STORAGE LIFIDS. IS INVOLVED IN THE REDUCTION OF CYTOCHROME P-450 AND MAY THEREFORE BE INVOLVED IN FLAVONOID BIOSYNTHESIS IN THE PETALS.
-I- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE CYTOCHASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
-I- TISSUE SPECIFICITY: IS HIGHLY EXPRESSED IN DEVELOPING SEEDS, MODERATELY EXPRESSED IN ELEVELS IN THE PETALS.

-I- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE CYTOCHASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
-I- TISSUE SPECIFICITY: IS HIGHLY EXPRESSED IN DEVELOPING SEEDS, MODERATELY EXPRESSED IN ELEVELS IN THE LEAP.
                                                                                         Homo sapiens (Human
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrictuse by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and f
                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cytochrome b5 outer mitochondrial membrane is
                                                                                                                                                                                                                                                       HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001199; Cyt_B5.
Pfam; PF00173; heme 1; 1.
ProDom; PD000612; Cyt_B5; 1.
PROSITE; PS00191; CYTOCHROME_B5_1;
PROSITE; PS00255; CYTOCHROME_B5_2;
Electron transport; Transmem5rane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <del>-</del>
                                                                                                                                         CYB5M OR OMB5.
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EMBL; X68140; CAA48240.1; -.
HSSP; P04166; 1B5M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vitro protein targeting.";
Plant Mol. Biol. 25:527-537(1994)
              Ishibashi K.
                            TISSUE=Testis;
                                              SEQUENCE FROM N.A.
                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Multigene family.
TRANSMEM 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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64
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105
                                                                                            Chordata;
Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  16;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 142.5; DB 1;
Pred. No. 4.9e'-05;
6; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
LA -> EF (IN REF. 1; CAA48240).
MISSING (IN REF. 1; CAA48240).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DACE9EA695B2835F CRC64;
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                                                                                                                                                                                                                                    146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Iron; Microsome;
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                                                                                                                                                                                                                                                                                                                                                                                   63
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'Cytochrome b5 and aquaporins share

the last transmembrane amino acids

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Search completed: January 1,
Job time : 9.90156 secs
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Best Local Similarity
Matches 43; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
TRANSMEM
METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AB009282; BAA23735.1; ...
HSSP; P04166; IBSM.
InterPro; IPR001199; Cyt_B5.
Pfam; pP00173; heme 1; 1.
PRINTS; PR00363; CYTOCHROMEB5.
PrODOM; PD000612; Cyt_B50; 1.
PROSITE; PS00191; CYTOCHROME B5 1; 1.
PROSITE; PS00191; CYTOCHROME B5 2; 1.
Electron transport; Mitochondrion; Outer membrane; Transmembrane;
Heme; Iron. 1 11 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence.";
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: CYTOCHROME B5 IS A MEMBRANE BOUND HEMOPROTEIN WHICH
FUNCTION AS AN ELECTRON CARRIER FOR SEVERAL MEMBRANE BOUND
OXYGENABES (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity).
-!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - 1- SUBCELLULAR LOCATION: Mitochondrial outer membrane (By
                                                                                                                                       115
                                                                                                                                                                                       122 VAVMELIVLYGVLRCTSVWAH----LGSGMLLGLLW 153
                                                                                                                                                                                                                                                                                                                        63 IAYHPGTAWSHLEKFFTG-YHLSDFKVSEVSKDYRKLASEFSKLGLFDTKGHVTSCTLAS 121
                                                                                                                                                                                                                                                                                                                                                                                                    16 VETSVTYYRLEBVAKRNSLKELMLVIHGRVYDVTRFLNEHPGGEEVLLEQAGVDASBSFE
                                                                                                                                                                                                                                                                    76 DVGHSSDAREMLKQYYIGDIHPSDLKPESGSKDPSQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VEKEKKYITSEELKGHNKEGDLWISIQGKVYNVSDWVKEHPGGDVPISNLAGQDVTDAF-
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119
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79
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146
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136
55
79
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                                                                                                                                ---CKSCWAYWILPIIGAVLLGFLY 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.8%; Score 141.5; DB 1; Length 146; 27.6%; Pred. No. 6.4e-05; tive 22; Mismatches 50; Indels 41
                               2004, 06:30:56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
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CYTOCHROME BS OUTER MITOCHONDRIAL
MEMBRANE ISOFORM.
HEME-BINDING.
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Title:
Perfect score:
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Maximum DB seq length: 200000000
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
    1887
1801.5
1749.5
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Match L
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1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*
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2449
1 MEVVEKEKKYITSEELKGHN......RDLTNPAPKNLLWEAVNTHG
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Gapop 10.0 , Gapext 0.5
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     sp_invertebrate:*
sp_mammal:*
sp_mhc:*
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sp_phage:*
sp_plant:*
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                                                                                                                                                                                                                                                                     sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_acteriap:*
sp_acrheap:*
    GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                              DB
     Q9ZRP7
Q8LB96
Q9ZRP8
Q9FR82
Q43449
Q43449
Q9ELLD7
Q8UZZZ
Q9SAU55
Q8UZZZ
Q9SAU55
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Q9SAU56
Q8UZZZ
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Q9fr82 borasgo offi
Q43469 helianthus
Q9zry9 ricinus com
Q8lld7 aquilegia v
Q8vzz2 echium gent
Q9sau5 borago offi
Q8vzz1 echium pita
Q8tri7 argania spi
Q9ztu8 triticum ae
Q9hdg8 mucor rouxi
Q8nkg9 saccharomyc
Q9lem9 ceratodon p
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17.7	17.8	17.8	17.8	17.8	17.9	17.9	18.0	18.0	18.2		18.3	18.4		18.5	18.6	18.6	20.1	20.1	20.1	20.1	٠	•		•	20.9		22.2	
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Nguyen M., Onodera C.S., Paim C.J., Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,	Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka	Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,	Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,		SEQUENCE FROM N.A.	[4]	Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.	EU Arabidopsis sequencing project;	SEQUENCE FROM N.A.		Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.	0.000	De Haan M. Maarge A C. Grivell I. A. Mewes H W. Lemcke K	SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF		J. Biol. Chem. 273:28590-28596 (1998).	,	"A sphingolipid desaturase from higher plants. Identification of a new	Sperling P., Zaehringer U., Heinz E.;		STRAIN=cv. Columbia; TISSUE=Flower, MAINLY GREEN PARTS, and Root;	SEQUENCE FROM N.A.	[1]	NCBI TaxID=3702;	eurosids II; Brassicales; Brassicaceae; Arabidopsis.	edons; core e	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Arabidopsis thaliana (Mouse-ear cress).	SLD1 OR F2A19.180 OR AT3G61580.		(TrEMBLrel. 23, Last		01-MAY-1999 (TrEMBLrel. 10, Created)	Q9ZRP7;	Q9ZRP7 PRELIMINARY; PRT; 449 AA.	RP7	JLT 1

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Matches 334
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A Carninci P., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M.,

A Deng J.M., Hayashizaki Y., Hsuan V.W., Lee J.M., Ishida J., Kamiya A.,

A Kawai J., Kim C.J., Narusaka M., Quach H.L., Sakurai T., Satou M.,

A Seki M., Shinn P., Tang C.C., Toroumi M., Wallender E.K., Wong C.,

AW H.C., Yamada K., Yu G., Yuan S., Shinozaki K., Ecker J.,

A Theologis A., Davis R.W.,

A Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.

-- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.

EMBL; AL132962; CAB11858.1; --

EMBL; AF428420; AAM116189.1; --

EMBL; AF428420; AAM17419.1; --

EMBL; BT000442; AAM17419.1; --
                       Q8LB96;
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EMBL;
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ProDom; PD001081; FA desat fam; 1.
PROSITE; PS50255; CYTOCHROME_B5_2;
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InterPro; IPRO05804; FA desat_fam.
Pfam; PF00487; FA desaturase; 1.
Pfam; PF00173; heme_1; 1.
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4; Mismatches 58;
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InterPro; IPR005804; FA_desat_fam.
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Pfam; PP00173; heme_1; 1.
ProDom; PD0010612; Cyt B5; 1.
ProDom; PD001081; FA_desat_fam; 1.
PROSITE; PS50255; CYTOCHROME_B5_2; 1
                       Q9ZRP8;
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-!- SIMILARITY: BELONGS TO THE CYTOCHROME
EMBL; AY087345; AAM64895.1; -.
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Brover V., Troukhan M., Alexandrov N.,
Feldmann K.;
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Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alex.
Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
"Full-length messenger RNA sequences greatly improve annotation.";
Genome Biol. 0:0-0(2002).
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                               MDWFFGGLQFQLEHHLFPRLPRCHLRKVSPVVQELCKKHNLPYRSMSWFEANVLTINTLK
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74.7%;
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01-MAY-1999
01-MAR-2003
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ProDom; PD001081; FA desat fam; 1.
PROSITE; PS50255; CYTOCHROME_B5_2; 1.
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Interpro; IPR001199; Cyt_B5.
Interpro; IPR005804; FA_desat_fam.
Pfam; PF00487; FA_desat_urase; 1.
Pfam; PF00173; heme_1; 1.
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J. Biol. Chem. 273:28590-28596 (1998)
-i-SIMILARITY: BELONGS TO THE CYTOC
EMBL; AJ224160; CAA11857.1;
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STRAIN=cv. Drakkar; TISSUE=Ripening
MEDLINE=99003197; PubMed=9786850;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
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                                      PRELIMINARY;
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Pred. No. 3.9e-166;
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Arch. Biochem. Biophys. 388:293-298(2001).
-!- SIMILARITY: BELONGS TO THE CYTOCHROME B5
EMBL; AF133728; AAG43277.1;
-- HSSP; P00171; 115U.
InterPro; IPR001199; Cyt B5.
IInterPro; IPR005804; FA desat fam.
Pfam; PF00487; FA desaturase; 1.
Pfam; PF00173; heme_1; 1.
Pfam; PF00173; heme_1; 1.
ProDom; PD001081; FA desat fam; 1.
ProDom; PD001081; FA desat fam; 1.
PROSITE; PS50255; CYTOCHROME_B5_2; 1.
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SEQUENCE FROM N.A.
MEDLINE=21092516; PubMed=11162428;
Libisch B., Michaelson L.V., Lewis
"Chimeras of Delta6-fatty acid and
pionhys. Res. Commun. 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Borago officinalis (Bourrache) (Borage).
Eukaryota; Viridiplantae; Streptophyta; Embry
Spermatophyta; Magnoliophyta; eudicotyledons;
Asteridae; lamiide; Boraginaceae; Borago.
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Sperling P., Libisch B., Zaehringer U
"Functional identification of a delta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VEKEKKYITSEELKGHNKEGDLWISIQGKVYNVSDWVKEHPGGDVPISNLAGQDVTDAFI
                                                                               RTAALQARDLTNPAPKNLLWEAVNTHG
                                                                                                                                                     SMDWFFGGLQFQLEHHLFPRLPRCQLRKISPLVSDLCKKHNLPYRSLSFWEANQWTIRTL
                                                                                                                                                                                                    CLPNWNERVLFVLTCFSVTALQHIQFTLNHFAADVYVGPPTGTNWFEKQAAGTIDISCSS
                                                                                                                                                                                                                      CLPNWPERVMFVLASFAVCSIQHIQFCLNHFAANVYVGPPSGNDWFEKQTSGTLDISCAS
                                                                                                                                                                                                                                                                                                                                                                                                                              LLLCGCVYGVLCSNSLWVHMLSGAMLGMCFIQAAYLGHDSGHYTMMSSKGYNKFAQVLNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEGTKKYISVGELEKHNOLGDVWISIQGKVYNVTDWIKKHPGGDVPIMNLAGODATDAFI
                                                      RTAALQARDLT-VVPQNLLWEAFNTHG
                                                                                                                                                                                                                                                                          LSRFLVSYQHFTIYLVMIFGRINLYVQTFLLLFSTRKVPDRALNIIGILVYWTWFPYLVS
                                                                                                                                                                                                                                                                                                                                                      NCLTGISIAWWKWTHNAHHIACNSLDYDPDLQHLPVFAVPSSFFKSLTSRFYGRELTFDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    446 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                QFQLEHHLFPRMPRCQLRNISPIVQDYCKKHNLPYRSLSFFDANVATIKTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50926 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ewis M.J., Shewry P.R., 1 and Delta8-sphingolipid 279:779-785(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EBD579F03SA3AF0C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U., Napier J.A.,
ta 8-sphingolipid
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desaturase from
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Best Local Similarity 71.6
Matches 317; Conservative
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Q43469;
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=cv. inbred line HA89;
TISSUB=Cotyledons of developing sunflower fruits;
MEDLINE=21116801; PubMed=11171153;
Sperling P., Blume A., Zaehringer U., Heinz E.;
"Further characterization of delta 8-sphingolipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Helianthus annuus (Common sunflower).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;

Asteridae; campanulids; Asterales; Asteraceae; Asteroideae;

Heliantheae; Helianthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Delta-8 sphingolipid desaturase.
                                                                                                                                                                                                                                                                                              Pfam; PF00487; FA_desaturase; 1.
Pfam; PF00173; heme 1; 1.
ProDom; PD000612; CYt_B5; 1.
ProDom; PD001081; FA_desat_fam; 1.
PROSITE; PS50255; CYTOCHROME_B5_2;
                                                                                                                                                                                                                                                                                                                                                 EMBL; X87143; CAA60621.1; -. HSSP; P00171; 1F03. InterPro; IPR001119; Cyt B5. InterPro; IPR005804; FA desat
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TISSUE-Cotyledons of developing;
MEDLINE-96028121; PubMed-7588718
Sperling P., Schmidt H., Heinz E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "A cytochrome b5-containing fusion desaturases.";
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                                                                                                                                                                       GTAWSHLEKFFTGYHLSDFKVSEVSKDYRKLASEFSKLGLFDTKGHVTSCTLASVAVMFL
            WPERVMFVLASFAVCSIQHIQFCLNHFAANVYVGPPSGNDWFEKQTSGTLDISCASSMDW
                                      GISIAWWKWTHNAHHIACNSLDHDPDLQHMPVFAVSSRFFNSITSHFYGRKLEFDFIARF
                                                                                                                               KKYITSEELKGHNKEGDLWISIQGKVYNVSDWVKEHPGGDVPISNLAGQDVTDAFIAYHP
                                                                                                                                                                                                                                                                                                                                                                                                     Soc. Trans.
WPERVAFVLVSFCVTGIQHIQFTLNHFSGDVYVGPPKGDNWFEKQTRGTIDIACSSWMDW
                                                                             GISIAWWKWTHNAHHIACNSLDYDPDLQHLPMLAVSSKLFNSITSVFYGRQLTFDPLARF
                                                                                                                     ACVYGVLYSGSFWIHMLSGAILGLAWMQIAYLGHDAGHYQMMATRGWNKFAGIFIGNCIT
                                                                                                                                                           GTAWKHLDKLFTGYHLKDYQVSDISRDYRKLASEFAKAGMFEKKGHGVIYSLCFVSLLLS
                                                                                                                                                                                                   KKYITSKELKKHNNPNDLWISILGKVYNVTEWAKEHPGGDAPLINLAGODVTDAFIAFHP
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71.6%; Pro
tive 55;
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Pred. No. 3
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Matches 306
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MEDLINE=97268723; PubMed=9108131;

Sayanova O., Smith M.A., Lapinskas P., Stobart A.K., Dobson G.,

Christie W.W., Shewry P.R., Napier J.A.;

"Expression of a borage desaturase cDNA containing an N-terminal cytochrome b5 domain results in the accumulation of high levels of delta6-desaturated fatty acids in transgenic tobacco.";

Proc. Natl. Acad. Sci. U.S.A. 94:4211-4216(1997).
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O9ZTY9; PRANCHIMINARY; PRT; 446 AA.

O1-MAY-1999 (TrEMBLrel. 10, Created)
O1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
O1-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Desaturase/cytochrome b5 protein.
Ricinus communis (Castor bean).
Ricinus communis (Castor bean).
Rikaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosida
eurosids I; Malpighiales; Euphorbiaceae; Ricinus.

NCBI TaxID=3988;
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                                                                                                                                                                                                                                                                                                                                         GTAWSHLEKFFTGYHLSDFKVSEVSKDYRKLASEFSKLGLFDTKGHVTSCTLASVAVMFL 127
WGERVMFVAASFSVTRIQHVQFCLNHFSSSVYLGLLIANDWFENQTKGTLDITCSSWMDW
                      WPERVMFVLASFAVCSIQHIQFCLNHFAANVYVGPPSGNDWFEKQTSGTLDISCASSMDW
                                                                                                                                                        GISIAWWKWNHNTHHIACNSLDEDPDLQHMPFFAVSSKEFSSITSYFYERKMNFDCAARF
                                                                                                                                                                                                                                    IVLYGVLRCTSVWAHLGSGMLLGLLWMQSAYVGHDSGHYVVMTTNGFNKVAQILSGNCLT 187
                                                                                                                                                                                                                                                                                                                    GTAWQYLDKFFTGYHLKDYSVSETSKDYRRLVAEFSKLG-FEKKGHIAFITLVSMVMLLA
                                                                                                                                                                                                                                                                                                                                                                                              KKYITSEELKGHNKEGDLWISIQGKVYNVSDWVKEHPGGDVPISNLAGQDVTDAFIAYHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 2.1e
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1749.5;
Pred. No. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A1954FDB2DDB600F CRC64;
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1es 78;
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(PSEQUENCE FROM N.A.)

(A LONGMAN A.J., Michaelson L.V., Napier J.A.;

(A LONGMAN A.J., Michaelson L.V., Napier J.A.;

(A LONGMAN A.J., Michaelson L.V., Napier J.A.;

(A TISOlation and characterization of a cDNA encoding a delta 8

(A TISOlation and characterization of a cDNA encoding a delta 8

(A TISOLATION ACCUPATION                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last samotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Sphingolipid long chain base delta 8 desaturase.
Aquilegia vulgaris.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermattophyta; Magnoliophyta; eudicotyledons; Ranunculales;
Ranunculaces; Aquilegia.
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                             DWFFGGLQFQLEHHLFPRLPRCQLRKISPLVSDLCKKHNLPYRSLSFWEANQWTIRTLRT 425
  DWFHGGI
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51273 MW; 76366DB0EB956D09 CRC64;
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01-MAR-2002 (TrEMBLr
01-MAR-2002 (TrEMBLr
01-OCT-2002 (TrEMBLr
Delta-6-desaturase.
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SEQUENCE
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Boraginaceae; Echium.
NCBI_TaxID=173991;
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ProDom; PD001081; FA desat_fam; 1.
PROSITE; PS50255; CYTOCHROME_B5_2;
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287; Conserv
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Q9SAU5;
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SEQUENCE
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Spermatophyta; Magnoliophyta; eudicotyledons;
Asteridae; lamiids; Boraginaceae; Borago.
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ProDom; PD001081; FA_desat_fam; 1.
PROSITE; PS50255; CYTOCHROME_B5_2;
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InterPro; IPR005804; FA desat fam.
Pfam; PP00487; FA desaturase; 1.
Pfam; PF00173; heme_1; 1.
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Nunberg A.N.,
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63.4%; Pred. No. 9.66
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Borago officinalis (Bourrache) (Borage).
Borago officinalis (Bourrache) (Borage).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamids; Boraginaceae; Borago.
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01-JUL-1997 (TrEMBLrel. 04,
01-OCT-2002 (TrEMBLrel. 22,
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MEDLINE=97268723; PubMed=9108131;
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PROSITE; PS50255; CYTOCHROME_B5_2; 1.
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InterPro; IPR001199; Cyt_B5.
InterPro; IPR005804; FA_desat_
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"Cloning and Molecular Characterization of the D6-Desaturase fro

T Echium: Functional Expression in Yeast and Tobacco.";

Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

C -!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.

R EMBL; AY055118; AAL23581.1; -.

R InterPro; IPR001199; Cyt B5.

R InterPro; IPR001199; Cyt B5.

R InterPro; IPR005804; FA desat fam.

Pfam; PF00487; FA desat fam.

Pfam; PF00173; heme 1; 1.

R ProDom; PD001081; FA desat fam; 1.

R ProDom; PD001081; FA desat fam; 1.

R PROSITE; PSS0255; CYTOCHROME B5 2; 1.
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01-CCT-2002 (TrEMBLrel. 2:
01-MAR-2003 (TrEMBLrel. 2:
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Boraginaceae; Echium.
NCBI_TaxID=174255;
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Best Local S
Matches 273
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Submitted (JUL-2002) to the EMBL/Genl Submitted (JUL-2002) to the EMBL/Genl Submitted (JUL-2002) to the EMBL/Genl Submitted (JUL-2002) to the EMBL; AY131238; AAM94345.1; -. InterPro; IPR001199; CYL B5. InterPro; IPR005804; FA_desat_fam. Pfam; PF00487; FA_desat_fam. Pfam; PF00173; heme_1; 1. Pfam; PF00173; heme_1; 1. ProDom; PD000181; FA_desat_fam; 1. ProDom; PD000181; FA_desat_fam; 1. PROSITE; PS50255; CYTOCHROME_B5_2; 1
                                                                                                              Q9ZTU8
Q9ZTU8;
Q9ZTU8;
01-MAY-1999
01-MAY-1999
01-MAR-2003
Triticum aestivum (Wheat).
Eukaryota; Viridiplantae; Stro
Spermatophyta; Magnoliophyta;
Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; Ericales; Sapotaceae; Argania.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
El Filali A., Anderson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=85884;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MSVYGVLRCEGVLVHLFSGCLMGFLWIQSGWIGHDPGHYMVVSDSRLNKFMGIFAANCLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASTWKNLDKFFTGYYLKDYSVSEVSKDYSKLVFEFSKMGLYDKAGHIMFATLCFIAMLFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KKYITSEELKGHNKEGDLMISIQGKVYNVSDMVKEHPGGDVPISNLAGQDVTDAFIAYHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTAWSHLEKFFTGYHLSDFKVSEVSKDYRKLASEPSKLGLFDTKGHVTSCTLASVAVMFL
                                                                                                                                                                                                                                                                                                            LQARDLTNPAPKNLLWEAVNTHG
                                                                                                                                                                                                                                                                                                                                                                    FHGGLQFQIEHHLFPKMPRCNLRTISPYVIELCKKHNLPYNYASFSKANEMTLRTLRNTA
                                                                                                                                                                                                                                                                                                                                                                                        FFGGLQFQLEHHLFPRLPRCQLRKISPLVSDLCKKKINLPYRSLSFWEANQWTIRTLRTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                              WGERIMFVIASLSVTGMQQVQFSLNHFSSSVYVGKPNGNNWFETQTDGTLDISCPPWMDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPERVMFVLASFAVCSIQHIQFCLNHFAANVYVGPPSGNDWFEKQTSGTLDISCASSMDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FVSYQHWTFYTIMCAARLNMYVQSLIMLLTKRNVSYRAHELLGCLVFSIWYPLLVSCLPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GISIGWSKWNHNAHHIACNSLEYDPDLQYIPFLVVSSKFFGSLTSHFYEKRLTIDSLSRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GISIAWWKWTHNAHHIACNSLDHDPDLQHMPVFAVSSRFFNSITSHFYGRKLEFDFIARF
                                                                                                                                                                                                                                                                                        LQARDITKPLPKNLVWEALHTHG
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                                                                                                              (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
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                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65.2%; Score 1597; DB 10; 61.6%; Pred. No. 2.8e-139; tive 78; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          n M., Abbas
I cloning of
                  Streptophyta; Embryophyta; Tracheophyta;
yta; Liliopsida; Poales; Poaceae; Pooidea
                                                                                                              Created)
Last sequence up
Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL/GenBank/DDBJ
THE CYTOCHROME B5 1
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delta-6-desaturase
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                      Pooideae;
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Saccharomyces

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RESULT 14

Q9HDG

ID Q9HDG

AC Q9HDG

DT 01-M3

DT 01-M3

DT 01-M3

DT 01-M3

CS Mucozz

OC Eukaz

OC Mucozz

OX NCBI

RN (1)
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Best Local S
Matches 255
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InterPro; IPR005804; FA_desat_fam.
InterPro; IPR001092; HLH_basic.
Pfam; PF00487; FA_desaturase; 1.
Pfam; PF00173; heme_1; 1.
Pfam; PF00173; heme_1; 1.
PRINTS; PR00363; CYTOCHROME5.
PRODOm; PD000612; Cyt_B5; 1.
PRODOm; PD001081; FA_desat_fam; 1.
PROSITE; PS50255; CYTOCHROME_B5_2; 1
PROSITE; PS00038; HLH_1; 1.
                                                                Q9HDG8 PRELIMINARY;
Q9HDG8;
01-MAR-2001 (TrEMBLrel. 1
01-MAR-2001 (TrEMBLrel. 1
01-MAR-2003 (TrEMBLrel. 2
Delta-6 desaturase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.,
STRAIN=CV. ET3;
Delhaize E., Heb
                   Mucor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genes.";
Submitted (OCT-1997) to the EM
Submitted (OCT-1997) to THE
FINE STRICT : BELONGS TO THE
EMBL; AF031194; AAD10250.1; -.
HSSP; P00171; 115U
                                        Eukaryota; Fungi; Zygomycota;
                                                         Mucor rouxii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Aluminum tolerance
               _TaxID=29923
                                                                                                                                                                                                                              429
                                                                                                                                                                                                                                                        387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VLYGVLRCTSVWAHLGSGMLLGLLWMQSAYVGHDSGHYVVMTTNGFNKVAQILSGNCLTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KYITSEELKGHNKEGDLWISIQGKVYNVSDWVKEHPGGDVPISNLAGQDVTDAFIAYHPG
                                                                                                                                                                                                                                                       QAREATTGAAPKNLVWEALNTHG
                                                                                                                                                                                                                   QARD-LTNPAPKNLLWEAVNTHG
                                                                                                                                                                                                                                                                                                          WERVAFVLASFVITGIQHVQFCLNHFSSAVYVGPPKGNDWFERQTAGTLDIXCSPWMDWF
                                                                                                                                                                                                                                                                                                                        PERVMFVLASFAVCSIQHIQFCLNHFAANVYVGPPSGNDWFEKQTSGTLDISCASSNDWF
                                                                                                                                                                                                                                                                                                                                                             VSYQHWTFYPVMGFARINLLVQSIVFLITQKKVRQRWLEIAGVAAFWVWYPLLVSCLPNW
                                                                                                                                                                                                                                                                                                                                                                         ICYOHFTFYPVMCVARVNLYLQTILLLFSRRKVQDRALNIMGILVFWTWFPLLVSCLPNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALYCVLACSSTGAHMFAGGLIGFIWIQSGWIGHDSGHHQITRHPALNRLLQVVSGNCLTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SVRPLLRRFFVG-RITDYTVPPASADFRRLLAQLSSAGLFERVGHTPKFLLVAMSVLFCI
                                                                                                                                                                                                                                                                                                                                                                                                                 LGIAWWKFNHNTHHISCNSLDHDPDLQHLPLFAVSTKLFNNLWSVCYERTLAFDAISKFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59.7%; Solitarity 57.6%; Political Conservative 79;
                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hebb D.
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3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gardner R.C., Richards
                                                                                16,
16,
23,
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                                                                             Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1463; DB 10;
Pred. No. 7.6e-127;
9; Mismatches 107;
                                          Zygomycetes; Mucorales;
                                                                                                                                     PRT;
                                                                                                                                                                                                                               450
                                                                                                                                                                                                       469
                                                                                                                                     523
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                                           Mucoraceae;
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    RESULT 15
Q8NKG9
ID Q8NKG
AC Q8NKG
DT 01-OC
DT 01-OC
DT 01-MA
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Best Local S
Matches 147
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InterPro; IPR001199; Cyt_B5.
InterPro; IPR005804; FA_desat_fam.
Pfam; PF000487; FA_desat_trase; 1.
Pfam; PF00173; heme_1; 1.
Pfonom; PD0010612; Cyt_B5; 1.
ProDom; PD001081; FA_desat_fam; 1.
PROSITE; PS001095; C5_MTASE_2; 1.
PROSITE; PS00191; CYTOCHROME_B5_1; 1
PROSITE; PS00191; CYTOCHROME_B5_2; 1
PROSITE; PS00195; CYTOCHROME_B5_2; 1
    Q8NKG9;
Q8NKG9;
01-OCT-2002
01-OCT-2002
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Heme.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochem. Biophys. Res. Commun.
- SIMILARITY: BELONGS TO THE
EMBL; AF296076; AAG36960.1; -.
EMBL; AF290933; AAG36959.1; -.
HSSP; P00173; 1JEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=ATCC 24905;
MEDLINE=20563795; PubMed=11112411;
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                                                                                                                                     ANQWTIRTLRTAALQARDLTNPAPKNL-LWEAVNTH
                                                                                                                                                                           TIMDVDCPEWLDWFHGGLQYQAVHHLFPRLPRHNLRQCVPLVKKFCDEVGLHYYMYNFST
                                                                                                                                                                                        GTLDISCASSMDWFFGGLQFQLEHHLFPRLPRCQLRKISPLVSDLCKKHNLPYRSLSFWE
                                                                                                                                                                                                                          FVWFGSLLSTLPTWNIRIAYIMVSYMLTFPLHVQITLSHFGMSTEDRGPD-EPFPAKMLR
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    (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
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                                                         PRELIMINARY;
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Mucor rouxii with high similarity to pl
its heterologous expression in Saccharo
     22,
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    Last sequence update)
Last annotation update)
                              Created)
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Pred. No. 4.7e-55;
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CYTOCHROME B5 FAMILY
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Best Local Simi
Matches 141;
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Saccharomyces kluyveri (Yeast).
Saccharomycotina; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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PROSITE; PS50255; CYTOCHROME_B5_2; 1.
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InterPro; IPR005804; FA desat fam.
Pfam; PF00487; FA desaturase; 1.
Pfam; PF00173; heme 1; 1.
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--- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
EMBL; AB085689; BAB93117.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=IFO 1685;
Takakuwa N., Kinoshita M., Oda Y., Ohnishi M.;
Takakuwa N., Kinoshita M., Oda Y., Ohnishi M.;
"Isolation and characterization of the genes encoding delta 8-
sphingolipid desaturase from Saccharomyces kluyveri and Kluyveromyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                        VLASFAVCSIQHIQFCLNHFAANVY-VGPPSGNDWFEKQTSGTLDISCASSMDWFFRGGLQ 373
                                                                                                                                        GRENLYRLSWMHVLLGLGPRRGKAGWFRYFELCGLIFFNYWFFYLLVGCKLQTGWDRFQY 420
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                                 FQLEHHLFPRLPRCQLRKISPLVSDLCKKHNLPYRSLSFWEANQWTIRTLRTAALQARDL 433
                                                                                                                                                                           ARVNLY----LQTILLESRRKVQD--RALNIMGILVFWTW-FPLLVSC-LPNWPERVMF 314
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FOVVHHLFPRLPRHNLRAAOPYVIEFCEKVGIKYSIYGFSKGNGVVLTKLQEIAVOAKTM 538
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Search completed: January Job time : 41.588 secs ۲,

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US-08-834-033A-7
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US-09-363-526-2
US-09-363-526-2
US-09-363-526-2
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## ALIGNMENTS

US-08-934-254-27
; Sequence 27, Application US/08934254
; Patent No. 6355861
; GENERAL INFORMATION:

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                                                                                                                 Matches
                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                        TELEX: 230 901 SANS UR INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION UNMBER: 19,827
REFERENCE/DOCKET NUMBER: 8383
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSE: Scully, Scott, Murphy & Presser STREET: 400 Garden City Plaza
CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Thomas, Terry L.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID
TITLE OF INVENTION: DELTA 6-DESATURASE
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Garden Cit
STATE: New York
COUNTRY: United
ZIP: 11530
                                                                                                                                                                                                                                                                                                                                         ELECUTARY: (516)
                                                                                                                                                                                                                        LENGTH: 452 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11530
 GTAWSHLEKFFTG-YHLSDFKVSEVSKDYRKLASEFSKLGLFDTKGHVTSCTLASVAVMF 126
                                                         KKYITSEELKGHNKEGDLWISIQGKVYNVSDWVKEHPGGDVPISNLAGQDVTDAFIAYHP
                                       KKYITAEDLRRHNKSGDLWISIQGKVYDCSRWAAEHPGGEVPLLSLAGQDVTDAFIAYHP
                                                                                                               69.9%; Score 1712; DB 4; ilarity 69.6%; Pred. No. 7.1e-180; Conservative 54; Mismatches 78;
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                                                                                                                                                   Length 452;
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Length 448;

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### HOLECULE TYPE: DNA (genomic)

US-08-366-779-5
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US-08-366-779-5
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APPLICANT: Thomas,
APPLICANT: Reddy, I
APPLICANT: Nuccio,
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                                                                                                                                                                                                                                                COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/366,779
FILING DATE: 30-DEC-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
                                                                                                       TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                             NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 83
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
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TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID
TITLE OF INVENTION: DELTA 6-DESATURASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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Freyssinet, Georges L.
                                                                                                                                                               (516) 742-4366
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                                         DNA (genomic)
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Best Local Sim
Matches 280;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                       COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d:
                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: PRESSET, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 831
                                                                      APPLICATION NUMBER: US/08/789,936
FILING DATE: 28-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/366,779
FILING DATE: 30-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Freyssinet, Georges L.
APPLICANT: Numberg, Andrew N.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINGLENIC ACID BY
TITLE OF INVENTION: DELTA 6-DESATURASE
                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Scully, Scott, Murphy & Presser STREET: 400 Garden City Plaza CITY: Garden City
STATE: New York
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No. 5789220
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RESULT 4
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US-08-789-936-5
                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/08934254 Patent No. 6355861
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Best Local Similarity
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TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Thomas
             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,254
                                                                                                                                                  STREET: 400 CITY: Garden City
STATE: New York
TATE: neited St
                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
                                                                                                                                                                                                                                                  APPLICANT: Thomas, 7
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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LENGTH: 448 amino acid
                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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TELEPHONE: (516) 742-4343
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amino acid
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63.2%;
                                                                                                                                                                                                                                                                                   PRODUCTION OF GAMMA LINOLENIC
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Pred. No. 4.8e-173;
8; Mismatches 85;
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                                                                                                                                           PATENT NO. 5972664

GENERAL INFORMATION:
APPLICANT: KNUTZON, DEBORAH
APPLICANT: HURKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
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INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
TYPE: amino acid
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Best Local Similarity
                             TITLE OF LAVENTES. 12

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: RAF-VENTER LAW GROUP, P.C.

ADDRESSEE: ASF SERIDAN AVE, P.O. BOX 60039
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                                                                                                               TITLE OF INVENTION: METHODS AND CO
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CALIFORNIA
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COMPOSITIONS FOR SYNTHESIS IN POLY-UNSATURATED FATTY A

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TELECOMMUNICATION INFORMATION: TELEPHONE: (516) 742-4343
TELEPAX: (516) 742-4366
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                             LOARDLTNPAPKNLLWEAVNTHG 450
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LQARDITKPLPKNLVWEALHTHG 448
                                                                                                     FHGGSQFQIEHHLFPKMPRCNLRKISPYVIELCKKHNLPYNYASFSKANEMTLRTLRNTA
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compati

94306

COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS

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RESULT 6
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                                                                               Sequence 15, Application US/08834033A Patent No. 6075183
                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: N/A
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                 APPLICANT:
APPLICANT:
 APPLICANT:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 11-APR-1997
CLASSIFICATION: 435
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STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
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REFERENCE/DOCKET NUMBER: CGNE.123.00US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)328-4400
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NAME: RAE-VENTER, BARBARA
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KNUTZON, DEBORAH
MUKERJI, PRADIP
HUANG, YUNG-SHENG
THURMOND, JENNIFER
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Best Local (
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FILING DATE: 11-APR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
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SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
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CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
STREET: 2001 FERRY BUILDING
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MOLECULE TYPE:
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linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 328-4477
TELEFAX: (650) 328-4477
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INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/834,655 FILING DATE: 11-APR-1997 CLASIFICATION: 435 ATTORNEY ACCESS.
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TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
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242
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                                    FGGLQFQLEHH 379
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MURKERJI, PRADIP
HUANG, YUNG-SHENG
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252
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RESULT 8

RESULT 9
US-09-363-574-7
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Best Local Similarity
Matches 188; Conserv
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APPLICANT: KNUTZO
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,033/
FILING DATE: 11-APR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REGISTRATION NUMBER: 38,651
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INFORMATION FOR SEQ ID NO: 8:
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APPLICANT: MUKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
STREET: 2001 FERRY BUILDING
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LENGTH: 252 amino acids
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MEDIUM TYPE: Floppy disk
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STRANDEDNESS: not relevant
TOPOLOGY: linear
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CITY: SAN FRANCISCO
STATE: CA
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                                                                                                                                                                                    249 ICYQHFTFYPVMCVARVNLYLQTILLLFSRRKVQDRALNIMGILVFWTWFPLLVSCLPNW
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                                                                           PERFFFVFTSFTVTALQHIQFTLNHFAADVYVGPFTGSDWFEKQAAGTIDISCRSYMDWF
                                                                                                     PERVMFVLASFAVCSIQHIQFCLNHFAANVYVGPPSGNDWFEKQTSGTLDISCASSMDWF 368
FGGLQFQLEHH 252
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                                                                                                                                                                                                                                                                                                                                                                                       44.5%; Score 1091; DB 3
74.9%; Pred. No. 8e-112;
ative 31; Mismatches 3
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US-09-363-526-7

Sequence 7, Application US/09363526

; Patent No. 6410288

; GENERAL INFORMATION:
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                                                                     RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: N/A
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEPAX: (415) 433-8716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
STREET: 2001 FERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION: NAME: WARD, MICHAEL R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/363,574 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94111
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MURKERJI, PRADIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide
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US-08-834-655-2

Sequence 2, Application US/08834655
Patent No. 5968809
GENERAL INFORMATION:

APPLICANT:

KNUTZON, I

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TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-363-526-7
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
STREET: 2001 FERRY BUILDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,526
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
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ZIP: 94111
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                                                                                                                                              129 VLYGVLRCTSVWAHLGSGMLLGLLMMQSAYVGHDSGHYVVMTTNGFNKVAQILSGNCLTG
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                                                                                       PERVMFVLASFAVCSIQHIQFCLNHFAANVYVGPPSGNDWFEKQTSGTLDISCASSMDWF 368
                                                                                                                             VSYOHETYYPVNCFGRINLFIQTFLLLFSKREVPDRALNFAGILVFWTWFPLLVSCLPNW
                                                                                                                                                                                           ISIAWWKWTHNAHHLACNSLDYDPDLQHIPVFAVSTKFFSSLTSRFYDRKLTFGPVARFL
FGGLQFQLEHH
                              FGGLQFQLEHH 379
                                                             PERFFFVFTSFTVTALQHIQFTLNHFAADVYVGPPTGSDWFEKQAAGTIDISCRSYMDWF
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                                                                                                                                                                                                                                                                                                                                                                                                                                      not relevant
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                                                                                                                                                                                                                                                                                                                       44.5%; Score 1091; DB 4; 74.9%; Pred. No. 8e-112; vative 31; Mismatches 32;
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425 VRYHTTGMIE 434

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PATENTIA Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,655
FILING DATE: 11-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.124.00US
TELEPAX: (650) 328-4477
TELEPAX: (650) 328-4477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: N/A
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
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TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: not relevant TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 457 amino acids
TYPE: amino acid
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                                                                                              346 N-DWFEKQTSGTLDISCASSMDWFFGGLQFQLEHHLFPRLPRCQLRKISPLVSDLCKKHN
                                                                                                                                                                                                                                                                                                                                                              190 GAFLGGVCQGFSSSWWKDKHNTHHAAPNVHGEDPDIDTHPLLTWSEHALEMFSDVPDEEL
                                                                                                                                                                                                                                                                                                                                                                                                              179 QILSGNCLTGISIAWWKWTHNAHHIACNSLDHDPDLQHMPVFAVSS---RFFNSITSHFY 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 FLIVLYGVLRC-----TSVWAHLGSGMLLGLLWMQSAYVGHDSGHYVVMTTNGFNKVA 178
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405 LPYRSLSFWE 414
                                                                                                                                                                                                       288 IMGILVFWTWFPLLVSCLPNWP-ERVMFVLASFAVC-SIQHIQFCLNHFAANVYVGPPSG
                                                                                                                                                                                                                                                                                                           236 GRKLEFDFIARFLICYOHFTFYPVMCVARVNLYLOTILLLF-----SRRKVODRALN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 ITSEELKGHNK--EGDLWISIQGKVYNVSDWVKEHPGGDVPISNLAGQDVTDAFIAYHPG
                                                   DMDFFTKQIITGRDVHPGLFANWFTGGLNYQIEHHLFPSMPRHNFSKIQPAVETLCKKYN
                                                                                                                                                         QLSLAMHWTWYLATMFLFIKDPVNMLVYFLVSQAVCGNLLAIVFSLNHNGMPVISKEEAV
                                                                                                                                                                                                                                                             TR-----MWSRFMVLNQTWFYFPILSFARLSWCLQSILFVLPNGQAHKPSGARVPISLVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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Patent No.
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Best Local Similarity
Matches 130; Conserv
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NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-8716
TELEPAX: (415) 433-8716
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APPLICATION NUMBER: US/08/834,033A
FILING DATE: 11-APR-1997
CLASSIFICATION: 800
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APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JERNIFER
APPLICANT: CHAUDHARY, SUNITA
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STRANDEDNESS: not
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                                                                                                                                                                                                                                                                                      69 TAWSHLEKFFTG---YHLSDFKVSEVSKDYRKLASEFSKLGLFDTKGHVTSCTLASVAVM
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                                        GRKLEFDFIARFLICYOHFTFYPVMCVARVNLYLQTILLLF-----SRRKVQDRALN 287
                                                                                                                                                                                                        FLIVLYGVLRC-----TSVWAHLGSGMLLGLLWMQSAYVGHDSGHYVVMTTNGFNKVA 178
                                                                                                                                                                                                                                                 AAWETLANFYVGDIDESDRDIKNDDFAAEVRKLRTLFQSLGYYD-----SKAYYAFKVS 129
TR-----MWSRFMVLNQTWFYFPILSFARLSWCLQSILFVLPNGQAHKPSGARVPISLVE 304
                                                                                                                        QILSGNCLTGISIAWWKWTHNAHHIACNSLDHDPDLQHMPVFAVSS---RFFNSITSHFY 235
                                                                                                                                                                   FNLCIWGLSTVIVAKWGQTSTLANVLSAALLGLFWQQCGWLAHDFLHHQVFQDRFWGDLF 189
                                                                                 GAFLGGVCQGFSSSWWKDKHNTHHAAPNVHGEDPDIDTHPLLTWSEHALEMFSDVPDEEL
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US-09-363-574-2
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Best Local Similarity
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ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION UNMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
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                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: N/A
INFORMATION FOR SEQ ID NO:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
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TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 18
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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126 FLIVLYGVLRC----
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                                                                                                                                                                     11 ITSEELKGHNK--EGDLWISIQGKVYNVSDWVKEHPGGDVPISNLAGQDVTDAFIAYHPG 68
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                                                         AAWETLANFYVGDIDESDRDIKNDDFAAEVRKLRTLFQSLGYYD-----SSKAYYAFKVS 129
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                                                                                              TAWSHLEKFFTG---YHLSDFKVSEVSKDYRKLASEFSKLGLFDTKGHVTSCTLASVAVM 125
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HUANG, YUNG-SHENG
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TSVWAHLGSGMLLGLLWMQSAYVGHDSGHYVVMTTNGFNKVA 178
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US-09-363-526-2
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 Matches 130;
                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 457 amino acids
                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
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                                                                                                                 TOPOLOGY: lir
                                                                                                                                                  TYPE: amino acid
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Conservative
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linear
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20.5%; Score 502.5;
30.2%; Pred. No. 1.5
tive 72; Mismatches
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   Mismatches
                   ..5e-46;
                                     DB 4;
                                     Length 457;
   37;
   Gaps
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Sequence 18, Application US/09330235

Patent No. 6459018

GENERAL INFORMATION:

APPLICANT: KNUTZON, Debbie

TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN

FILE REFERENCE: MOCO.156.00US

CURRENT APPLICATION NUMBER: US/09/330,235

CURRENT FILING DATE: 1999-06-10

PRIOR APPLICATION NUMBER: 60/089,043

PRIOR APPLICATION NUMBER: 60/089,043

PRIOR APPLICATION NUMBER: 60/089,043

PRIOR FILING DATE: 1998-06-12

NUMBER OF SEQ ID NOS: 22

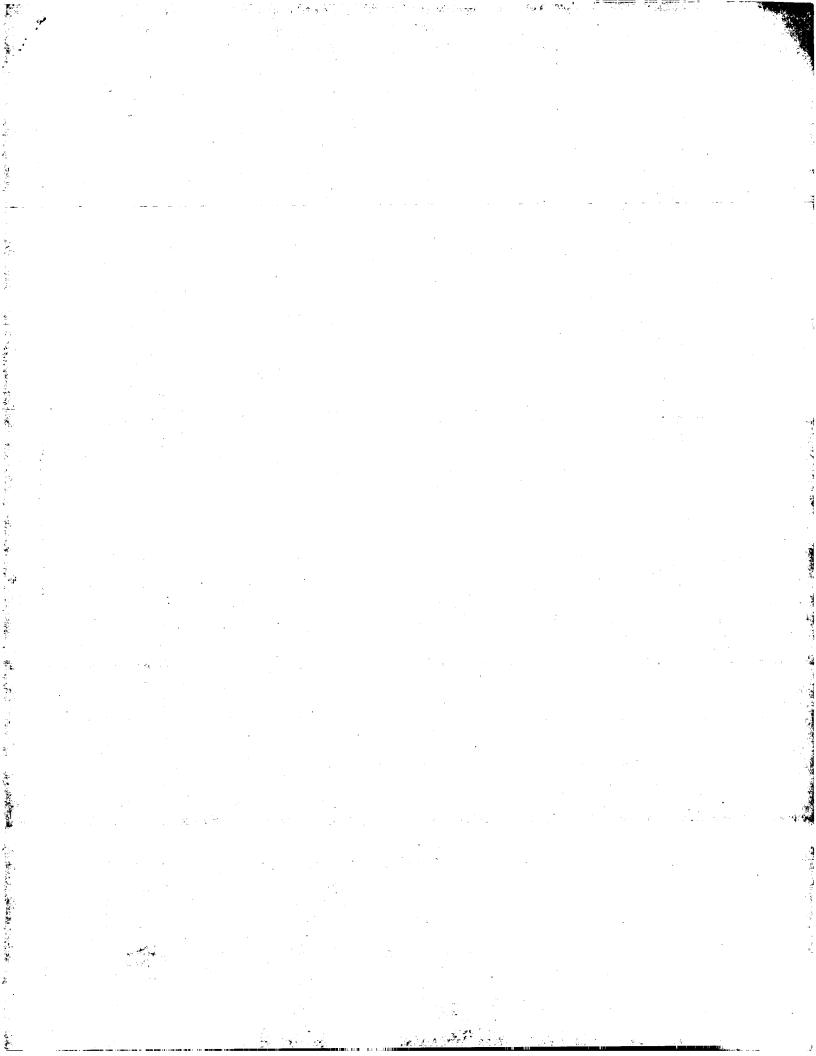
SOFTWARE: Patentin version 3.0

SEQ ID NO 18

LENGTH: 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Mortierella alpina
US-09-330-235-18
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US-09-330-235-18
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Best Local Similarity
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190 GAFLGGVCQGFSSSWWKDKHNTHHAAPNVHGEDPDIDTHPLLTWSEHALEMFSDVPDEEL
                                             179 QILSGNCLTGISIAWWKWTHNAHHIACNSLDHDPDLQHMPVFAVSS---RFFNSITSHFY 235
                                                                                                                                  126 FLIVLYGVLRC-----TSVWAHLGSGMLLGLLWMQSAYVGHDSGHYVVMTTNGFNKVA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             405 LPYRSLSFWE 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 FLIVLYGVLRC-----TSVWAHLGSGMLLGLLWMQSAYVGHDSGHYVVMTTNGFNKVA 178
                                                                                                                                                                                                                                                                         16 LNAEALNEGKKDAEAPFLMIIDNKVYDVREFVPDHPGGSVILTHV-GKDGTDVFDTFHPE
                                                                                                                                                                                                                                                                                                        11 ITSEELKGHNK--EGDLWISIQGKVYNVSDWVKEHPGGDVPISNLAGQDVTDAFIAYHPG
                                                                                                                                                                                 75 AAWETLANFYVGDIDESDRDIKNDDFAAEVRKLRTLFQSLGYYD-----SKAYYAFKVS 129
                                                                                                                                                                                                                              69 TAWSHLEKFFTG---YHLSDFKVSEVSKDYRKLASEFSKLGLFDTKGHVTSCTLASVAVM 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75 AAWETLANFYVGDIDESDRDIKNDDFAAEVRKLRTLFQSLGYYD-----SKAYYAFKVS
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                                                                                                                                                                                                                                                                                                                                                              20.5%; Score 502.5; DB 4; Length 457; 30.2%; Pred. No. 1.5e-46; vative 72; Mismatches 191; Indels 37
                                                                                                                                                                                                                                                                                                                                                                   191; Indels 37;
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                       405 LPYRSLSFWE 414
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                                                                                                                                                     250 TR----MWSREMVLNQTWFYFPILSFARLSWCLQSILFVLENGQAHKPSGARVFISLVE
                                                                                                                                                                       236 GRKLEFDFIARFLICYQHFTFYFVMCVARVNLYLQTILLLF------SRRKVQDRALN
                                                                                                    305 QLSLAMHWTWYLATMFLFIKDPVNMLVYFLVSQAVCGNLLAIVFSLNHNGMPVISKEEAV 364
VRYHTTGMIE
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Search completed: January 1, 2004, 06:38:15 Job time: 16.834 secs



Copyright

GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.

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No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                    1650
560.5
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1 MEVVEKEKKYITSEELKGHN.....RDLTNPAPKNLLWEAVNTHG
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                                                                                                                                                                                                                                                                                                                                       Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10:
12:
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67.6
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22.9
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20.5
20.5
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| (gn126/ptodata/I/pubpaa/US07_PUBCOMB.pep:*
| (gn26/ptodata/I/pubpaa/ECT_NEW_PUB.pep:*
| (gn26/ptodata/I/pubpaa/US06_NEW_PUB.pep:*
| (gn26/ptodata/I/pubpaa/US06_PUBCOMB.pep:*
| (gn26/ptodata/I/pubpaa/US06_PUBCOMB.pep:*
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| (gn26/ptodata/I/pubpaa/ECTUS_PUBCOMB.pep:*
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/ Cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
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/ Cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
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/ Cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
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/ Cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
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      US-10-340-779A-11
US-10-29-756-27
US-10-340-779A-13
US-10-369-493-4137
US-99-67-477B-8
US-09-769-863-14
US-10-264-534B-14
US-10-278-391-4
US-10-278-391-4
US-10-191-513A-11
US-10-262-617-1
US-10-262-617-1
US-10-262-617-1
US-10-262-617-3
US-10-191-513A-12
                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                   Description
Sequence 11, Appl
Sequence 27, Appl
Sequence 13, Appl
Sequence 5, Appli
Sequence 4, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 4, Appli
Sequence 11, Appl
Sequence 11, Appl
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Sequence 11, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 12, Appli
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## ALIGNMENTS

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PRIOR APPLICATION NUMBER: PCT/GB98/03895
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: UX 9814034.6
PRIOR FILING DATE: 1998-06-29
PRIOR APPLICATION NUMBER: UX 9727256.1
PRIOR FILING DATE: 1997-12-23
NUMBER OF SEQ ID NOS: 23
SOPTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11, Application US/10340779A
Publication No. US20030152983A1
GENERAL INFORMATION:
APPLICANT: Napier, Johnathan A.
APPLICANT: Michaelson, Louise
APPLICANT: Stobart, Keith
TITLE OF INVENTION: Desaturase
FILE REFERENCE: 005407.00004
CURRENT FILING DATE: 2003-03-24
PRIOR APPLICATION NUMBER: US 09/502,034
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-12-19
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                                                                                                                                                                                                                                               LENGTH: 458
TYPE: PRT
CORGANISM: Helianthus annus
US-10-340-779A-11
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US-10-340-779A-11
                                                                                                                                                                              Query Match
Best Local 9
                                                                                                                                                           Matches
                                                                                                                                                    tch 73.5%; Score 1801; DB 12; al Similarity 71.6%; Pred. No. 1.5e-174; 317; Conservative 55; Mismatches 71;
68 GTAWSHLEKFFTGYHLSDFKVSEVSKDYRKLASEFSKLGLFDTKGHVTSCTLASVAVMFL 127
                                                                 Indels 0;
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0,

Indels

4.

Gaps

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SEQUENCE DESCRIPTION: SEQ ID NO: US-10-029-756-27
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Sequence 27, Application US/10029756
; Publication No. US20020108147A1
; GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S
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  Query Match
                                                                                                                                                         NAME: Presser_Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 8383ZYXWVU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEY 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/934,254
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/029,756
FILING DATE: 21-Dec-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Thomas, Terry L.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINGLENIC ACID BY A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FVSYQHYLYYPIMCVARVNLYLQTILLISKRKIPDRGLNILGTLIFWTWFPLLVSRLPN 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IVLYGVLRCTSVWAHLGSGMLLGLLWMQSAYVGHDSGHYVVMTTNGFNKVAQILSGNCLT 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPERVAFVLVSFCVTGIQHIQFTLNHFSGDVYVGPPKGDNWFEKQTRGTIDIACSSWMDW
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                                                                                                                        LENGTH: 452 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: New York
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                                                                                               TOPOLOGY: linear
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  69.9%;
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  Score 1712;
                                                            27:
  DB 14;
  Length 452;
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                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13, Application US/10340779A Publication No. US20030152983A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 69.6 Matches 311; Conservative
                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: PCT/GB98/03895
PRIOR TILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: UK 9814034.6
PRIOR FILING DATE: 1998-06-29
PRIOR APPLICATION NUMBER: UK 9727256.1
PRIOR FILING DATE: 1997-12-23
NUMBER OF SEQ ID NOS: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 005407.00004
CURRENT APPLICATION NUMBER: US/10/340,779A
CURRENT FILING DATE: 2003-03-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Napier, Johnathan A APPLICANT: Michaelson, Louise
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 09/582,034 PRIOR FILING DATE: 2000-12-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Stobart, Keith TITLE OF INVENTION: Desaturase
                                                                                                                                                                                                           LENGTH: 448
TYPE: PRT
ORGANISM: Borago officinalis
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                                       KKYITSEELKGHNKEGDLMISIQGKVYNVSDWVKEHPGGDVPISNLAGQDVTDAFIAYHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAVOARDLNSAPCPKKLGYGEAYNTHG 452
  GTAWSHLEKFFTGYHLSDFKVSEVSKDYRKLASEFSKLGLFDTKGHVTSCTLASVAVMFL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AALQARDLTN-PAPKNILW-EAVNTHG 450
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                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                      for Windows Version
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                                                                                                                    67.6%; Score 1655; DB 12; 63.4%; Pred. No. 1.1e-159; tive 78; Mismatches 84;
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4; Mismatches 78;
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425

366

305

245

185

365

Length Indels

448; 0

Gaps

Gaps

0

65

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TOPOLOGY: linear
HOLECULE TYPE: Protein
SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-029-756-5
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Publication No. US20020108147A1
GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
TITLE OF INVENTION: PRODUCTION OF GAMMA
                                                                                                                             TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: U9/10/029,756

FILING DATE: 21-Dec-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/934,254
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Mur.
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
                                                                                                                                                                                                           REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 83
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GISIAWWKWTHNAHHIACNSLDHDPDLQHMPVFAVSSRFFNSITSHFYGRKLEFDFIARF 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MSVYGVLFCEGVLVHLFSGCLMGFLWIQSGWIGHDAGHYMVVSDSRLNKFMGIFAANCLS 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 448 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                NAME: Presser, Leopold
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                                                                                                                                                                                                                                                  ; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 4137
; LENGTH: 366
; TYPE PRT
; ORGANISM: Neurospora crassa
US-10-369-493-4137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-369-493-4137; Sequence 4137, Application US/10369493; Publication No. US20030233675A1
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Best Local Similarity
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Best Local 9
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
CURRENT FILING DATE: 2003-02-28
                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/360,039 PRIOR FILING DATE: 2,002-02-21
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                                         148 LIGILWMQSAYVGHDSGHYVVMTTNGFNKVAQILSGNCLTGISIAWWKWTHNAHHIACNS 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 306 WGERIMFVIASLSVIGMQQVQFSLNHFSSSVXVGKPKGNNWFEKQIDGILDISCPPWNDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246 FVSYQHWTFYPIMCAARLNMYVQSLIMLLTKRNVSYRAQELLGCLVFSIWYPLLVSCLPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             188 GISIAWWKWTHNAHHIACNSLDHDPDLQHMPVFAVSSRFFNSITSHFYGRKLEFDFIARF 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 MSVYGVLFCEGVLVHLFSGCLMGFLWIQSGWIGHDAGHYMVVSDSRLNKFMGIFAANCLS
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56 CLGSFWHQLVFTAHDAGHMGITHHFHVDTVIGIIIADFIGGLSLGWWKRNHNVHHIITNS
                                                                                                                           91 VSKDYRKLASEFSKLGLFDTKGHVTSCTLASVAV---MFLIVLYGVLRCTSVWAHLGSGM 147
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63.2%; Pred. No. 3.6e-159;
tive 78; Mismatches 85;
                                                                                                                                                                61;
                                                                                                                                                                                        Score 560.5; DB 1
Pred. No. 2.6e-48;
                                                                                                                                                                  Mismatches 148;
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427

365 367 305 307 245 185

425

23;

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CURRENT APPLICATION NUMBER: US/09/967,477B
CURRENT FILING DATE: 2002-04-16
PRIOR APPLICATION NUMBER: 60/236,303
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 60/297,562
PRIOR FILING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
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US-09-967-477B-8
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Best Local Similarity
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APPLICANT: Haiping Hong
TITLE OF INVENTION: FAD4, FAD5, FAD5-2, AND FAD6, NOVEL
TITLE OF INVENTION: FATTY ACID DESATURASE FAMILY MEMBERS AND
FILE REFERENCE: BNZ-001
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                                                             HIQFCLNHFAANVYVGPPSGNDWFEKQTSGTLDISCASSMDWFFGGLQFQLEHHLFPRLP 385
                                                                                                                                                                                                                         LOHMPVFAVSSRFFNSITSHFYGRKLEFDFIARFLICYOHFTFYPVMCVARVNLYLOTIL
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                       ALVESIGHNGMSVYERETKPDFW-QLQVTTTRNIRASVFMDWFTGGLNYQIDHHLFPLVP
                                                                                                                                           LLFSR-----RKVQDRALNIMGILVFWTW-FPLLVSCLPNWPERVMFVLASFAVCS-IQ 325
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                                                                                                                                                                                 IDTMPLLAWSKEMARKAFESAHG------PFFIRNQAFLYFPLLLLARLSWLAQSFF
                                                                                                                                                                                                                                                                    HDFLHNQVCENRTLGNLIGCLVGNAWQGFSVQWWKNKHNLHHAVPNLHSAKDEGFIGDPD
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APPLICANT: Pereira, Suzette L.
FITTLE OF INVENTION: DESATURASE GENES AND USES THE
FILE REFERENCE: 6763.US.O1
CURRENT FILING DATE: 2001-01-25
CURRENT FILING DATE: 2001-01-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 453
TYPE: PRT
ORGANISM: Saprolegnia diclina
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                                                           US-10-054-534B-14
US-10-054-534B-14
; Sequence 14, Application US/10054534B
; Publication No. US20030167525A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
APPLICANT: Abbott Laboratories APPLICANT: Mukerji, Pradip APPLICANT: Huang, Yung-Sheng
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Huang, Yung-Sheng
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; TYPE: PRT
; ORGANISM: Saprolegnia diclina
US-10-054-534B-14
APPLICANT: Thurmond, Jennifer
APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: DESATURASE GENES AND USES THI
FILE REFERENCE: 6763.US.01
CURRENT APPLICATION NUMBER: US/10/431,952
CURRENT FILLING DATE: 2003-05-08
PRIOR APPLICATION NUMBER: US/09/769,863
PRIOR APPLICATION NUMBER: US/09/769,863
PRIOR APPLICATION OF SEQ 01-01-25
NUMBER OF SEQ 1D NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: US 09/769,863
PRIOR FILING DATE: 2001-01-25
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                       APPLICANT: Mukerji, Pradip
APPLICANT: Huang, Yung-Sheng
APPLICANT: Das, Tapas
                                                                                                                                                                                                                           APPLICANT: Abbott Laboratories APPLICANT: Mukerji, Pradip
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TITLE OF INVENTION: DESATURASE GENES AND
FILE REFERENCE: 6763.US.P1
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Pred. No. 1.2e-43;
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US-10-278-391-4
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; ORGANISM: Saprolegnia diclina
US-10-431-952-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/10278391 Publication No. US20030159164A1 GENERAL INFORMATION:
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Best Local Similarity
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           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,391
FILING DATE: 23-Oct-2002
                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LI
STREET: 220 MONTGOMERY STREET,
                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                         CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NHFAANVYVGPPSGNDWFEKQTSGTLDISCASSMDWFFGGLQFQLEHHLFPRLPRCQLRK 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGGTFDKVQYPLLERAGLLLYYGWNLGLVYAANMSLLQAAAFLFVSQASCGLFLAMVFSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AWSLK----MAQHAVDSP-----VGLFFMRYQAYLYFPILLFARISWVIQSAMYAFYNVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YDSSKLYYLYKCASTLSIALVSAAICLHFDSTAMYMVAAVILGLFYQQCGWLAHDFLHHQ 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FHPSSALKLLEQYYVGDVDQSTAAVDTSISD----EVKKSQSDFIASYRKLRLEVKRLGL
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     CLASSIFICATION: 800
                                                                                                                                                                    ZIP: 94104
                                                                                                                                                                                         COUNTRY: UNITED STATES
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                                                                                                                                                                                                                                                                                                                                          INVENTION: COMPOSITIONS
SYNTHESIS OF
                                                                                                                                                                                                                                                                                                                                                                                     KELDER, BRUCE
HUANG, YUNG-SHENG
KIRCHNER, STEPHEN J
                                                                                                                                                                                                                                                                                                                                                                                                                                         KOPCHIK, JOHN J.
KELDER, BRUCE
                                                                                                                                                                                                                                                                                                                                                                                 MUKERJI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21.1%; Score 516; DB 12; 29.0%; Pred. No. 1.2e-43;
                                                                                                                                                                                                                                                                                                                                                                                 PRADIP
                                                                                                                                                                                                                                                                                                                        PRODUCTS
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                                                                                                                                                                                           AMERICA
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                                                                                                                                                                                                                                                                   LLP
                                                                                                                                                                                                                                                 SUITE 2200
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                                                                           #1.30
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Sequence 11, Application US/10191513A

Publication No. US20030104596A1

GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pardip
APPLICANT: Heonard, Amanda E.
APPLICANT: Huang, Yung-Sheng
APPLICANT: Tapas, Das
FILLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
FILE REFERENCE: 6295.US.D3

CURRENT APPLICATION NUMBER: US/10/191,513A

CURRENT FILING DATE: 2002-09-25
PRIOR APPLICATION DATE: 1999-01-08
                                                                                                                                                                                                                                                                                                                                                             RESULT 11
US-10-191-513A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-278-391-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: No. US20030159164A1 Relevant
TOPOLOGY: No. US20030159164A1 Relevant
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/087,578
FILING DATE: 29-MAY-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    346 N-DWFEKQTSGTLDISCASSMDWFFGGLQFQLEHHLFPRLPRCQLRKISPLVSDLCKKHN 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        288 IMGILVFWTWFPLLVSCLPNWP-ERVMFVLASFAVC-SIQHIQFCLNHFAANVYVGPPSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 GRKLEFDFIARFLICYQHFTFYPVMCVARVNLYLQTILLLF-----SRRKVQDRALN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190 GAFLGGVCQGFSSSWWKDKHNTHHAAPNVHGEDPDIDTHPLLTWSEHALEMFSDVPDEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 LNAEALNEGKKDAEAPFLMIIDNKVYDVREFVPDHPGGSVILTHV-GKDGTDVFDTFHPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75 AAWETLANFYVGDIDESDRDIKNDDFAAEVRKLRTLFQSLGYYD-----SSKAYYAFKVS 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 TAWSHLEKFFTG---YHLSDFKVSEVSKDYRKLASEFSKLGLFDTKGHVTSCTLASVAVM 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 ITSEELKGHNK--EGDLWISIQGKVYNVSDWVKEHPGGDVPISNLAGQDVTDAFIAYHPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LPYRSLSFWE 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QILSGNCLTGISIAWWKWTHNAHHIACNSLDHDPDLQHMPVFAVSS---RFFNSITSHFY
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REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OHU-03348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VRYHTTGMIE 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DMDFFTKQIITGRDVHPGLFANWFTGGLNYQIEHHLFPSMPRHNFSKIQPAVETLCKKYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QLSLAMHWTWYLATMFLFIKDPVNMLVYFLVSQAVCGNLLAIVFSLNHNGMPVISKEEAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TR-----MWSRFMVLNQTWFYFPILSFARLSWCLQSILFVLPNGQAHKPSGARVPISLVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72; Mismatches 191; Indels
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Pred. No. 2.9e-42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37;
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; ORGANISM: Homo sapiens
; FEATURE:
; NAMB/KEY: VARIANT
; LOCATION: (458) . . . (458)
; OTHER INFORMATION: Xaa = Unknown or other at position 458
US-10-191-513A-11
APPLICANT: Huang, Yung-Sheng
APPLICANT: Tapas, Das
APPLICANT: Tapas, Das
TITLE OF INVENTION: HUMAN DESATURASE GENE AND USI
FILE REFERENCE: 6295.US.D3
CURRENT APPLICATION NUMBER: US/10/191,513A
CURRENT FILING DATE: 2002-09-25
PRIOR APPLICATION NUMBER: US 09/227,613
PRIOR FILING DATE: 1999-01-08
PRIOR FILING DATE: 1999-01-08
PRIOR APPLICATION NUMBER: US 08/833,610
PRIOR APPLICATION NUMBER: US 08/833,610
PRIOR APPLICATION NUMBER: US 08/833,610
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US-10-191-513A-41
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PRIOR FILING DATE: 1998-04-10
PRIOR APPLICATION NUMBER: US 08/833,610
PRIOR APPLICATION NUMBER: US 08/833,610
PRIOR FILING DATE: 1997-04-11
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 41, Application US/10191513A Publication No. US20030104596A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                     APPLICANT: Abbott Laboratories APPLICANT: Mukerji, Pardip
                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH: 458
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Local Similarity 30.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 TAWSHLEKFFTG---YHLSDFKVSEVSKDYRKLASBFSKLGLFDTKGHVTSCTLASVAVM 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 INAEALNEGKKDAEAPFLMIIDNKVYDVREFVPDHPGGSVILTHV-GKDGTDVFDTFHPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PNICIWGLSTVIVAKWGQTSTLANVLSAALLGLFWQQCGWLAHDFLHHQVFQDRFWGDLF 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VRYHTTGMIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QLSLAMHWTWYLATMFLFIKDPVNMLVYFLVSQAVCGNLLAIVFSLNHNGMPVISKEEAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAFLGGVCQGFSSSWWKDKHNTHHAAPNVHGEDPDIDTHPLLTWSEHALEMFSDVPDEEL 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DMDFFTKQIITGRDVHPGLFANWFTGGLNYQIEHHLFPSMPRHNFSKIQPAVETLCKKYN
                                                                                                                                                                                                                                                                                                              Mukerji, Pardip
Leonard, Amanda E.
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Pred. No. 2.9e-42;
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Sequence 1, Application US/10262617
Publication No. US20030077747A1
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
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; NAME/KEY: VARIANT
; LOCATION: (458)...(458)
; OTHER INFORMATION: Xaa = Unknown or other at position
US-10-191-513A-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 41
                                                                                                                                    NUMBER OF SEQ ID NOS: 4
SOFTWARE: PERL Program
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                 APPLICAMY: Shah, PUIVI
APPLICAMY: Shah, PUIVI
TITLE OF INVENTION: DELTA-6 DESATURASE HOMOLOGS
FILE REFERENCE: PF-0494-1 DIV
CURRENT APPLICATION NUMBER: US/10/262,617
CURRENT FILING DATE: 2002-09-30
FRIOR APPLICATION NUMBER: 09/048,888
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20030077747A1 2451043CD1
                                                                                            LENGTH: 445
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                     ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75 AAWETLANFYVGDIDESDRDIKNDDFAAEVRKLRTLFQSLGYYD-----SSKAYYAFKVS 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRKLEFDFIARFLICYQHFTFYPVMCVARVNLYLQTILLLF-----SRRKVQDRALN 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QILSGNCLTGISIAWWKWTHNAHHIACNSLDHDPDLQHMPVFAVSS---RFFNSITSHFY 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FLIVLYGVLRC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAWSHLEKFFTG---YHLSDFKVSEVSKDYRKLASEFSKLGLFDTKGHVTSCTLASVAVM 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LNAEALNEGKKDAEAPFLMIIDNKVYDVREFVPDHPGGSVILTHV-GKDGTDVFDTFHPE 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ITSEELKGHNK--EGDLWISIQGKVYNVSDWVKEHPGGDVPISNLAGQDVTDAFIAYHPG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VRYHTTGMIE 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LPYRSLSFWE 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DMDFFTKQIITGRDVHPGLFANWFTGGLNYQIEHHLFPSMPRHNFSKIQPAVETLCKKYN 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QLSLAMHWTWYLATMFLFIKDPVNMLVYFLVSQAVCGNLLAIVFSLNHNGMPVISKEBAV 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMGILVFWTWFPLLVSCLPNWP-ERVMFVLASFAVC-SIQHIQFCLNHFAANVYVGPPSG 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TR-----MWSRFMVLNQTWFYFPILSFARLSWCLQSILFVLPNGQAHKPSGARVPISLVE 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAFLGGVCQGFSSSWWKDKHNTHHAAPNVHGEDPDIDTHPLLTWSEHALEMFSDVPDEEL 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FNLCIWGLSTVIVAKWGQTSTLANVLSAALLGLFWQQCGWLAHDFLHHQVFQDRFWGDLF 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 502.5; DB 15;
Pred. No. 2.9e-42;
2; Mismatches 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 15; Length 458;
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유정

18 RYFTWDEVAQRSGCEERWLVIDRKVYNISEFTRRHPGGSRVISHYAGQDATDPFVAFHIN

9 KYITSEELKGHNKEGDLWISIQGKVYNVSDWVKEHPGGDVPISNLAGQDVTDAFIAYH---

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TITLE OF INVENTION: DEUTA-6 DESATURASE HOMOLOGS
FILE REFERENCE: PF-0494-1 DIV
CURRENT APPLICATION NUMBER: US/10/262,617
CURRENT FILLING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: 09/048,888
PRIOR APPLICATION NUMBER: 09/048,888
PRIOR FILING DATE: 1998-03-26
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Best Local S
Matches 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/10262617 Publication No. US20030077747A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
                                                                                                                                                                                                               ORGANISM: Homo sapiens
FEATURE:
FANME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20030077747A1 2056310CD1
                                             Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 BELKGHNKEGDLWISIQGKVYNVSDWVKEHPGGDVPISNLAGQDVTDAFIAYHPGTAWSH 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --IGHEKHRDWVSSQLAATCNVEPSLFTNWFSGHLNFQIEHHLFPRMPRHNYSRVAPLVK 405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A---MEVLAWLLIYLLGPGWVPSALA----AFILAISQAQSWCLQHDLGHASIFKKSWWN 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCTLASVAVMFLIVLYGVLRCTSVWAHLGSGMLLGLLWMQSAYVGHDSGHYVVMTTNGFN 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEKFFTGYHLSDFKVSEVS-----KDYRKLASEFSKLGLFDTK-----GHVT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQIRAHDQPGDKWLVIERRVYDISRWAQRHPGGSRLIGHHGAEDATDAFRAFHQDL--NF 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MLVCMQWADLLWAASFYARFFLSYLPFYGVPGVLLFFVAVRVLESHWFVWITQMNHIPKE
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17.5%; Score 429; DB 15; 28.3%; Pred. No. 8.7e-35; tive 68; Mismatches 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.8%; Score 436; DB 15; 28.4%; Pred. No. 1.7e-35;
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                                                                                 Length 444;
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FILE REFERENCE: 6295.US.D3
CURRENT APPLICATION NUMBER: US/10/191,513A
CURRENT FILING DATE: 2002-09-25
PRIOR APPLICATION NUMBER: US 09/227,613
PRIOR PILING DATE: 1999-01-08
PRIOR PILING DATE: 1999-01-08
PRIOR FILING DATE: 1998-04-10
PRIOR APPLICATION NUMBER: PCT/US98/07422
PRIOR FILING DATE: 1998-04-10
PRIOR APPLICATION NUMBER: US 08/833,610
PRIOR APPLICATION NUMBER: US 08/833,610
PRIOR PILING DATE: 1997-04-11
NUMBER OF SEQ ID NOS: 54
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 444
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Best Local Similarity
Matches 123; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pardip
APPLICANT: Leonard, Amanda E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Huang, Yung-Sheng
APPLICANT: Tapas, Das
TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
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                                                                                                                                                                                                                                                              17.4%; Score 425; DB 15; Length 444; al Similarity 27.3%; Pred. No. 2.2e-34; 1ndels 7
                                      121 SVAVMFLIVLYGVLRC------TSVWAHLGSGMLLGLLWMQSAYVGHDSGHYVV 168
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                                                                                                                                67 PGTAWSHLEKFFTGY-----HLSDFKVSEVSKDYRKLASEFSKLGLFDTKGHVTSCTLA 120
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ANHVFFLLYLLHILLLDGAAWLTLWVFGTSFLPFLLCAVLLSAVQAQAGWLQHDFGHLSV 186
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                                                                                                                                                                                                                         287 NI-MGILVFWTWFPLL------VSCL-PNWPERVMFVLASFAVCSIQHIQFCLNH 333
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                                                                                                                   FAANVYVGPPSGNDWFEKQTSGTLDISCASSMDWFFGGLQFQLEHHLFPRLPRCQLRKIS 393
                                         PLVSDLCKKHNLPYRSLSFWEANQWTIRTLR 424
                                                                                                                                                                                                                                                                     VELGKOKKKYMPYN-----HOHKYFFLIGPPALLPLYFOWYIFYFVIORKKWVDLAW 298
                                                                                                                                                                                                                                                                                                            SITSHFYGRKLEFDFIARFLICYOHFTFYPVMCVARVNLYLQTILLLF--SRRKVQDRAL 286
PLVQSLCAKRGIEYQSKPLLSAFADIIHSLK 431
                                                                                       -----DRNMDWVSTQLLATCNVHKSAFNDWFSGHLNFQIEHHLFPTMPRHNYHKVA 400
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Search completed: January 1, 2004, 06:58:37 Job time: 86.7267 secs

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Minimum
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1 (bases 1 to 1788) Delhaize, E., Hebb, D.M., Gardner, R.C. and Richards, K.D. Aluminum tolerance in yeast conferred by over-expression of wheat	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticeae; Triticum.	Triticum aestivum	Triticum aestivum (bread wheat)		AF031194.1 GI:4104055	AF031194	Triticum aestivum S276 (S276) mRNA, complete cds.	AF031194 1788 bp mRNA linear PLN 29-JAN-1999		-

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Delhaize,E., Hebb,D.M.,
Direct Submission
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ASFVITGIQHVQFCLNHFSSAVYVGPPKGNDWFERQTAGTLDIKCSPWMDWFHGGLQF
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Direct Submission

AL Submitted (23-UUL-2002) Takuji Sasaki, National Institute of
Agrobiological Sciences, Rice Genome Research Program; Kannondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan

(E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7469.

The nucleotide sequence of this BAC clone was generated by
combining Monsanto and RGP-Japan sequencing data.

NOTE: It currently consists of 1 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces is believed
to be correct as given, however the sizes of the gaps between them
are based on estimates that have provided by the submitter. This
sequence will be replaced by the finished sequence as soon as it is
available and the accession number will be preserved.

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Oryza satīva (japonica cultivar-group)
Oryza satīva (japonica cultivar-group)
Oryza satīva (japonica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Oryza sativa (japonica cultivar-group)
OJ1118 Al0, *** SEQUENCING IN PROGRESS
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                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                  /organism="Oryza sativa (
/mol_type="genomic DNA"
/culTivar="Nipponbare"
/db xref="taxon:39947"
/chromosome="9"
                                                                                                                                                                                                                                                                                                                            /clone="OJ1118_A10"
21050 c 21390 g
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                                                                                                                                                                          Direct Submission
Submitted (10-FEB-2003) Crop Performance & Improvement, Submitted (10-FEB-2003) Crop Performance & Improvement, Research Station, Long Ashton, Bristol BS41 9AF, UK
Location/Qualifiers
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Primula farinosa sphingolipid
                                                                                                                                                                                                                                           2 (bases 1 to 1681)
Sayanova, O.V., Beaudoin, F.,
Napier, J.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Primula farinosa
Primula farinosa
                                                                                                                                                                                                                                                                                                                 substrate preferences(1) FEBS Lett. 542 (1-3), 10
                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; Ericales; Primulaceae; Primulaceae; Primulaceae; Dases 1 to 1681)
                                                                                                                                                                                                                                                                                                                                            Identification of Primula fatty acid
                                                                                                                                                                                                                                                                                                                                                            Napier,J.A.
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                                          /codom_start=1
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/protein_id="AAP23033.1"
/db_xref="GI:30350275"
                                                                                                                                                        organism="Primula farinosa"
                                                                                                 note="cytochrome b5 fusion desaturase"
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1 delta-8 desaturase mRNA, complete
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Similarity
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AAATCCCACACCACCTGCTTCACGTTCGTCGCCATGGTAGTCTTGTTCTTCCTCAGCCT
                                                                                            ACCTCCTCCGACTACCGCAAACTCCTCCACAACTTCCATAAACTCGACCTTTTCCAGACC
                                                                                                                                                                                           GCCCGTCTCCTCCTCTCTCCGCCAACCTCCTTCTAGAACACTACTCCGTCTCCCCC
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                                          CGTCGGCACACCCCCAAGTTCCTGCTCGTCGCAAAGTCNGTGCTCTTCTGCATCGGCCT
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MPPFVVSSKFENSLTSRFYDRKLINPDGYSRL
LFSSRKVPDRVQBIFGIGVFWWYBYDLVSCLPLWGGRIMFVVAASFSVFNGIQHVQFCHL
LFSSRKVPDRVQBIFGIGVFWWYBLLVSCLPLWGGERIMFVVAASFSVFGIQHVQFCHL
HFSAEVYLGPPEGNDWFEKQTAGTLNISCHSWNDWFHGGLQFQIEHHLFPRLPRSQLR
KCVSPFVRDLCKKGNNLPYNVTSFTMANVLTLKTLRNAAIQARDLSNPTFKNLVWEAVNT
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1385 Primula vialii sphingolipid d AY234126 Primula vialii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicottyledons; core eudicots;
Asteridae; Ericales; Primulaceae; Primula.

1 (bases 1 to 1385)
Sayanova,O.V., Beaudoin,F., Michaelson,L.V., Shewry,P.R. and Submitted (10-FEB-2003) Crop Performance Research Station, Long Ashton, Bristol BS Sayanova, O.V., substrate preferences(1) FEBS Lett. 542 (1-3), 10 Napier, J.A. Identification of Primula fatty acid Napier, J.A. Primula vialii (bases 1 to 1385) Submission Location/Qualifiers
1. .1385 /note="cytochrome b5 fusion desaturase" /codon_start=1 /product="sphingolipid delta-8 desatura GI:30350278 . 1385 Beaudoin, F., 100-104 35 bp m 1 delta-8 Michaelson, L.V., (2003)Bristol BS41 9AF, UK mRNA linear desaturase mRNA, Delta(6)-desaturases linear Shewry, P.R. PLN 04-MAY-2003 complete cds. Long and with n-3

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REFERENCE
AUTHORS
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Direct Submission
Submitted (10-FEB-2003) Crop Performance & Improvement,
Research Station, Long Ashton, Bristol BS41 9AF, UK
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                         Napier, J.A.
                                                                                                                                                                                                                                                                                         substrate preferences(1)
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HPGGSAPLMALAGHDVTDAFLAYHPBSTRALLPPLSTRULLQNHSVSPTSSDYRKLH
NPHKIGLFOYTGHTTVTFVANVALFFLSLYVEVFCSDSAWHLAGSGVMGVAMIQSGW
LGHDSGHYQIMSSRKTNRFAQVLSGNCLAGISIAWKWNHNAHHLACNSLDYDDDLQH
MPFFVVSSKFFGSLTSRFYDRKLRFDSVSRFLVSYQHWSFYFVMCLARINLFAQSFML
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HFSARVYLGPDEGNDWFEKQTAGTLNISCPSWMDWFHGGLQFQLEHHLFPRLPRSQLR
HFSARVYLGPDEGNUWFEKQTAGTLNISCPSWMGERIMFVVASFRVTGIQHVQFCUNT
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Beaudoin, F.,
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                                                                                                                                                                                                                                                                                                100-104 (2003)
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                                                                                                                                                     Michaelson, L.V.,
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AR200409
                                                                            Production of gamma linolenic acid by a Patent: US 6359861-A 26 12-MAR-2002; Coation/Qualifiers
1. 1702
                                                                                                                                                                                           Thomas, T.L.
                                                                                                                                                                                                                                              Unclassified
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                      /organism="unknown"
471 c 446 g
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RKISPFVRDLCKKHNLPYNIASFTKANVLTLKTLRNTAIEARDLSNPTPKNMVWEAVH
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/db_xref="taxon:175103"
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/product="fatty acid delta-6 desaturase"
join(36. .522,744. .1618)
/note="cytochrome_b5 fusion desaturase; has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Primula vialii"
/mol_type="genomic DNA"
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Primula farinosa fatty acid
                                                                                                                                                                                                                                                                                                                                                                                          Submitted (10-FEB-2003)
                                                                                                                                                                                                                                                                                                                                                                                                                       Sayanova,O.V., Beaudoin,F., Michaelson,L.V., Napier,J.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identification of Primula fatty acid
substrate preferences(1)
FEBS Lett. 542 (1-3), 100-104 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 1410)
Sayanova,O.V., Beaudoin,F., Michaelson,L.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; Ericales; Primulaceae; Primula.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primula
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                                                  YIPLLVVSPKFFNSLTSRFYDKKLNFDGVSRFLVCYQHWTFYPVMCVARLNMLAQSFI
TLFSSREVCHRAQEVFGLAVFWVWFPLLLSCLPNWGERIMFLLASYSVTGIQHVQFSL
NHFSSDVYVGPPVGNDWFKKQTAGTLNISCPAMMDWFHGGLQFQVEHHLFPRMPRGQF
                                                                                               /tränslation="MANKSPPNPKTGYITSSDLKSHNKAGDLMISIHGQVYDVSSWAA
LHPGGTAPLWALAGHDVTDAFLAYHPBSTARLLPBLSTYLLLCHSVGYBYSVSPTSSDYRKLL
DNFHKHGLFRARGHTAYATFVFMIAWELMSVTGVULGBDSAWYHLASGGAMGFANIOCD
WIGHDSGHYRIMSDRKWNWFAQILSTNCLQGISIGWWKWNHNAHHIACNSLDYDPDLQ
                                                                                                                                                                                                                                                                                                                                                                       Station, Long
                               RKISPFVRDLCKKHNLPYNIASFTKANVFTLKTLRNTAIEARDLSNPLPKNMVWEALK
                                                                                                                                                                /product="fatty acid delta-6 desaturase"
/protein_id="AAP23034.1"
/db_xref="GI:30350277"
                                                                                                                                                                                                                                                                                                                                                   Station, Long Ashton,
Location/Qualifiers
                                                                                                                                                                                                                                    for n-3 fatty acid
                                                                                                                                                                                                                                                                                                                      organism="Primula farinosa"
                                                                                                                                                                                                                                                    note="cytochrome b5 fusion desaturase;
                                                                                                                                                                                                                                                                                     db_xref="taxon:133892"
                                                                                                                                                                                                                      codon_start=1
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62.3%;
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n, Bristol BS41 9AF, UK
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AUTHORS
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KEYWORDS
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Sequence split into 10 fragments
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Best Local S
Matches 179
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RN52A06_04
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RN52A06_07
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Rattus norvegicus
Eukaryota; Metazoa; Chordata;
Eukaryota; Mutheria; Rodentia;
                                                                                                                                                                Submitted (23-MAY-2003) GBF, Dept. of Genome Analysis, Mascheroder Weg 1, D-38124 Braunschweig, Germany, E-mail: info.genome@gbf.de All annotations in this database entry are developed by computational tools. It is therefore not explicitly noted in the feature lines that evidence is not experimental.
Sequencing vector: ###;
Chemistry: Dye-terminator-amersham:
                                                                                              Web site: http://genome.gbf.de/
Contact: info.genome@gbf.de
                                                                                                                                 Center: GBF, Braunschweig
Center code: GBF
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Schoen, O., Conrad, A., H
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HTG; HTGS_PHASE1; HTGS_I
                                                Center project name:
Center clone name: RP32-52A06
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Best Local S
Matches 178
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TITLE
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136 AAGGCAAAGTCTACGACGTCTCCCACTGGGTCAAATCCCATCCCGGAGGCGAAGCAGCGA 195
                                                                                                                                 Brassica napus (rape)
Brassica napus (rape)
Brassica napus
Brassica napus
Brassica napus
Brassica napus
Brassica napus
Embryophyta; Tracheo
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                        Brassica napus mRNA for
AJ224160
AJ224160.1 GI:3819707
delta-8 sphingolipid des
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Sphingolipid-desaturase
Patent: WO 0000593-A 1 06-JAN-2000;
ZAEHRINGER ULRICH (DE); HEINZ ERNST (DE);
                                                                                Sperling, P.,
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sphingolipid desaturase from higher plant
ew cytochrome b5 fusion protein
. Biol. Chem. 273 (44), 28590-28596 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGATCTCCACCAAGGAGCTGCAGGCGCCACGCCGCGGACGACCTCTGGATCTCCATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCGCCTCCGCCGACTTCCGCCGCCCTCCTCGCGCAGCTCTCCTCCGCGGGCCTCTTCGA 496
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llarity 59.7%;
Conservative
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ADVYTGPPNGNDWFEKQTAGTLDISCRSYMDWFFGGLQFQLEHHLFPRLPRCHLRGVS
PVVQELCKKHNLPYRSLSWWEANVWTLRTLRKAAVQARDVTNPVLENLLWEALNTHG"
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/db_xref="GI:9995106"
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mol_type="genomic DNA"
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                                                                                Zahringer, U. and Heinz, B
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Pred. No. 0.024;
0; Mismatches 117;
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TITLE
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                             202 TGATCTCCACCAAGGAGCTGCAGGCGCACGCCGCCGGACGACCTCTGGATCTCCATCT 261
AC084799 303091 bp Mus musculus chromosome 16 clone SEQUENCE, 101 unordered pieces. AC084799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (13-FEB-1998) Sperling P., Physiologie, Institut fuer Aligemeine Botanik der Universitaet Hamburg, Ohnhorststrasse 18, D-22609 Hamburg, GERMANY Related sequence: X87143.
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                       AAGGCAAAGTCTACGACGTCTCCCACTGGGTCAAATCCCCATCCCGGAGGCGAAGCAGCGA 195
                                                                                                                                           ACGTGTCGCGTGACTACCGTCGTTTAGCCGCGGAGTTTTCCAAACGCGGACTCTTCGA 373
                                                                                                                                                                        CCGTGCGCCCCCTCCCCCCCCTTCTTCGTCGGCCGCCTCACCGACTACACTGTCCCCC 438
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/product="delta-8 sphingolipid desaturase"
/protein_id="CaAl1857.1"
/protein_id="CaAl1857.1"
/db_xref="GI:3819708"
/db_xref="GI:3819708"
/db_xref="SFTREMBL:09ZRP8"
/db_xref="SFTREMBL:09ZRP8"
/translation="MSEQTKKRFITSDDLKKHNOPGDLWISIQGKVYDVSHWVKSHPG
CERAILMILAGDVYDLAFIAYHPGTAWRHLENLHINGHYWCHHYBOVSRDYRLLAAEFS
KRGLFDKKGHYTLYTLTCVAAMLAAVUYGVACTSIMAHLISAVLLGLLHODDLQHIPV
LAVSNKFFKSMTSRFYGRKLTSDDLARFLISYQHWSFYPIMCYRINLFIQTLLHFS
LAVSNKFFKSMTSRFYGRKLTSDDLARFLISYQHWSFYPIMCYRINLFIQTLLHFS
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/gene="sld1"
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51. .1400
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ADVYTGPPNGNDWFEKQTAGTLDISCRSYMDWFFGGLQFQLEHHLFPRLPRCHLRGVS
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Consensus quality: 152568 bases at least Q40
Consensus quality: 175579 bases at least Q30
Consensus quality: 186949 bases at least Q20
Consensus quality: 186949 bases at least Q20
Estimated insert size: 198300; agarose-fp estimation
Estimated insert size: 293091; sum-of-contigs estimation
Quality coverage: 4.85 in Q20 bases; agarose-fp estimation
Quality coverage: 3.88 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 101 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (17-NOV-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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Center Project Name: 0
Center clone name: RPCI-23_197M9
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Mus musculus (house mouse)
Mus musculus
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DOE Joint Genome Institute.
Sequencing of Human Chromosome
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HTG; HTGS_PHASE1; HTGS 1
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Mammalia; Eutheria; Rodentia;
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                                                                                                          136
                                                     94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage : CP 5706 91057 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
The cDNA library to be analyzed within the framework of this project was created using a Botrytis cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal situation for B. cinerea during its development on its host plant. The library was produced in an oriented direction, in the pBSII
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                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 144979)
Birren,B., Linton,L., Nusbaum,C., Lander,E.,
Baldwin,J., Barna,N., Beckerly,R., Boguslavk
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Institute/ MIT Center for Genome Research

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* NOTE: This record contains 138 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
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Pred. No. 0.01;
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                                                                                                                                                                                                                                                                                                                       108409 bp
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                                                                                                                                                                       Herpesviridae;
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Virologie, Universitaet Erlangen-Nuernberg, Schlossgarten 4,
Erlangen, Bayern 91054, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Albrecht, J.-C. and Fleckenstein, B. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                           APLIFFACQTGHITSLAQMSDMPVTQAFQMKMLHAHLINLKCSSKPTIQGFFRQVPSDL
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                                                                                                                                                                                                                                                                                                                                                                                                      EKFESRWSNIYIPENTKAIAPQSLKNSLLPCWTQGTHLRFYHPKPMLEKMAEHGMVSS
MFYGHNLASGPAQHYPLTPNGSNATAGICSADGRHLALLHDPSLCNNICQWPYVPPTD
                                                                                                                                                                                                                                                                                                                                           7470. .8552
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                                                                                                                                                                                                                                                                                                                                                                                     PPLKVSPWKTMFLDLHKWGITVQGASPPPSRTDDPLRSLVF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KNSRLGIVLDIDYWTPWSSTNILYEGLYNVEKGVVYTFGGFTQTPNLMGVLNMALHWR
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complement (2752.
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/note="TIO; similar to TIP and STP-C of herpesvirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (2144.
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                                                                   note="orf 06"
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                                                                                       .12591
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                     protein"
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KQALNEKLGPRCSYQTELVKKKILSRYDPDEHEVFKVTISSSHSVYKVSDYLVANGCE
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14627. .17050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LETMFREYNYYAQSISGLRKDFDNSQRNNRDRIIQDFSEILADLGSIGKVIVNIASSA
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12598. .14640
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/note="orf 09"
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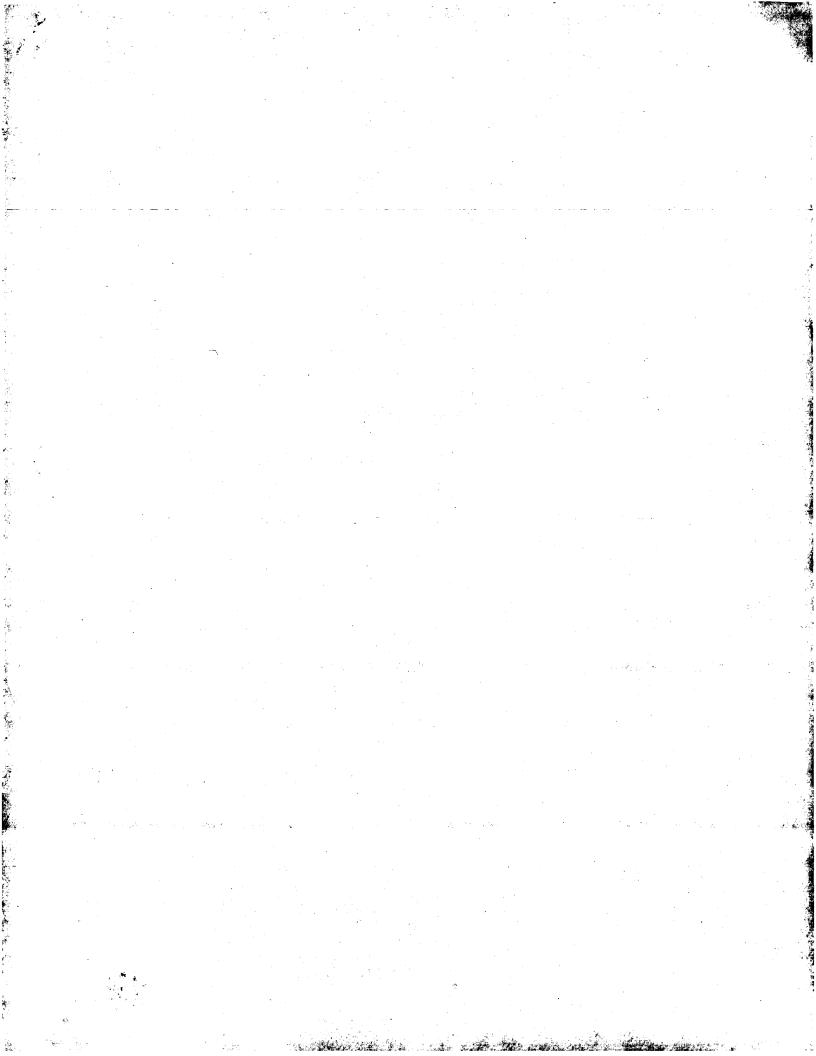
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Best Local Similarity
Matches 260; Conserv
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CCCCGCCTCCGCCGACTTCCGCCGCCGCCTCCTCGCGCAGGCCTCTTCGA 496
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                                                                                  CGTCGCCCCCTCTTCCCAGTCTCCCCCGTCGCCCCCCTCTTCCCCCGTCTCCCCCGTCTC
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SIBSIIDKRVSHGLVGTLLQFQQYTNSVPAVFSDTSEQPCKFYVLPWFTSDFINFLVV
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VEISFSFVFNRGLVDTNQSALFVASSNHTTKYVVKPQIWYFITPLSITVYNPGNRIIF
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GLPDGFLKVIDILNESYENLRTGKVSMDDLTFSTELSRPISSYKTENLPHLTVYKKII
KRQEEPPQIHDRIPYVFVGKTATCISTMAEDFTYAVQHNIPIARDLYFDKLIHGVANI
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KHIQTSLLSKILTVWLSKRKAI RQKLAQCEDQTKTI ILDKQQLAI KYTCNAVYGFTGV
ASGLLPCI SI JAETVYLQSGTWLESKSAF I EBROTYKTI ILDKQLAI VHKLNHEHEAKFRY I YE
DTDSLFVECVGYSVDTVVRFGDFLATFTSEKLFNAPIKLESEKTFQCLLLLAKKRY I G
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DHCIGAKKEDVSYKDILPLFMSGPEGRAKIGRYCVIDSVLVLKLLMFFKTHVEISEIA
KLAKIPTRRVLTDGQQIRVFSCLLAAARAENYILPVSNNVNTDGFQGATVITPIPGFY
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/db_xref="GI:4019237"
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IKRGFCVAVAVPCFFYLKAPGQDCEDKVTLDSQTSSIHWSDVLIKPGEGGPIVHAHHL
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/db_xref="GI:4019236"
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/note="orf 11; similar
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	Project Information Center Project Name: 0 Center Project Name: 0 Center clone name: RPCI-23_6K21 Center clone name: RPCI-23_6K21  Center clone name: RPCI-23_6K21  Summary Statistics Consensus quality: 156592 bases at least Q30 Consensus quality: 187032 bases at least Q30 Consensus quality: 187032 bases at least Q20 Consensus quality: 187032 bases at least Q20 Consensus quality: 187032 bases at least Q20 Consensus quality: 187032 bases at least Q20 Consensus quality: 187032 bases at least Q30 Consensus quality: 187032 bases at least Q30 Consensus quality: 187032 bases at least Q30 Consensus quality: 187032 bases at least Q30 Consensus quality: 187032 bases at least Q30 Consensus quality: 187032 bases at least Q30 Consensus quality: 187032 bases at least Q30 Consensus quality: 187032 bases at least Q30 Consensus quality: 187032 bases at least Q30 Consensus quality: 187032 bases at least Q30 Consensus quality: 187032 bases at least Q30 Consensus quality: 187032 bases at least Q30 Consensus quality: 187032 bases at least Q30 Consensus quality: 187032 bases at least Q30 Consensus quality: 187032 bases at least Q30 Consensus quality: 187032 bases at least Q30 Consensus quality: 187032 bases at least Q30 Consensus quality: 187032 bases at least Q30 Consensus quality: 187032 bases at least Q30 Consensus quality: 187032 bases at least Q30 Consensus quality: 187032 bases at least Q30 Consensus quality: 187032 bases at least Q30 Consensus quality: 187032 bases at least Q30 Consensus quality: 187032 bases at least Q30 Consensus quality: 187032 bases at least Q30 Consensus quality: 187032 bases at least Q30 Consensus quality: 187032 bases at least Q30 Consensus quality: 187032 bases at least Q30 Consensus quality: 187032 bases at least Q30 Consensus quality: 187032 bases at least Q30 Consensus quality: 187032 bases at least Q30 Consensus quality: 187032 bases at least Q30 Consensus quality: 187032 bases at least Q30 Consensus quality: 187032 bases at least Q30 Consensus quality: 187032 bases at least Q30 Consensus quality:	ACCESSION AC074307 VERSION AC074307.1 GI:9454523 KEYWORDS SOURCE ORGANISM Mus musculus (house mouse) ORGANISM Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. TITLE TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS DOE Joint Genome Institute.  TITLE JOURNAL COMMENT COMMENT Center: Joint Genome Institute Center: Joint Genome Institute Center: Joint Genome Institute Center: Joint Genome Institute Center: Joint Genome Institute Center: Joint Genome Institute Center: Joint Genome Institute Center: Joint Genome Institute Center: Joint Genome Institute Center: Joint Genome Institute Center: Joint Genome Institute Center: Joint Genome Institute Center: Joint Genome Institute Center: Joint Genome Institute Center: Joint Genome Institute Center: Joint Genome Institute Center: Joint Genome Institute Center: Joint Genome Institute Center: Joint Genome Institute	Ž C 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
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					מ"		desaturase;						Streptomyces roseo Platenolide syntha	Streptomyces freno	Saprolegnia diclin	Primer used in the	Florida bitterbush Nucleotide seguenc	Human colon cancer	Listeria monocytog Human thrombopoiet	S. chrysomallus ac	S. kaniharaensis D	Arabidopsis thalia A. thaliana sldl D	Arabidopsis thalia	Pythium irregulare	Mycobacterium tube	Mycobacterium tube	Seed development e Contig 109 DNA enc	Nucleotide sequenc	Oligonucleotide fo	Sphingolipid desat	Streptomyces nours	Arabidopsis thalia Human PAL-18 polyn	Mycobacterium tube	Human colon cancer	gene ex

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polynucleotide encoding delta-6 desaturase enzyme useful for producing transgenic plants and for producing antibodies specific to which is
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enic plant; fatty acid; ss.
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                                                                                                 Conservative
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/product= "Sphingolipid
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94.6%;
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                                                                                              Score 552; DB 21;
Pred. No. 3.5e-88;
0; Mismatches 27;
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                                                                                                                                                                                                           Corn sphingolipid desaturase cDNA
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                                                                                                                                                                                                                                                                                                                        TCGCCGGGGGCTCATTGG----CTTATCTGGTCAGTCGGGCTGGATTGGC 642
                                                                                                                                                                                                                                                                                                                                                           TGCTCTTCTGCATCGGCCTCTACTGC-TCCTCGCCTGCTCAA--CACCGGGGCCACATGT
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                                                              99WO-US28589
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89..1477
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/product= "Sphingolipid desaturase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polynucleotide encoding delta-6 desaturase enzyme useful for producing transgenic plants and for producing antibodies specific to which is useful for screening cDNA expression libraries -
delta6-desaturase; sunflower; soybean; maize; tobacco;
peanut; carrot; oil seed rape; gamma linolenic acid; GLA;
                                              DNA encoding Evening primrose delta6-desaturase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1764 BP; 310 A; 602 C; 456 G; 396 T; 0 other;
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P-PSDB; AAY71552.
                                                                              15-JUL-2002
                                                                                                                                           ABK49503 standard; DNA; 1702 BP
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                                                                             (first entry)
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Pred. No. 1.3e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
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                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 187
                                                                                                                                                                                                                                                                                                                                                          The invention describes an isolated nucleic acid encoding an evening primrose Delta6-desaturase. The nucleic acid and a vector expressing the nucleic acid are useful for producing a plant such as sunflower, soybean, maize, tobacco, peanut, carrot or oil seed rape plant, with increased gamma linolenic acid (GLA) content, and also for inducing or increasing production of GLA in a bacteria or plant deficient, lacking in or producing low levels of GLA. The nucleic acid is also useful for inducing chilling tolerance in plants. This sequence encodes the evening primrose delta6 desaturase involved in the production of gamma linoleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel nucleic acid encoding evening primrose delta6-desaturase which converts linoleic acid to gamma linolenic acid useful for producing gamma linolenic acid in transgenic plant or bacteria
                                                                                                                                                                                                                                                                                                                                      Sequence 1702 BP; 358 A; 471 C; 446 G; 427 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-JAN-1992;
14-SEP-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-OCT-1992;
10-OCT-1991;
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                                                                                                                                                                                                                                                                                  187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Column 41-46;
                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                             ATCACCCTCGCCGGCCAGGACGCCACCGACGCCTTCATGGCCTACCACCCGCCCTCCGTG
                                                                                                                                                                                                                                        ATCTCCACCAAGGAGCTGCAGGCGCACGCCGCCGCGGACGACCTCTGGGATCTCCATCTCC
 GAGATCTCCAAGGACTACCGGAGGCTTTTGAACGAGATGTCGCGGGTCCGGGGATCTTCGAG
                                                                               cecceercecececececerrerrerree-----ceecereaceacracacratereece
                                                                                                                                                                 GGCAAGGTCTACGACTGCTCTCGGTGGGCGGCGGAGCACCCCGGCGGCGAGGTCCCGCTC
                                                                                                                                                                                             GGGGACGTCTACGACGTCACGCCCTGGCTGCCCACCACCCGGCGGCGAGGTCCCGCTC
                           CCCGCCTCCGCCGACTTCCGCCGCCTCCTCGCGCAGCTCTCCTCCGCGGGCCTCTTCGAG
                                                    TGGCGGCATCTGGATCCGCTCTTCACCGGCTACTACTACCTCAAGGACTTCGAAGTGTCG
                                                                                                            CTCAGTCTGGCCGGCCAGGACGTCACCGACGCCTTCATTGCGTACCACCCGGGCACGGCG
                                                                                                                                                                                                                        tolerance;
                                                                                                                                                                                                                                                                                 Conservative
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91US-0774475.
92US-0817919.
94US-0307382.
97US-0789936.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "delta6-desaturase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene;
                                                                                                                                                                                                                                                                                              13.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53pp;
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                                                                                                                                                                                                                                                                                                           Score 106.8; DB 24;
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                                                                                                                                                                                                                                                                                               Pred.
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                                                                                                                                                                                                                                                                                               3.4e-10;
                                                                                                                                                                                                                                                                                 107; Indels
                                                                                                                                                                                                                                                                                                         Length 1702;
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371
                            497
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RESULT 5 ABX15367

323

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Best Local S
Matches 187
                                                                                                                                                          Sequence 1702
                                                                                                                                                                                              for producing a plant (such as sunflower, soybean, maize, tobacco, peanut, carrot or oil seed rape plant) with increased gamma-linolenic acid (GLA) content by transforming a plant cell with the nucleic acid or vector and regenerating a plant with increased GLA content from the plant cell, for inducing or increasing production of GLA in an organism lacking in or producing low levels of GLA and for inducing production of octadecatetraenoic acid in at least one of a plant deficient or lacking in or producing low levels of octadecatetraenoic acid, a bacterium which produces alpha-linolenic acid or a bacterium which exhibits a delta-15-desaturase activity on a GLA substrate. This sequence represents
                                                                                                                                                                                                                                                                                                                                          The invention relates to a nucleic acid encoding an evening primrose delta-6-desaturase polypeptide. The nucleic acid, a vector comprising nucleic acid or a nucleic acid encoding delta-12-desaturase, is useful
                                                                                                                                                                                                                                                                                                                                                                                                                            Novel nucleic acid encoding evening primrose delta-6-desaturase, for producing plant with increased gamma linolenic acid content, for inducing octadecatetraenoic acid production in plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-066659/06
P-PSDB; ABG73416.
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                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; Fig 10; 55pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-JAN-1997;
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14-SEP-1994;
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                 264
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                                            72
                                                                                                  l Similarity
187; Conserv
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GGGGACGTCTACGACGCCCTGGCTGCGCCACCACCCGGGCGGCGACGTCCCGCTC
                                                                ATCTCCACCAAGGAGCTGCAGGCGCACGCCGCGGGACGACCTCTGGATCTCCATCTCCC
                                            biennis.
                                                                                                   Conservative
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92US-0817919
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97US-0934254
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                                                                                                                                                        358 A; 471 C; 446 G;
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                                                                                                Score 106.8; DB 25;
Pred. No. 3.4e-10;
0; Mismatches 107;
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                                                                                                                                                           427
                                                                                                                              DB 25;
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                                                                                                                                                                                    polypeptide
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                                                                                                Gaps
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This invention describes a novel sphingolipid desaturase that selectively controduces a double bond into the sphingolase of the ceramide residue of sphingolipids and capnoids. A DNA sequence encoding the sphingolipid desaturase, or a vector containing the DNA sequence, can be used to produce transgenic plants, especially crop plants, with an increased or decreased delta-8-unsaturated long-chain base content or an altered delta-8-unsaturated long-chain base content or an altered contents are specially to compensate for a delta-8-unsaturated long-chain base deficiency, to exclude production of delta-8-unsaturated bases, to increase tolerance or resistance to soil salinity, ion stress or texicity, drought, wet conditions, cold or frost and/or phytopathogenic microorganisms, or to alter size growth and flowering time. Cells, transgenic organisms or plants containing the DNA sequence can be used to produce sphingolipids and capnoids with unsaturated sphingobases. The sphingolipids or capnoids can be used in cosmetics, pharmaceuticals and foods and as chemical raw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B. napus sld1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transgenic plant; crop plant; delta-8-unsaturated long-chain base; tolerance; resistance; soil salinity; ion stress; toxicity; drought; cold; frost; phytopathogenic microorganism; flowering time; cosmetic; pharmaceutical; food; chemical raw material; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sphingolipid desaturase; sld1; sphingobase; ceramide; capnoid
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                                                                                                                                                                                                                                                                              Claim 11; Fig 1; 62pp; German
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)B; AAY51333.
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                                                                                                                                                      Isolated nucleic acid comprises bacterial promoters modified to have altered activity in at least one gram-positive organism, e.g. Bacillu anthracis or Clostridium botulinum, useful for regulating gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ds; promoter; gram positive bacteria; fusion promoter; T5; CP25; P59; P1P2; PL; xy10; tet0; trp0; mal0; lambdac10; cellular prolif
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06-SEP-2001; 2001US-0948993
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Leuconostoc mesentero:
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                                                                                                                                                                                                                                                                                                                                                                            (ELIT-) ELITRA
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                                                                                                                                                                                                                                                                                                                                                                            PHARM INC
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Pred. No. 4.
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The invention relates to an isolated nucleic acid promoter comprising at least one promoter that is

comprising a fus modified to have

fusion

expression in bacteria

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224-227;

246pp;

English.

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CC of xylo, teto, trpo, malo or lambdacio, where at least one operator is constitued so binding of a repressor to an operator represses constitued so binding of a repressor to an operator represses constitued are vectors and constitued in cellular proliferation or required for proliferation of a compound in cellular proliferation or required for proliferation of a compound that reduces the activity or level of a compound identifying a compound that reduces the activity or level of a compound identified by the methods, a method of inhibiting the vector, a compound identified by the methods, a method of inhibiting the vector, a compound identified by the methods, a method of inhibiting the vector, a compound identified by the methods, a method of inhibiting the vector, a compound identified by the methods, a method of inhibiting the vector or cell consolidation of a gene in an operon required for proliferation using the vector, manufacturing an antibiotic comprising using the vector or cell and identifying a nucleic acid with promoter activity in Enterococcus consolidation, particularly for regulating gene expression in batteria and for identifying proliferation-required genes or molecules with potential antibiotic activity. The modified promoters are also
                                                                                                              useful for replacing endogenous promoters to create cells with specific regulatable genes. The present sequence is vector (or fragment) incorporating a fusion promoter sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           altered activity in at least one gram-positive organism, or comprising T5, CP25, P32, P59, P1P2 or P1 linked to at least one operator consist of xylO, tetO, trpO, malO or lambdaclO, where at least one operator is
Sequence 12733 BP; 3549 A; 2567 C; 3207 G; 3409 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  consisting
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5051 5231 395 275 262; 35 CGATCTCCCTTCNCCCCTCCCTTCCTTCCTCCTGAGTCCTGACCACCCCTCCTCGCGC Similarity всявестверановодительной подпоратородительной подпоратородительном подпоратородительном подпоратородительном подпоратородительном подпоратородительном подпоратородительном подпоратородительном подпоратородительном подпоратородительном подпоратородительном подпоратородительном подпоратородительном подпоратородительном подпоратородительном подпоратородительном подпоратородительном подпоратородительном подпоратородительном подпоратородительном подпоратородительном подпоратородительном подпоратородительном подпоратородительном подпоратородительном подпоратородительном подпоратородительном подпоратородительном подпоратородительном подпоратородительном подпоратородительном подпоратородительном подпоратородительном подпоратородительном подпоратородительном подпоратородительном подпоратородительном подпоратородительном подпоратородительном подпоратородительном подпоратородительном подпоратородительном п AGCCGACGCAATGCCGGCCGGCCAGCAAGGACGCCGACGTCCGCATGATCTCCCACCAA TCCAGCTAAATCCACGCCACCGATGGCCCGCACGGGCTTCGCGGACGCAACGGCGCCGGA 154 CGGCCAGGACGCCACGACGCCTTCATGGCCTACCACCCGCCCTCCGTGCGCCCCGCTCCT Conservative 10.4%; <u>,</u> Score 85.6; DB 24; Length 12733; Pred. No. 1.7e-06; 0; Mismatches 296; Indels 0; 394 454 4992 5052 5112 5172 214 5232 5292 94

밁 5 밁 Ş 밁 S 밁 S δ 밁 밁 δ В á 밁 δ Matches Query Match Best Local 4871 4811 4991 CCCCCCCCCCCCCCC 4794 GCTCAACACCGGGGCCAC coccedencecedencecedencecedencecedencecedencecedencecedence AAGTTCCTGCTCGCAAAGTCNGTGCTCTTCTGCATCGGCCTCTACTGCTCCTCGCCT 574 CCGCCGCCTCCTCGCGCAGCTCTCCTCCGCGGGCCTCTTCGAGCGCGTCGGCACACCCCC 592 4872 514

RESULT 8 ABK98592/c ID ABK98592 standard; DNA; 12739 BP

> 27-DEC-2000; 2000US-259434P 06-SEP-2001; 2001US-0948993 21-DEC-2001; 2001WO-US50250. WO200251982-A2 Bacteriophage lambda Escherichia coli. antibiotic; ds; promoter; gram positive bacteria; fusion promoter; T5; CP25; P32; P59; P1P2; PL; xyl0; tet0; trp0; mal0; lambdac10; cellular proliferation; Vector pEPEF1 containing XylR/XylO/CP25 ABK98592; (ELIT-) ELITRA PHARM INC vector. (first entry) sequences

Isolated nucleic acid comprises bacterial promoters modified to have altered activity in at least one gram-positive organism, e.g. Bacillus anthracis or Clostridium botulinum, useful for regulating gene expression in bacteria

WPI; 2002-575374/61. Haselbeck R, Wall D,

Gross

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Example 1; Page 206-209; 246pp; English

cc promoter comprising at least one promoter that is modified to have

cc altered activity in at least one gram-positive organism, or comprising

cc 75, CP25, P32, P59, P1P2 or PL linked to at least one operator is

cc of xylo, teto, trpo, malo or lambdaclo, where at least one operator is

cc positioned so binding of a repressor to an operator represses

cc transcription from the fusion promoter. Also included are vectors and

cc host cells comprising the fusion promoters, a method of identifying genes

cc involved in cellular proliferation or required for proliferation of a

cc prokaryotic cell using the vector, a method of identifying compounds that

cc inhibit the proliferation of a prokaryotic cell using the vector, a

cc method of identifying a compound that reduces the activity or level of a

cc ompound identified by the methods, a method of inhibiting the vector, a

cc compound identified by the methods, a method of inhibiting the vector, a

cc or expression of a gene in an operon required for proliferation using the

cvetor, manufacturing an antiblotic comprising using the vector or cell

cc and identifying a nucleic acid with promoter activity in Enterococcus

cc faccalis. The fusion promoters are useful for regulating nucleic acid or

cc polypeptide expression, particularly for regulating gene expression in

cc with potential antibiotic activity. The modified promoters are also

cuseful for renlacion and orenversor and college with energiful useful for replacing endogenous promoters to create cells with regulatable genes. The present sequence is vector (or fragment) incorporating a fusion promoter sequence of the invention. The invention relates to an isolated nucleic acid comprising a promoter comprising at least one promoter that is modified to

Sequence 12739 BP; 3543 A; 2572 C; 3211 G; 3413 T; 0 other;

Ś 밁 Matches Query Match Best Local ( Similarity cearcrecerrence en cercerrecerrecerreceres de la concerce de concerce en cerceres en concercer en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en concerce en conc 10.4%; 47.0%; Score 85.6; DB Pred. No. 1.7e-( 0; Mismatches 2 1.7e-06 24; 0 Gaps 5298 94 0

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28-JAN-1998;
24-FEB-1998;
31-MAR-1998;
Crkvenjakov R, Dickson M, Drmanac R, Drmanac S;
Escobedo J, Garcia PD, Garcia V, Gises K, Innis MA;
Jones WL, Kassam A, Kennedy GC, Kita D, Labat I;
Lamson G, Leshkowitz D, Pot D, Randazzo F, Reinhard
Stache-Crain B, Sudduth-Klinger J, Williams LT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genetic analysis; colorectal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene; gene expression product; diagnosis; therapion; mapping; tissue typing; profiling; forensic;
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98US-0072910.
98US-0075954.
98US-0080114.
98US-0080515.
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WPI; 1999-494092/41
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Novel human genes and their expression products which differentially expressed in different cell types

Claim 1; Page 2250-2251; 2479pp; English

CC comprising the sequences given in AAZI2532 to AAZI7779. Also described is camerined of detecting differentially expressed genes correlated with the cancerous state of a mammalian cell, comprising detecting at least one cdifferentially expressed gene product in a test sample from a cell cuspected of being cancerous, where the gene product is encoded by one cof the 5248 polymucleotide sequences given in AAZI2532 to AAZI7779. The cDlymucleotides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, can be used for raising antibodies for experimental, diagnostic and therapeutic purposes. The polymucleotides may also be used to construct can be used for raising antibodies for experimental, diagnostic and therapeutic purposes. The polymucleotides may also be used to construct can encoded protein); and to detect differences in expression levels between colls (e.g. to identify abnormal or diseased tissue in a human, to colorer). The polymucleotides of the invention are especially used in the Cdiagnosis, prognosis and management of colorectal cancer, breast cancer, cand lung cancer. The polynucleotides can also be used to screen for epitide analogues and antagonists. 18

Sequence 1337 BP; 42 A; 577 C; 27 G; 22 T; 669 other;

Query Match 10.0%; Best Local Similarity 31.2%; Matches 181; Conservative

<u>,,</u>

Score 82.2; DB 20; Pred. No. 7.1e-06; 0; Mismatches 400;

Indels Length

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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is a cDNA encoding sphingolipid desaturase from clone ssl.pk0017.D4:fis isolated from soybean seedling cDNA library, ssl. The present sequence is useful for producing transgenic plants having altered levels of sphingolipid desaturase which in turn would alter the fatty acid composition. The enzyme is useful for producing polyclonal or monoclonal antibodies. The polymucleotide is also useful as primer or probe for screening cDNA libraries to isolate desired full-length cDNA clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polynucleotide encoding delta-6 desaturase enzyme useful for producing transgenic plants and for producing antibodies specific to which is useful for screening cDNA expression libraries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1934 BP; 505 A; 367 C; 448 G; 614 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
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15-MAY-1998;
21-OCT-1998;
27-OCT-1998;
                                                        The polynucleotides sequences can be used in a method for detecting differentially expressed genes correlated with a cancerous state of a mammalian cell. The polynucleotides can also be used as probes for detecting and mapping related genes. They can be used in diagnosis and prognosis of diseases and disorders (e.g. identification of pre-metastatic or metastatic cancerous states, stages of cancer, or responsiveness of cancer to therapy). This is particularly for breast cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-negative breast cancer, negative breast cancer, lung cancer, and colon cancer.
                                                                                                                                                                                                                                                                                                                                 AAA00010 to AAA02716 represent polynucleotides isolated from cDNA libraries constructed from human colon cancer cell lines. The present invention also describes a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polynucleotide library used to determine cancerous states
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breast cancer; oes
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Randazzo F, Kennedy GC, Pot D, Ke
Crkvenjakov R, Dickson M, Drmanac
Garcia V, Jones LW, Stache-Crain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
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Query Match

Sequence 1000 BP; 21 A; 53 C; 574 G; 22 T; 330 other;

9.7%;

Score

79.6;

BB

21;

Length 1000;

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                                                                  KINDERS R J.
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 Mycobacterium tuberculosis
                             Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome; variation; epidemiology; patient treatment; epidemic monitoring; d
                                                                                                                   15-JAN-2002
                                                                                                                                                   AAI99682;
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Pred. No. 5.
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The present invention relates to human PAL-18 polypeptides and polynucleotides. The PAL-18 gene is found on chromosome 1q41. The sequences can be used to diagnose, monitor and treat cancers, particularly breast, colon and prostate cancers. The present sequence a PAL-18 polynucleotide shown in the invention.
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Mycobacterium tuberculosis strain H37Rv genome
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Matches 263; Conserv
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                                                                                                                                                                                                                                                                                               Claim 1; Page 50-51; 150pp; English.
                                                                                                                                                                                                                                                                                                                           New isolated PAL-18 polypeptide, useful for diagnosing, characterizing, and treating disease and in determining disease susceptibility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; PAL-18; cancer; chromosome 1q41; prostate cancer; colon cancer; breast cancer; cytostatic; gene; ds.
                                                                                                                                                                            Sequence 1065 BP; 98 A; 606 C; 36 G; 210 T; 115 other;
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218;
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                                                                                                                h 8.8%; Score 72.4; DB 24; Length 1065;
Similarity 43.8%; Pred. No. 0.00037;
18; Conservative 0; Mismatches 274; Indels 6;
                          TCCTCCTGAGTCCTGACCACCCTCCTCGCGCTCCAGCTAAATCCACGCCACCGATGGCC
                                                       CACGTGACTACCGTCGTTTAGCCGCCGAGTTCTCCAAACGCGGCCTCTTCGA 438
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                                                          TCCTCCGCGGGCCTCTTC 494
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Triticum.
1 (bases 1 to 642)
1 (bases 1 to 642)
1 Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z.,
Miao,G., Caraher,N. and Hanafey,M.K.
DuPont Wheat cDNA Sequence
                                                                                                                                                                                                                                                                                                  642 bp mRNA linear EST 23-NOV-200: wleln.pk0080.d7 wleln Triticum aestivum cDNA clone wleln.pk0080.d7 5' end, mRNA sequence.
  Crop Genetics
E. I. DuPont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104,
Tel: 302-631-2602
Fax: 302-631-2607
                                                                                                                Unpublished
Contact: Scott V. Tingey
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EST 23-NOV-2002

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CA710447 wdk2c.pk0
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CD239012 SS1 43 D0
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BX46454 BX46454
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Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
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Sequences have been trimmed
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//lab host="E. coli SOLR"
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//clome_lib="Wheat CS whole plant cDNA library"
//clome_lib="Wheat CS whole plant cDNA library"
//clome_lib="Wheat CS whole plant collected phagemid palluescript SK(-); Site_l: EcoRI; Site_2: khol; plant tissues from wheat cv. CS grown to full tillering stage in greenhouse were collected at University of California, Davis (Jan Dvorak's lab, K. Deal and E. Akhunov). Total RNA was prepared from leaves (young leaf and third leaf), whole roots, crown, steam and sheath tissues, and then equal quantities of RNA were pooled from the these samples. PolyA was purified from the pooled RNA, a cDNA library was made, and the cDNA clones were in vivo excised to give paluescript SK(-) phagemids in J. Dvorak's lab (E. Akhunov, J. Dvorak) at the University of California, Davis. Colony plating, plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
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/tissue_type="Roots, leaves,
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/cultivar="Chinese
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Query Match  56.7%; Score 466.6; DB 13; Length 563; Best Local Similarity 96.4%; Pred. No. 9.1e-83; Matches 509; Conservative 0; Mismatches 15; Indels 4; Gaps 3;  Qy  84 CCTCCTCGCGCTCCAGCTAAATCCACGCCACCGATGGCCCACGGGCTTCGCGGACGCA 143	/organism="Triticum aestivum" /mol_type="MRNA" /cultivar="Wyuna" /db_xref="taxon:4565" /tissue_type="endosperm" /tissue_type="endosperm" /dev_stage="developing endosperm tissue 8, 10 and 12 DPA /dev_stagt="developing endosperm library"  /days_post anthesis)" /clone_lib="wheat_EST_endosperm library"  BASE_COUNT	JOURNAL Funct. Integr. Genomics 3 (1-2), 33-38 (2003) MEDLINE 22478026  PUBNED 12590341  COMMENT Contact: Lambrecht M  COMMENT The Arabidopsis Information Resource Carnegie Institution of Washington, Dept. of Plant Biology 260 Panama Street, Stanford, CA 94305, USA Tel: 1 650 325 1521 x 251  Fax: 1 650 325 3748  Email: rhee@acoma.stanford.edu. FEATURES Location/Qualifiers  source 1. 563	ON BRY 2718 wheat EST endosperm library Triticum aestiv mRNA sequence.  NEGO6843  REG606843.1 GI:21556172  EST.  Triticum aestivum (bread wheat)  Triticum aestivum  Ebkaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Po; Triticae; Triticum.  1 (base; Triticum.)  1 (base; 1 to 563)  1 Clarke, B., Lambrecht, M. and Rhee, S.Y.  Arabidopsis genomic information for interpreting whe sequences	-CTTATCTGGTCAGTCGGG	Oy  435 CCCCCCGCCTCCGCCGCTCCTCCGCCGCTTCTTCGTCGGCGG
/mol_type="mRNA"  /culfivar="Chinese Spring"  /db_xref="taxon:4565"  /clone="wHE4048 E08 J16"  /tissue_type="Anther"  /dev stage="Meiotic stages pre-meiosis-metaphase I"  /dev stage="Meiotic anther cDNA library"  /clone_lib="wheat meiotic anther cDNA library"  /clone_lib="wheat meiotic anther cDNA library"  /clone_lib="wheat meiotic anther cDNA library"  /clone_lib="wheat meiotic anther cDNA library"  /clone_lib="wheat meiotic anther cDNA library"  /clone_lib="wheat meiotic anther cDNA library"  /clone_lib="wheat meiotic anther cDNA library"  /clone_lib="wheat meiotic anther cDNA library"  /clone_lib="wheat meiotic anther cDNA library"  /clone_lib="wheat meiotic anther cDNA library"  /clone_lib="wheat meiotic anther meiotic stage was determined by removing anthers from individual primary florets. One anther was sacrificed for microscopic staging, and if determined to be between (and including) meiotic stages pre-meiosis and metaphase I, the remaining two	West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA Tel: 5105595773 Fax: 5105595818 Email: oandersn@pw.usda.gov Email: oandersn@pw.usda.gov Sequences have been trinmed to remove vector sequence and low quality sequence with phred score less than 20 Seq primer: T7 primer. FEATURES Location/Qualifiers 50urce 1. 665 FYGGANIANGE TRIFFICIUM APASTIVUM"	ORGANISM Triticum asetivum  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Triticum.  REFERENCE 1 (bases 1 to 665) AUTHORS Anderson,O.D., Chao,S., Crossman,C., Langridge,P., Lazo,G.R., Pham ,J., Rausch,C.J., Sutton,T., Woo,J. and Wilson,C.  TITLE The structure and function of the expressed portion of the wheat genomes - Meiotic anther cDNA library  JOURNAL Unpublished Contact: Olin Anderson US Department of Agriculture, Agriculture Research Service, Pacific	Qy 563 TGC-TCCTCGCCTGAACACCGGGCCACATGTTCGCCGGGGC 607	Oy  444 TCCGCCGACTTCCGCCGCCTCCTCGCGCAGCTCTCCTCCGCGGGCCTCTTCGAGCGCGTC 503	Db 121 ATCTCCACCAAGGAGCTGCAGGCGCACCGGACGACCTCCTGGATCTCCATCTCC 180  Qy 264 GGGGACGTCTACGACGTCACGCCCTTGGCTGCCCACCACCACCGGGCGAGGTCCCGCTC 323

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Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier,S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,P., Herrmann,R.G., Holton,T., Jacquemin,J.M., Jia,J., Joudrier,P.,
                                                         Spermatophyta; Magnoliophyta; ; Triticeae; Triticum.
                                                                    Eukaryota, Viridiplantae, Streptophyta, Em
Spermatophyta, Magnoliophyta, Liliopsida,
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BASE COUNT
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Matches 506; Conserv
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Contact: Holton T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Centre for Plant Conservation Genetics, PO Box 157, Lismore NSW 2480 AUSTRALIA Tel: 61 2 6620 3409
Fax: 61 2 6622 2080
Email: tholton@scu.edu.au
International Triticeae EST Cooperative
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Location/Qualifiers
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TGTTCGCCGGGGGC 607
                                                                        GTCNGTGCTCTTCTGCATCGGCCTCTACTGCTCCTCGCCTGCTCAACACCGGGG-CCACA
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                                               GTCGGTGCTCTTCTGCATCGCCTCTACTGCGTCCTCGCCTGGTCAGCACCGGGGCCCACA
                                                                                                                        CTCCTTCGCGGGCCTCTTCGAGCGCGTCGGCCACACCCCCAAGTTCCTGCTCGTCGCAAT
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/culTivar="Myuna"
/db xref="taxon:4565"
/clone="SCU008.G07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="endosperm"
/clone_lib="ITEC_SCU_wheat_Endosperm_Library"
/note="Vector: Bluescript_II_SK(-)"
/note="Vector: Bluescript_II_SK(-)"
/note="Vector: Bluescript_II_SK(-)"
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Best Local Similarity
Matches 445; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Molecular Markers Group, Department Genbank Institute of Plant Genetics and Crop Plant | Corrensetr. 3, 06466, Gatersleben, Germany Tel: 039482-5522
Fax: 039482-5595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
; Triticeae; Hordeum.
1 (bases 1 to 500)
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HX07011r HX Hordeum vulgare subsp.
5-PRIME, mRNA sequence.
CA030713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: stein@ipk-gatersleben.de
Insert Length: 500 Std Error: 0.00
Plate: 7 row: O column: 11
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EST.
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                  CACCGACGCCTTCATGGCCTACCACCCGCCCTCCGTGCGCCCGCTCCTCCGCCGCTTCTT
                                                                              CTGGCTGCGCCACCCGGGCGGGCGAGGTCCCCGCTCATCACCCTCGCCGGCCAGGACGC
                                                                                                                                             GCACGCCGCGGGACGACCTCTGGATCTCCATCTCCGGGGACGTCTACGACGTCA
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                                                                                                                                                                                                                                                                                                                                                                                            /dev stage="apex (3-5 mm in size)"
//lab host="XL10-Gold"
//lab host="XL10-Gold"
//clone_lib="HX"
//clone_lib="HX"
//note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of cDNA); Site_2: XhoI (3'-end of cDNA); Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRIadapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BanHI, SalI, PstI). NOTE: Also due to the cloning system used Blue/white selection for recombinate is not 100% reliable."
61 a 225 c 135 g 79 t
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/db_xref="taxon:112509"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="HX07011"
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/cultivar="barke"
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Pred. No. 9.3e-75;
0; Mismatches 14;
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vulgare
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Best Local Similarity
Matches 458; Conserv
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wrel.pk0004.c7 wrel Triticum
end, mRNA sequence.
CA637422
CA637422.1 GI:25215718
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Tingey,S.V., Powell,W., Wolters,P.,
Miao,G., Caraher,N. and Hanafey,M.K.
DuPont Wheat CDNA Sequence
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Crop Genetics
E. I. DuPont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark,
Tel: 302-631-2602
Fax: 302-631-2607
Email: Scott. V.Tingey@USA.dupont.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Triticum aestivum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: M13
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AGGACGCCGCCGACGATCGCATCATCTCCACCAAGGAGCTGCAGGCGCACGCCGCCGCGG 240
                                                                       CTTCCTGAGTCCTGACCACCCCTCCTCGCGCTCAGCTAAATCCACGCCACCGATGG
                                                                                                                                                                                                                             CTCCCTAACAAACCTCCGTTGCTGTTTAAGATCCGGATCTCCCCCTTCNCCCCTCCC
                                                                                                                              CTTCCTCCTGAGTCCTGACCACCCCTCCTCGCGCTCCAGCTAAATCCACGCCACCGATGG
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218 c 119 g
                                                                                                                                                                                                                                                                                                                                                                                                           /clone_llb="wrel"
/note="Vector; pBluescript SK+; Site_1: EcoRI; Site_2: XhoI; Wheat (Triticum aestivum L.) root; 7 day old
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:4565"
/clone="wre1.pk0004.c7"
/tissue_type="root"
/clone_lb="wre1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Triticum aestivum"
/mol_type="mRNA"
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95.0%;
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Pred. No. 6.1e-72;
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aestivum cDNA clone wre1.pk0004.c7
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AUTHORS
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Best Local Similarity
Matches 419; Conserv
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 12
                              17
                                                                                                                                                                                                                                                                                                                                                                                                      Tel: (204) 983-2340
Fax: (204) 983-24604
Email: scloutler@em.agr.ca
was cloned directionally, not all sequences generated with reverse
primer were from the 5' end (same with forward primer and 3' end).
Average insert size is >2.0 kb
Plate: 038 row: F column: 05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cereal Research Centre, Agriculture and Agri-food Canada
195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Stro
Spermatophyta; Magnoliophyta;
; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BQ238994 453 bp mRNA linear EST 03-MAY-200: TaE05038F05R TaE05 Triticum aestivum cDNA clone TaE05038F05R, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Dr. Sylvie Cloutier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wheat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BQ238994.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cloutier, S.
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CGTTCCTGTTTTAAGATCCGAGCTCCCCTTGCCCCCTCCCCTCCCCTCCCCTTCC
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                                                                                                                                                62
                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            functional genomics - Glenlea developing seeds
                                                                                                                                           /tissue_type="developing seeds"
/dev_stage="5 days after anthesis"
/lab_host="5 days after anthesis"
/clone_lib="TaE05"
/note="Vector: pSPORT-P (Invitrogen Technologies);
NotI; Site_2: MluI; mRNA obtained from wheat seeds cultivar Glenlea 5 days post-anthesis"
a 214 c 109 g 68 t
                                                                                                                                                                                                                                                                               /clone="TaE05038F05R"
                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/cultivar="Glenlea"
                                                                                                                                                                                                                                                                                                                                                                             ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                organism="Triticum aestivum"
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                                                                              47.9%;
94.8%;
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                                                             Score 394.2; DB
Pred. No. 2e-68;
0; Mismatches
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yta; Liliopsida;
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a; Poales; Poaceae; Pooideae
                                                                Indels
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RESULT 9
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AUTHORS
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Query Match 41.6%;
Best Local Similarity 86.6%;
Matches 388; Conservative
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                                                                                                                                                                                                                                                     260 Panama Street, Stanfo
Tel: 1 650 325 1521 x 251
Fax: 1 650 325 3748
                                                                                                                                                                                                                                                                                                                                                                                                 , Triticeae; Triticum.

1 (bases 1 to 697)

Clarke, B., Lambrecht, M. and Rhee, S.Y.

Arabidopsis genomic information for interpreting
                                                                                                                                                                                                                                                                                      Contact: Lambrecht M
The Arabidopsis Information Resource
Carnegie Institution of Washington, Dept. (
260 Panama Street, Stanford, CA 94305, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BQ605802
BRY_1370 wheat EST endosperm
                                                                                                                                                                                                                           Email: rhee@acoma.stanford.edu.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                             Integr.
                                                                        /db xref="taxon:4565"
/tissue_type="endosperm"
/dev stage="developing endosperm tissue
(days post anthesis)"
/clone_lib="wheat EST endosperm library"
217 c 177 g 189 t
                                                                                                                                                               /organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Wyuna"
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Score 342.2; DB Pred. No. 4.3e-58 0; Mismatches 5
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Zea mays
Zea mays
                                                                                                                   Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA

If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.ntigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB:
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                                                                                                                                                                                                                      Coe, E.H.
Direct Submission
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2 (bases 1 to 1764)
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Overgo Probes
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                                   /mol_type="mRNA"
/db_xref="MaizeDB:634923"
/db_xref="taxon:4577"
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1 (bases 1 to 634)

Klein, R.R., Cordonnier-Pratt, M.-M., Gingle, A., Sudman, M. and Pratt
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
Tel: 706 542 1860
Pax: 706 583 0210
                                                                                                                                                                                                                                                 Sorghum bicolor (sorghum)
Sorghum bicolor
                                                                                       Contact: Cordonnier-Pratt
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ETH1_42 C07.g1_A002 Ethylene-treated seedlings Sorghum clone ETH1_42_C07_A002 5', mRNA sequence.
CD463185
CD463185.1 GI:31384453
EST.
Sorghum bicolor (sorghum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for high quality sequence in
20. Three-prime sequences, which are obtained with PolyTMix or T7
                                                                                                               CD463185
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/note="Organ: Developing preanthesis pannicles; Vector:
/note="Organ: Developing preanthesis pannicles; Vector:
/note="Organ: Developing preanthesis pannicles; Vector:
/note="Organ: Tist of the pannicles of the pannicles; Vector: Annicles of the pannicles of the prepared by mass excision."

297 c 171 g 95 t
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/mol_type="mRNA"
/cultivar="BTX623"
/db_xref="taxon:4558"
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Pred. No. 2.2e-51;
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Best Local Similarity
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 744)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mmpratt@uga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science; plant material and RNA prepared at Texas A & M University;
sequencing done in the Laboratory for Genomics and Bioinformatics,
University of Georgia. Sequence ends have been trimmed to exclude
vector and regions below Phred quality 16. Three-prime sequences
are presented as their reverse complement and have been trimmed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Cottoolman Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
The University of Georgia, Department of Plant Biology
The Coiences Building, Rm. 2502, Athens, GA 30602-7271,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cordonnier-Pratt, M.-M., Wentzel, V., Suzuki, Y., S., R.R., Liang, C., Sun, F., Sullivan, R., Shah, M., S., N., Gonzalez, M., Lane, S., Miller, V., Nanda, P., Eastman, A. and Pratt, L.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: Sug5 (CTTCTGCTCTAAAAAGCTGCG).
Location/Qualifiers
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Contact: Cordonnier-Pratt MM
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                            CGGCGAGGTCCCGCTCATCACCCTCGCCGGCCAGGACGCCACCGACGCCTTCATGGCCTA 367
                                                                                                                                                                                                                  CGCAATGCCGCCCTCTGTCGACGCAATGCCGGCCCCCGGAGGAGGAGACGCCGCGGGCGC
CGGCGACCTCCCGCTCATCACCCTCGCGGGGCAGGACGCCACCGACGCCTTCGCCGCCTA
                                                                                                                                                                                CTGGATCTCCATCTCCGGCGACGTCTACGACGTCACGCCCTGGCTCCCCCCACCACCCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102
                                                                                                                                                                                                                                                                                                                                                                      Conservative
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/note="Vector: pMEJBS-FLJ; Site 1: XhoI; Site 2: XhoI; The library was prepared from polyA+ RNA from seedlings grown in hydroponic culture. At 8 days of age, medium was supplemented with 0.5 mM 1-aminocyclopropane-1-carboxylic acid (ACC) to induce endogenous ethylene (ETH) production. Roots and shoots were harvested after 27 and 72 hr and material from both time points was combined prior to RNA isolation. Double-stranded cDNA was cloned unidirectionally into different braIII sites of the pMEJBS-FL3 vector (5-prime DraIII site is CACTGTGTG, 3-prime DraIII site is CACTGTGTG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:4558"
/clone="ETH1_42_C07_A002"
/lab_host="DH10B-T1_phage-resistant_E._coli"
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                                                                                                                                                                                                                                                                                                                                                                                         37.3%;
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Pred. No. 4.5e-51;
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Salzman, R., Chua
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RESULT 13
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JOURNAL
                                                                                    Matches 372;
                                                                                                         Query Match
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Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC344270 576 bp DNA linear GSS 16-MI OGMBO60TV ZM 0.7 1.5 KB Zea mays genomic clone ZMMBMa0385I23. genomic survey sequence.
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    (bases 1 to 576)

                                                                                                                                                                                                                                                                                                      9712 Medical Center Drive, Tel: 301-838-5843
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                                                                                                                                                                                                                                                                                                                                     Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                             Fax: 301-838-0208
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                                                                                                                                      /organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
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 AGGGGCCACGGCCGCCAATGCCGCCCTCTGCCGACGCAATGCCGGCCCCC
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79.7%;
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                                                                                  Score 289.8; DB Pred. No. 1e-47; 0; Mismatches 8
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                                                                                               BASE COUNT
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           wdk2c.pk015.k22 wdk2c Triticum aestivum cDNA clone wdk2c.pk015.k22 send, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                  E. I. DuPont de Nemours and Company
1 Innovation Way, P.O. Box 6104, New
Tel: 302-631-2607
Fax: 302-631-2607
Email: Scott.V.Tingey@USA.dupont.com
                                                                                                                                                                                                                                                                                                                                                   Seq primer: M13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Scott V. Tingey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Miao,G., Caraher,N. and na.
DuPont Wheat cDNA Sequence
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                                                                  Similarity
CAGCTCTCCTCCGCGGGCCTCTTCGAGCGCGTCGGCACACCCCCAAG 517
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/clone_lib="wdk2c"
                                                                                                                                                                       /note="Vector: pBluescript SK+; Site_1: EcoRI;
XhoI; Wheat (Triticum aestivum L.) developing )
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199 c 111 g
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                                               Score 285.4; DB 14;
Pred. No. 7.7e-47;
0; Mismatches 42;
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CTCCCTAACAAACCTCCGTTGCTGTTTTAAGATCCGATCTCCCCCTTCCCCCTCC

BASE COUNT 46 a ORIGIN  Query Match Best Local Similarity Matches 318; Conser  Qy 182 GGACGCCGC Qy 184 GGGCGCCGC Db 41 GGGCGCCGC	Tel: Fax: Fax: Email Seq [ High High POLY/ FEATURES SOURCE	REFERENCE 1 (L) AUTHORS Cord TITLE An ES JOURNAL Unput COMMENT Labo The	ACCESSION BG158 VERSION BG158 KEYWORDS EST. SOURCE Sorgh ORGANISM Sorgh Eyen Cladd	Qy 358 TCJ Db 374 GNJ RESULT 15 RESULT 15 LOCUS BG158 DEFINITION RHIZZ	Db 254 ACC	Qy 181 AGC Db 194 AGC Qy 241 ACC	Qy 61 CTT
Clones to be sequenced to the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the	Tel: 706 542 1860 Fax: 706 583 0210 Email: mmpratteyga.edu Seq primer: JEN REV High quality sequence stop: 297 POLYA=NO. Location/Qualifiers 1400 /organism="Sorghum propinquum" /mol_type="mRNA" /db_xref="taxon:132711" /clone="lib="Rhizomes; Vector: pBl fap II; Site_1: XhoI; Site_2: EcoRI	1 (bases 1 to 400) Cordonnier-Pratt, MM., Gi LH. An EST database from Sorgh Unpublished Contact: Cordonnier-Pratt Laboratory for Genomics ar The University of Georgia, Plant Sciences Wilding	GI:12692662 inquum inquum inquum inquum a; Maiplantae a; Mappoliop a; Andr	CCT 366	ACGACCTCTGGATCTCCATCTCCC CACCCGGGCGGCGAGGTCCCGG	ACGCCGCCGACGTCCGCATGI	CCTCCTGAGTCCTGACCACCA
Clones to be sequenced were prepared by mass excision 46 a 188 c 112 g 54 t  34.5%; Score 283.6; DB 10; Length 400; imilarity 88.6%; Pred. No. 1.7e-46; imilarity 88.6%; Pred. No. 1.7e-46; Conservative 0; Mismatches 40; Indels 1; Gaps GGACGCCGCGCACGATGATCTCCCACCAAGGAGCTCCGCGCGACGCCCGCC	, ue	P Q A	phyta; Embry	400 bp mRNA line	ACGACCTCTGGATCTCCATCTCCGGGGACGTCTANGGACGTCACGCCGTGGTTGCGCCACCACCATCACCCGGGCGGGCGACGTCCCCTCATCACCCTCGCCGGCCAGGACGCCACCGACGCCTCATCACCTCNTCGGCCAGGACGCCAANNACGCCACCN	AGGACGCCGACGTCCGCATGATCTCCACCAAGGAGCTGCAGGCGCACGCCGCGGGGIIIIIIIIII	CTTCCTCCTGAGTCCTGACCACCCCTCCTCGCGCTCCAGCTAAATCCACGCCACCGATCG
d by mass excision."  Length 400;  ndels 1; Gaps 1;  GGCGCACGCCGCGGGA 241	cript II from Lambda he library was made	dman,M hizome hizogy logy	a; Tracheoph	ar EST Of	SCGTGGTTGCGCCAC 313 SACGCCACCGACGCCT 357	CCTGGCTGCGCAC 299	CCACGCCACCGATGG 120

дь	δ	Дb	δ	뮹	Ş	Db	δ	D _P	Ş
341 CGCGGCCTCTTCGAGCGCGTCGGCCCCACCCCCAAGGTCCAGCTCGGCCTCATGGCCG 399	482 CGCGGGCCTCTTCGAGCGCGTCGG-CACACCCCCAAGTTCCTGCTCGTCGCAAAGTCNG 539	281 CGACTACACCGTCTCCCCCGGGTGCGCCGACTACCGCCGCCTCCTCGCGCGAGCTCTCCTC 340	422 CGACTACACTGTCCCCCCCCCCCCCCCCCCGCCTCCCGCCCCCCCC	221 CGCCTACCACCCGCCCTCGGCGCCCGCTCCTCCGCCGCTTCTTCGTCGGCCGCC	362 GGCCTACCACCCGCCCTCCGTGCGCCCCCTCCGCCCGCTTCTTCGTCGGCCGCC	161 CCCCGGCGGACCTCCCGCTCATCACCCTCGCGGGGCAGGACGCCACCGACGCCTTCGC 220	302 CCCGGGCGGCGAGGTCCCGCTCATCACCCTCGCCGGCCAGGACGCCACCGACGGACG	CCATCTCCGGCGACGTGT	242 CGACCTCTGGATCTCCATCTCCGGGGACGTCTACGACGTCACGCCCTGGCCTGCGCCACCA 301

Search completed: December 31, 2003, 23:59:29 Job time : 1259.26 secs

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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                      61.8
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6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*
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US-09-249-585A-4
US-09-130-1114-2
US-08-232-463-14
US-09-410-551B-1
US-09-410-551B-1
US-09-103-840A-2
US-09-103-840A-1
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7.2	7.2	7.2	7.2	7.2	7.2	7.2	7.2	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.4	7.4	7.5
1071	1071	1027	1896	2064	675	320	318	6085	2481	1717	2612	1193	1020	939	1158	320	152331
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US-08-997-362-180	US-08-997-080-180	US-09-674-741-9	US-09-311-626B-15	US-08-343-428-1	US-08-998-416-723	US-09-165-264-11	US-09-165-264-12	US-09-029-603-4	US-09-894-998A-35	US-09-048-888-2	US-09-105-390-7	US-09-372-422A-23	US-09-105-390-61	US-09-105-390-45	US-09-372-422A-21	US-09-165-264-14	US-09-128-155-16
-	Sequence 180, App	Sequence 9, Appli	Sequence 15, Appl	Sequence 1, Appli	Sequence 723, App	Sequence 11, Appl	Sequence 12, Appl	Sequence 4, Appli	Sequence 35, Appl	Sequence 2, Appli	Sequence 7, Appli	Sequence 23, Appl	Sequence 61, Appl	Sequence 45, Appl	Sequence 21, Appl	Sequence 14, Appl	Sequence 16, Appl

## ALIGNMENTS

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LOCATION:
US-08-934-254-26
                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEPAX: (516) 742-4343
TELEPAX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 1702 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 26, Applicat:
Patent No. 6355861
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,254
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                            NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Thomas, Terry L.

APPLICANT: Thomas, Terry L.

TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC
TITLE OF INVENTION: DELTA 6-DESATURASE
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
                                                                                                                                                                        MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Garden Cit
STATE: New York
COUNTRY: United
ZIP: 11530
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REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 8383ZYXWVU
                                                                                                                                                                                                                                                      TYPE: nucleic acid
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5. 6355861
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WRITE, Obn C.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 4411529
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
 1217800
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GCGCCCCTCGCCGGCCGCCCCCCCCTGCCGCCACGGCCGCTGTCGCCGGCCCGGCCCCG
                                                                     GCGGCGCCGGCCCGCCGTCACCGCCGTGCCCGCCGGTGCCCACCAGCAGCCCGGCG
                                                                                                                                          CGGCCGCCAGCGCCGATGCCCGTGCCGGCCGGCCGCCGTCACCGCCCTTGACG
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                                AGGTCCCGCTCATCACCCTCGCCGGCCAGGACGCCACCGACGCCTTCATGGCCTACCACC
                                                                                                    TCTCCATCTCCGGGGGACGTCTACGACGTCACGCCTGGCTGCCGCCACCACCCGGGCGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 75.2; DB 3; Pred. No. 1.6e-06;
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US-09-130-114-2

Sequence 2, Application US/09130114 Patent No. 5976807

GENERAL INFORMATION:
APPLICANT: Horlick, Robert A
APPLICANT: Damaj, Bassam B.
APPLICANT: Robbins, Alan K.

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SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
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GENERAL INFORMATION:
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TITLE OF INVENTION: METHOD FOR MAINTENANCE
FILE REFERENCE: 0867/0D905
CURRENT APPLICATION NUMBER: US/09/249,585A
CURRENT FILING DATE: 1999-02-11
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LOCATION: (1)..(1926)
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ORGANISM: Epstein Barr Virus
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Pred. No. 1.1e-06;
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; LENGTH: 1931
; TYPE: DNA
; ORGANISM: EENA
US-09-130-114-2
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Best Local Similarity
Matches 162; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/130,114
CURRENT FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                          APPLICATION NUMBER: EP 9
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 435
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 22313-0299
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Conservative
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Pred. No. 1.1e-06;
0; Mismatches 129;
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1 LENGTH: 77536

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US-08-232-463-14
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Best Local (
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APPLICANT: WU, KAI
TITLE OF INVENTION: CONSTRUCTS THEREFOR
TITLE OF INVENTION: CONSTRUCTS THEREFOR
FILE REFERENCE: 30062-20026.00
CURRENT APPLICATION NUMBER: US/09/410,551B
CURRENT FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: US 60/139,650
PRIOR PILING DATE: 1999-06-17
PRIOR APPLICATION NUMBER: US 60/123,810
PRIOR APPLICATION NUMBER: US 60/123,810
PRIOR APPLICATION NUMBER: US 60/123,810
PRIOR APPLICATION NUMBER: US 60/123,810
PRIOR PILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 60/102,748
PRIOR FILING DATE: 1998-10-02
NUMBER: US 60/102,748
PRIOR FILING DATE: 1998-10-02
NUMBER: US 60/102,748
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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US-09-434-288-5/c
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SEQ ID NO 5
LENGTH: 1881
TYPE: DNA
ORGANISM: Streptomyces narbonensis
S-09-434-288-5
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Best Local Similarity 49.8%;
Matches 227; Conservative
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Best Local Similarity
Matches 186; Conserv
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TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES
TITLE OF INVENTION: CONSTRUCTS THEREFOR
FILE REFERENCE: 30062-20030.00
CURRENT APPLICATION NUMBER: US/09/434,288
CURRENT FILING DATE: 1999-11-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1998-11-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
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LOCATION: (52275)...(71465)
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                                                                                                                                                                                                                                                                                                                     Score 68.6; DB 4;
Pred. No. 1.5e-05;
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Pred. No. 8.1e-06;
0; Mismatches 192;
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APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
ITITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
ITITLE OF INVENTION: TUBERCULOSIS
ITITLE OF ENVENTION: TUBERCULOSIS
ITITLE OF ENVENTION: TUBERCULOSIS
ITITLE OF INVENTION: UBORCULOSIS
ITITLE OF ENVENTION: 100807.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTMARE: PATENTIN VET. 7
SEQ ID NO 2
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OTHER INFORMATION: "n" bases at various positions throughout the sequence; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
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Best Local Similarity
Matches 227; Conserv
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                                   CACAGTCCACCGACCCCGCCTCCCCCCGCCGGTGCCGAGTACGGTGCTGGCTCCGCCG
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Pred. No. 3.7e-05;
0; Mismatches 247
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Best Local Similarity 48.0
Matches 193; Conservative
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LENGTH: 4403765
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TITLE OF INVENTION: DUB SEQUENCES FOR STRATITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
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APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
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OTHER INFORMATION: "n" bases at
OTHER INFORMATION: represent a,
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48.0%;
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Pred. No. 5.4e-05;
0; Mismatches 209;
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GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: HHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
APPLICANT: VENTER, JOHN C.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
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US-09-103-840A-1
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                                                                                                                                                                                                   RESULT 11
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                                                                                                                 Sequence 8, Application US/09165264
Patent No. 6197510
GENERAL INFORMATION:
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
                                                        APPLICANT: Vinayagamoorthy, TITLE OF INVENTION: Multi-Lc FILE REFERENCE: 44747
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TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
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                                                              ON: Multi-Loci Genomic 44747
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48.0%;
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Pred. No. 5.4e-05;
0; Mismatches 209;
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SOFTWARE: PA SEQ ID NO 8 LENGTH: 319 TYPE: DNA

PatentIn

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                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/985,586
PILING DATE: 03-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/406,030;
FILING DATE: 17-MAR-1995
CLASSIFICATION: 45
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/243,391
FILING DATE: 13-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                    FILING DATE: 03-DEC-
PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                               PRIOR APPLICATION DATA:
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                                                                                                                                          FILING DATE:
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Selden, Richard F
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
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APPLICATION NUMBER: US 0
FILING DATE: 05-NOV-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: TK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Pred. No. 8.7e-05;
0; Mismatches 241;
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; Sequence 13, Application US/09165264
; Patent No. 6197510
; GENERAL INFORMATION:
APPLICANT: Vinayagamoorthy, Thuraiayah
; TITLE OF INVENTION: Multi-Loci Genomic Analysis

RESULT 13 US-09-165-264-13/c

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FILE REFERENCE: 44747
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 320
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
FEATURE:
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US-08-804-227C-7
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US-09-165-264-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 7.7%;
Best Local Similarity 50.0%;
Matches 158; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Applic
Patent No. 587699:
                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
APPLICANT:
                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCI(DOS) Text only
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,227C
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                           ADDRESSEE: THOMAS G.
                                                                                                                                                                                                                                                                                                                                    APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
FITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                               FILING DATE: Fe CLASSIFICATION:
                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                              CITY: INDIANAPOLIS
                                                                                                                                                                                                                                                                             STREET:
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                                                                                                                                                                                                                                                                           E: THOMAS G. PLANT 1501
LILLY CORPORATE CENTER
                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                           DeHoff, Bradley S.
                                                                                February 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>,</u>
   X-8231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 63.2; DB 3;
Pred. No. 0.00015;
0; Mismatches 158
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                                                                                                                                                                                              Sequence 1, Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 153;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                  GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
                                                                                               APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                 CORRESPONDENCE ADDRESS:
                                                                                APPLICANT: ROSTECK, Paul R., Jr.
TITLE OF INVENTION: PLATENOLIDE SYNTHASE GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
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                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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LOCATION:
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LOCATION:
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                                ADDRESSEE:
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                                                                                                                                                                                                   , Application US/08804198
5945320
INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                                                                GGTCTTCGACCACCCCACCCCCGCCGCGCGCTGTCCTCGCACCTCGACGGCCTGCTGGCCCC 31013
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                  E: PAUL R. CANTH
                                                                                                                             Burgett, Stanley G.
Kuhstoss, Stuart A.
Rao, Nagaraja R.
                                                                                                              Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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70 NO: 7:
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31329..36071
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350..14002
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50.5%;
                                  CANTRELL
                                                                                                              Mark A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 150; Indels
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Pred. No. 0.00028;
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STATE: I

OPERATING SYSTEM: Macintosh 7.0 SOFTWARE: Microsoft Word 5.1 CURRENT APPLICATION DATA:

US/08/804,198

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macinto

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; LOCATION:
; FEATURE:
; NAME/KEY:
; LOCATION:
US-08-804-198-1
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Search completed: January 1, 2004, 00:05:52 Job time: 63.8386 secs
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FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CANTRELL, PAUL R.
REGISTRATION NUMBER: 36,470
REFERENCE/DOCKET NUMBER: P9113
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3885
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 44377 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOTECULE TYPE: DATE: 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 7.7%; Score 63; DB 2; Length 44377; Best Local Similarity 50.5%; Pred. No. 0.00028; Matches 153; Conservative 0; Mismatches 150; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: CDS
LOCATION: 350..14002
FEATURE:
NAME/KEY: CDS
LOCATION: 14046..20036
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FEATURE:
NAME/KEY:
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                                                                                 31014 GGC 31016
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14046..20036
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31329..36071
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Database :
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq length: 0
seq length: 2000000000
                                                                                                                                                                                                                                                                                Maximum.
Listing first --

Published_Applications_NA:*

1: /cgn2 6/ptcdata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptcdata/2/pubpna/US06_NEW PUB.seq:*

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/cgn2_6/ptcdata/2/pubpna/US07_NEW PUB.seq:*

/^/nubpna/US07_NEW PUB.seq:*

///nubpna/US07_NEW PUB.seq:*
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823
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/cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
/cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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	8. 6	8.6	8.8	9.2	9.2	9.4	9.5	9.5	10.3	10.3	10.4	10.4	10.6	10.6	13.0	Query Match Length
	520	77536	1065	1117	1117	1064	5452	5452	3133	3133	12739	12733	3163	3163	1702	Length
	15	13	10	13	12	10	13	12	13	12	15	15	13	12	14	BB
	US-10-184-644-332	US-09-940-316B-1	US-09-804-682-33	US-10-017-161-1403	US-10-292-798-1141	US-09-804-682-29	US-10-017-161-1481	US-10-292-798-1189	US-10-017-161-1483	US-10-292-798-1191	US-10-032-393-8	US-10-032-393-47	US-10-017-161-1857	US-10-292-798-1513	US-10-029-756-26	ID
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61.8	61.8	61.8	62	62	62.2	62.2	62.2	62.2	62.4	62.4	62.8	62.8	63	63	63	63.2	63.6	63.6	64.4	64.4	66	66.4	67.2	67.4	68.4	68.6	69.4	69.4	70.4
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US-09-940-316B-16	US-09-940-316B-20	US-10-108-915-33	US-10-156-761-2231	US-09-931-457A-44	US-10-156-761-15103	US-10-156-761-411	US-10-156-761-2716	US-09-887-576-781	US-10-156-761-6923	US-10-156-761-6338	US-10-156-761-2267	US-10-156-761-6190	US-10-431-952-13	US-10-054-534B-13	US-09-769-863-13	US-09-976-059-1	US-10-156-761-1	US-10-156-761-4706	US-10-027-632-31508	US-10-027-632-31508	US-09-931-457A-50	US-10-101-464A-861	US-09-938-842A-558	US-09-967-477B-7	US-10-156-761-1	US-10-271-889-5	US-10-369-493-42356	US-10-163-198-40	US-10-184-634-332
Sequence 16	Sequence 20	Sequence 33, A	Sequence 22										13	13	13	5	e	4	ω	31	50				Sequence 1				Sequence 33
, Appl	, Appl	, Appl	31, Ap	, Appl	15103, A	411, App	16, Ap			38, Ap	67, Ap	90, Ap	Appl	Appl	13, Appl	Appli	, Appli	4706, Ap	31508, A	508, A	, Appl	1, App		Appli	, Appli	Appli	356, A	40, Appl	2, App

## ALIGNMENTS

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US-10-029-756-26

US-10-029-756-26

Sequence 26, Application US/10029756

Sequence 26, Application US/10029756

Sequence 26, Application US/10029756

Publication No. US20020108147A1

GENERAL IMPORMATION: PRODUCTION OF GAMMA LINOLENIC ACID BY A

PILLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A

PUBLICANT: Thomas, Terry L.

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser

STREET: 400 Garden City

STATE: 400 Garden City

STATE: 400 Garden City

STATE: New York

COUNTRY: Garden City

STATE: New York

COUNTRY: United States

ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/10/029,756

FILING DATE: 21-Dec-2001

CLASSIFICATION ADTA:
APPLICATION NUMBER: US/10/029,756

FILING DATE: CUNKnown>

PRIOR APPLICATION NUMBER: 08/934,254

FILING DATE: CUNKnown>

PRIOR APPLICATION NUMBER: 19,827

REFERENCE/DOCKET NUMBER: 3883ZYXWVU

TELEPHONE: (516) 742-4343

TELEPHONE: (516) 742-4343

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:
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CURRENT APPLICATION NUMBER: US/10/292,798
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: 10/017,161
PRIOR FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: JP 2001-246789
PRIOR PLICATION NUMBER: JP 2001-246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2070
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 1513
LENGTH: 3163
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1513, Application US/10292798 publication No. US20030235833A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 187;
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SUWA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAWA, YUTAKA
APPLICANT: AKIYAWA, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REFERENCE: 084335/166
CURRENT APPLICATION NUMBER: US/10/292,798
                                                              FEATURE:
NAME/KEY: CDS
LOCATION: (201)...(2963)
                     NAME/KEY: modified base LOCATION: (556)..(655)
                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                          FEATURE:
                                                                                                                                OCATION: (1) .. (3163)
                                                                                                                                                                      LOCATION: source
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STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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SEQUENCE DESCRIPTION: SEQ ID
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INFORMATION: a, t,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                264 GGGGACGTCTACGACGTCACGCCCTGGCTGCGCCACCCGGGCGAGGTCCCGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      204 ATCTCCACCAAGGAGCTGCAGGCGCACGCCGCCGGACGACCTCTGGATCTCCATCTCC
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LOCATION:
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PEATURE:
NAME/KEY: modified base
(920)..(920)
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NAME/KEY: modified base
TORMITON: (892)..(892)
                                                                                                                                PEATURE: modified base LOCATION: (897)...(897) OTHER INFORMATION: a, t,
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                                          NAME/KEY: modified_base
LOCATION: (941)..(941)
OTHER INFORMATION: a, t,
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LOCATION: (843)..(843)
OTHER_INFORMATION: a, t,
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OTHER INFORMATION: a, t,
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OTHER INFORMATION: a, t,
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NAME/KEY: modified base
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OTHER INFORMATION: a, t,
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OTHER INFORMATION: a, t,
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LOCATION: (658)..(669)
OTHER INFORMATION: a, t,
FEATURE:
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LOCATION: (754)..(756)
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NAME/KEY: modified base LOCATION: (1130)..(1130)
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                                                                                                                                            NAME/KEY: modified base LOCATION: (1601)..(1601)
                                                                                                                                                                                    PEATURE: NAME/KEY: modified base LOCATION: (1544)...(1544) OTHER INFORMATION: a, t,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: modified base LOCATION: (1147)...(1147) OTHER INFORMATION: a, t,
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                                                                                                    NAME/KEY: modified base LOCATION: (1605)..(1605)
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LOCATION: (1162)..(1162)
OTHER_INFORMATION: a, t,
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OTHER INFORMATION: a, t,
                  OTHER INFORMATION: a, t,
                             NAME/KEY: modified base LOCATION: (1637)..(1637)
                                                           LOCATION: (1635)..(163
                                                                                           FEATURE:
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OTHER INFORMATION: a, t,
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LOCATION: (1082)..(1084
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ENERTAL INFORMATION

GENERAL INFORMATION

APPLICANT: SUWA, MAKIKO

APPLICANT: ASAI, KIYOSHI

APPLICANT: ASAI, KIYOSHI

APPLICANT: ASAI, KIYOSHI

APPLICANT: ASURATANI, HIROYUKI

TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS

FILE REFERENCE: 084335/0152

CURRENT APPLICATION NUMBER: US/10/017,161

CURRENT FILING DATE: 2002-12-18

PRIOR APPLICATION NUMBER: JP 2001/246789

PRIOR APPLICATION NUMBER: JP 2001/246789

PRIOR APPLICATION NUMBER: JP 2001/246789

PRIOR FILING DATE: 2001-06-18

NUMBER OF SEQ ID NOS: 2430

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 1857

LENGTH: 3163

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEV: SOURCE
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Sequence 1857, Application US/10017161
Publication No. US20030143668A1
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PRIOR FILING DATE: 2000-12-27
PRIOR APPLICATION NUMBER: 09/948,993
PRIOR FILING DATE: 2001-09-06
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
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APPLICANT: Gross, Molly
TITLE OF INVENTION: BACTERIAL PROMOTERS AND METHODS
FILE REFERENCE: ELITRA.010A
CURRENT APPLICATION NUMBER: US/10/032,393
CURRENT FILING DATE: 2001-12-21
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Pred. No. 1e-12;
0; Mismatches 296;
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TITLE OF INVENTION: BACTERIAL PROMOTERS AND METHODS OF USE
FILE REFERENCE: ELITRA.010A
CURRENT APPLICATION NUMBER: US/10/032,393
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/259,434
PRIOR FILING DATE: 2000-12-27
PRIOR APPLICATION NUMBER: 09/948,993
PRIOR FILING DATE: 2001-09-06
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 12739
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APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REFERENCE: 084335/166
CURRENT APPLICATION NUMBER: US/10/292,798
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: 10/017,161
PRIOR FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: JP 2001-246789
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NAME/KEY: modified base LOCATION: (231)(232) OTHER INFORMATION: a, t,	NAME/KEY: modified base LOCATION: (229)(229) OTHER INFORMATION: a, t, FEATURE.	NAME/KEY: modified base LOCATION: (222)(225) OTHER INFORMATION: a, t, FEATURE:	NAME/KEY: modified base LOCATION: (219)(219) OTHER INFORMATION: a, t, FEATURE:	NAME/KEY: modified base LOCATION: (214)(214) OTHER INFORMATION: a, t, FEATURE:	NAME/KEY: modified base LOCATION: (212)(212) OTHER INFORMATION: a, t, FRATURE.	NAME/KEY: modified base LOCATION: (210)(210) OTHER INFORMATION: a, t, ERATURE.	NAME/KEY: modified base LOCATION: (194)(195) OTHER INFORMATION: a, t,	NAME/KEY: modified base LOCATION: (192)(192) OTHER INFORMATION: a, t,	NAME/KEY: modified base LOCATION: (185)(188) OTHER INFORMATION: a, t,	NAME/KEY: modified base LOCATION: (182)(182) OTHER INFORMATION: a, t, ERATTRE.	NAME/KEY: modified base LOCATION: (179)(180) OTHER INFORMATION: a, t, FEATURE:	NAME/KEY: modified base LOCATION: (172)(172) OTHER INFORMATION: a, t, EPATTRE.	NAME/KEY: modified base LOCATION: (155)(155) OTHER INFORMATION: a, t, FRATURE.	NAME/KEY: modified base LOCATION: (151)(152) OTHER INFORMATION: a, t, FEATURE.	NAME/KEY: modified base LOCATION: (146)(148) OTHER INFORMATION: a, t, FRATURE:	NAME/KEY: modified base LOCATION: (139)(139) OTHER INFORMATION: a, t, FEATURE:	NAME/KEY: modified base LOCATION: (124)(129) OTHER INFORMATION: a, t, FEATURE.	
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SEQ ID NO 1483
LENGTH: 3133
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APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ABUARTANI, HIROYUKI
TITLE OF INVENTION: NOVEL G PRO
FILE REFERENCE: 084335/0152
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CURRENT FILING DATE: 2002-12-18
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APPLICANT: ASAI, KIYOSI
APPLICANT: AKIYAMA, YU
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LOCATION: (192)
OTHER INFORMATION: a, t,
                         NAME/KEY: modified_base
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                                                                    NAME/KEY: modified_base LOCATION: (185)..(188)
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TOTATION: (287)...(290)
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NAME/KEY: modified base
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LOCATION: (345) ..(363)
OTHER INFORMATION: a, t,
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OTHER INFORMATION: a, t,
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NAME/KEY: modified base
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LOCATION: (365)..(368)
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SEQ ID NO 1189
LENGTH: 5452
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APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ABUGATANI, HIROYUKI
TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REFERENCE: 084335/166
CURRENT APPLICATION NUMBER: US/10/292,798
CURRENT FILING DATE: 2002-211-13
PRIOR APPLICATION NUMBER: 10/017,161
PRIOR APPLICATION NUMBER: JP 2001-246789
PRIOR APPLICATION NUMBER: JP 2001-246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2070
                                                               NAME/KEY: modified_base
LOCATION: (145)..(145)
OTHER INFORMATION: a, t,
                                                                                                                                                                                                    NAME/KEY: modified base LOCATION: (1)..(140)
OTHER INFORMATION: a, t,
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NAME/KEY: modified_base
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FEATURE:

NAME/KEY: modified base

CONTION: (248)..(252)
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FEATURE:

NAME/KEY: modified_base

FORMTION: (218)..(218)
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NAME/KEY: modified_base
LOCATION: (162)...(162)
OTHER INFORMATION: a, t,
                                                                               NAME/KEY: modified_base
LOCATION: (246)..(246)
OTHER INFORMATION: a, t,
                                                                                                                             NAME/KEY: modified base LOCATION: (235)..(236) OTHER INFORMATION: a, t,
                                                                                                                                                                                                                           LOCATION: (229)..(229)
OTHER INFORMATION: a, t,
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LOCATION: (172)..(172)
OTHER INFORMATION: a, t,
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OTHER INFORMATION: a, t,
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NAME/KEY: modified base
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LOCATION: (359)..(359)
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GENERAL INFORMATION:
APPLICANT: SUWA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RE
FILE REFERENCE: 084335/015
CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18

RECEPTORS

APPLICATION NUMBER: JP 2001/246789 FILING DATE: 2001-06-18

US-10-017-161-1481/c

Sequence 1481, Application US/10017161 Publication No. US20030143668A1

RESULT 9

; NUMBER OF SEQ ID NOS: 2430; SOFTWARE: PatentIn Ver. 2.1; SEQ ID NO 1481; LENGTH: 5452; TYPE: DNA ORGANISM: Homo sapiens NAME/KEY: modified_base LOCATION: (199)
OTHER INFORMATION: a, t, c FEATURE:
NAME/KEY: modified_base LOCATION: (214)
OTHER INFORMATION: a, t, c FEATURE:
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OTHER INFORMATION: a, t, c, NAME/KEY: modified_base LOCATION: (221) OTHER INFORMATION: a, t, FEATURE: NAME/KEY: modified_base LOCATION: (168) OTHER INFORMATION: a, t, NAME/KEY: modified base LOCATION: (225)..(226) OTHER INFORMATION: a, t, c, NAME/KEY: modified_base LOCATION: (196) OTHER INFORMATION: a, t, FEATURE: NAME/KEY: modified base LOCATION: (191)..(193) OTHER INFORMATION: a, t, c, NAME/KEY: modified base LOCATION: (147)..(148) OTHER INFORMATION: a, t, c, FEATURE: NAME/KEY: modified_base LOCATION: (145) OTHER INFORMATION: a, t, c, FEATURE:
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Pred. No. 8.2e-11;
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Kinders, Robert

APPLICANT: Corey, Michael J.

FILE OF INVENTION: PAL-18 POLYPEPTIDES, NUCLEIC ACIDS

TITLE OF INVENTION: ENCODING THE SAME AND METHODS FOR SCR

TITLE OF INVENTION: MODULATING THE SAME

FILE REFERENCE: 130001.406

CURRENT APPLICATION NUMBER: US/09/804,682

CURRENT APPLICATION NUMBER: 2001-03-12

NUMBER OF SEQ ID NOS: 174

SOFTMARE: PASTUSE FOR WINDOWS VERSION 4.0

SEQ ID NO 29

LENGTH: 1064

TYPE: DAY
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LOCATION: 858, 878, 884, 886, 896, 897,
LOCATION: 957, 961, 965, 981, 991, 993,
LOCATION: 1043, 1049, 1049, 1051, 1054,
OTHER INFORMATION: n = A,T,C or G
US-09-804-682-29
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US-09-804-682-29
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Best Local S
Matches 238
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NAME/KEY: misc_feature
LOCATION: 485, 487, 488, 494, 496,
LOCATION: 583, 600, 611, 613, 623,
LOCATION: 694, 701, 713, 716, 720,
LOCATION: 744, 781, 782, 785, 789,
OTHER INFORMATION: n = A,T,C or G
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Patent No. US20020106765A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens FEATURE:
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Pred. No. 1.3e-10;
0; Mismatches 312;
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Sequence 1141, Application US/10292798

Sequence 1141, Application US/10292798

Publication No. US20030235833A1

GENERAL INFORMATION:
APPLICANT: SUWA, MAKIKO
APPLICANT: AKIYAWA, YUTAKA
APPLICANT: AKIYAWA, YUTAKA
APPLICANT: AKIYAWA, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
ITITLE OF INVENTION: GGANOSIME TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REFERENCE: 084315/166

CURRENT APPLICATION NUMBER: US/10/292,798
CURRENT APPLICATION NUMBER: 10/017,161
PRIOR APPLICATION NUMBER: 10/017,161
PRIOR APPLICATION NUMBER: J201-246789
PRIOR FILING DATE: 2001-12-18
PRIOR FILING DATE: 2001-06-18
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SOFTWARE: PatentIn Ver. 2.
SEQ ID NO 1141
LENGTH: 1117
                                                            OTHER INFORMATION: a, t,
                                                                                                FEATURE: modified base LOCATION: (351)..(356)
                                                                                                                                                                                                NAME/KEY: modified_base
LOCATION: (343)..(344)
COTHER INFORMATION: a, t,
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LOCATION: (173)..(173)
OTHER INFORMATION: a, t,
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LOCATION: (170)..(170)
OTHER INFORMATION: a, t, c,
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LOCATION: (207)..(306)
OTHER INFORMATION: a, t,
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LOCATION: (201)..(917)
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ORGANISM: Homo sapiens
NAME/KEY: modified_base
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LOCATION: (1)..(1117)
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FEATURE: NAME/KEY:
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                                 NAME/KEY: modified base LOCATION: (539)..(542) OTHER INFORMATION: a, t.
                                                                      NAME/KEY: modified base LOCATION: (532)..(533) OTHER INFORMATION: a, t, FEATURE:
                                                                                                                      LOCATION: (525)..(527)
OTHER INFORMATION: a, t,
FEATURE:
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NAME/KEY: modified_base
LOCATION: (509)..(510)
OTHER_INFORMATION: a, t,
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NAME/KEY: modified base
NAME/KEY: (398)..(399)
                                                                                                                                             NAME/KEY: modified base LOCATION: (525)..(527)
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LOCATION: (487)..(497)
OTHER INFORMATION: a, t,
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OTHER INFORMATION: a, t,
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LOCATION: (468)..(468)
OTHER INFORMATION: a, t,
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LOCATION: (464)..(465)
OTHER INFORMATION: a, t,
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LOCATION: (440)..(444)
OTHER INFORMATION: a, t,
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LOCATION: (405)..(405)
OTHER_INFORMATION: a, t,
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LOCATION: (401)..(402)
OTHER INFORMATION: a, t,
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OTHER INFORMATION: a, t,
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LOCATION: (380)..(383)
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OTHER INFORMATION: a,
FEATURE:
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LOCATION: (431)..(432)
OTHER INFORMATION: a, t,
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NAME/KEY: modified base LOCATION: (673)..(675) OTHER INFORMATION: a, t,
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OTHER INFORMATION: a, t,
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RESULT 12
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PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1403
LENGTH: 1117
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TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED
FILE REFERENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18
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APPLICANT: ASAI, KIYOS
APPLICANT: AKIYAMA, YU
                                                          NAME/KEY:
LOCATION:
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LOCATION: (1)..(1117)
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ORGANISM: Homo sapiens
FEATURE:
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NAME/KEY: modified base
LOCATION: (694)..(696)
OTHER INFORMATION: a, t,
LOCATION: (170)
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OTHER INFORMATION: a, t, FEATURE:
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OTHER INFORMATION: a, t,
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LOCATION: (577)
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LOCATION: (573)
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NAME/KEY: modified_base
LOCATION: (565)
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OTHER INFORMATION: a, t,
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Sequence 33, Application US/09804682
Patent No. US20020106765A1
GENERAL INFORMATION:
APPLICANT: Kinders, Robert
APPLICANT: Corey, Michael J.
APPLICANT: Corey, Michael J.
TITLE OF INVENTION: PAL-18 POLYPEPTIDES, NU
TITLE OF INVENTION: MODULATING THE SAME AND
TITLE OF INVENTION: MODULATING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 178
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LOCATION: (688)..(689)
OTHER INFORMATION: a, t,
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OTHER INFORMATION: a,
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Local Similarity 37.8%;
les 178; Conservative
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Pred. No. 2.7e-10;
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CURRENT APPLICATION NUMBER: US/09/804,682
CURRENT FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 174
SOFTWARE: FASUSEQ for Windows Version 4.0
SEQ ID NO 33
                                                                                                                                                                                                                                                                                                          Query Match 8.8%;
Best Local Similarity 43.8%;
Matches 218; Conservative
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Pred. No. 2.4e-09;
0; Mismatches 274;
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US-09-940-316B-1/c ; Sequence 1, Application US/09940316B ; Publication No. US20030175901A1

RESULT 14

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SEQ ID NO 1
LENGTH: 77536
TYPE: DNA
ORGANISM: Streptomyces hygroscopicus
FEATURE:
NAME/KEY: CDS
LOCATION: (52275)...(71465)
US-09-940-316B-1
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APPLICANT: RESUES, CHRISTOPHER
APPLICANT: CHU, DANIEL
APPLICANT: KHOSLA, CHAITAN
APPLICANT: SANTI, DANIEL
APPLICANT: WU, KAI
TITLE OF INVENTION: POLYKETIDES ENCODING THE £KBA GENE OF THE
TITLE OF INVENTION: GENE CLUSTER
FILE REFERENCE: 30062-20026.11
CURRENT APPLICATION NUMBER: US/09/940,316B
CURRENT FILING DATE: 2001-08-27
PRIOR APPLICATION NUMBER: US 60/13,650
PRIOR APPLICATION NUMBER: US 60/13,650
PRIOR APPLICATION NUMBER: US 60/13,810
PRIOR PILING DATE: 1999-06-17
PRIOR APPLICATION NUMBER: US 60/123,810
PRIOR PILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 60/123,748
PRIOR FILING DATE: 1999-03-11
PRIOR PILING DATE: 1999-03-11
PRIOR PILING DATE: 1999-03-11
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PRIOR PILING DATE: 1999-03-11
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US-10-184-644-332/c
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                                                                                               Sequence 332, Application US/10184644 Publication No. US20030044930A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 186; Conserv
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APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audre:
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Pred. No. 8.5e-09;
0; Mismatches 192;
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US-10-184-644-332
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 332
LENGTH: 520
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CURRENT FILING DATE: 2002-06-28
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X WPI; 2000-412336/35. N-PSDB; AADO1354. 03-DEC-1998; 08-JUN-2000 Triticum aestivum. Wheat; sphingolipid desaturase; membrane-bound desaturase; transgenic plant; fatty acid. 12-OCT-2000 AAY71556; Cahoon EB, Cahoon RE, 02-DEC-1999; WO200032790-A2. Wheat sphingolipid desaturase #2. AAY71556 standard; Protein; (DUPO ) DU PONT DE NEMOURS & CO E I. (first entry) 98US-0110784. 99WO-US28589 Hitz WD, 114 ₿ Kinney AJ;

Polynucleotide encoding delta-6 desaturase enzyme useful for producing transgenic plants and for producing antibodies specific to which is

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RESULT 2
AAY/1555
ID AAY/1555
ID AAY/1555
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The present sequence is a sphingolipid desaturase from clone wre1.pk0004.c7:fis isolated from wheat etiolated seedling root cDNA library, wre1.

The present sequence is useful for producing transgenic plants having altered levels of sphingolipid desaturase which in turn would alter the fatty acid composition. The enzyme is also useful for producing polyclonal or monoclonal antibodies. The polynucleotide is useful as primer or probe for screening cDNA libraries to
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transgenic plant; fatty acid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY71552 standard; Protein; 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                isolate desired full-length cDNA clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (DUPO ) DU PONT DE NEMOURS & CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000-412336/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sphingolipid desaturase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77
                          N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MPAASKDAADVRMISTKELQAHAAADDLWISISGDVYDVTPWLRHHPGGEVPLITLAGQD
                                                                          94;
                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
PAASKDAADVRMISTKELQAHAAADDLWISISGDVYDVTPWLRHHPGGEVPLITLAGQDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATDAFMAYHPPSVRPLLRRFFVGRLTDYTVPPASADFRRLLAQLSSAGLFERVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATDAFMAYHPPSVRPLLRRFFVGRLSDYTVPPASADFRRLLAQLSSAGLFERVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MPAASKDAADVRMISTKELQAHAAADDLWISISGDVYDVTPWLRHHPGGEVPLITLAGQD
                                                                                                                                                                              462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cahoon RE,
                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                              Ŗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A
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                                                                                                    84.6%;
83.2%;
                                                                          9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
Pred.
                                                                                                  Score 501; DB 21;
Pred. No. 1.8e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    membrane-bound
                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kinney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   588; DB 21;
No. 9.4e-61;
                                                                          10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    desaturase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                         Length 462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 469;
                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60
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RESULT 5
AAY51348
ID AAY5
XX
AC AAY5
XX
AC AAY5
XX
AC AAY5
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                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 52
                                                                                                                                                                                                                                                                                                                  The present sequence is a delta-6 fatty acid desaturase protein sequence from clone pps.bk0011.d5:fis isolated from Florida bitterbush developing seed cDNA library, pps. The delta-6 desaturase enzyme catalyses the formation of tariric acid, a fatty acid that has a triple bond at the delta-6 carbon. The present sequence is useful for producing transgenic plants having altered levels of delta-6 desaturase which in turn would alter the fatty acid composition. The enzyme is also useful for producing polyclonal or monoclonal antibodies. The polynucleotide is useful as primer or probe for screening cDNA libraries to isolate desired full-length cDNA clones.
 27-APR-2000
                           AAY51348;
                                                       AAY51348 standard;
                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 10; Page 40-41; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polynucleotide encoding delta-6 desaturase enzyme useful for producing transgenic plants and for producing antibodies specific to which is useful for screening cDNA expression libraries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAD01349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Picramnia pentandra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Florida bitterbush;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Florida bitterbush delta-6 fatty acid desaturase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY71551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY71551 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200032790-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Odbo ) bu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000-412336/35.
                                                                                                                           89
                                                                                                                                                    74
                                                                                                                                                                                                  14 ISTKELQAHAAADDLWISISGDVYDVTPWLRHHPGGEVPLITLAGQDATDAFMAYHPPSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EB,
                                                                                                                                                                                                                                        52;
                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                  RPLLRRFFVG-RLTDYTVPPASADFRRLLAQLSSAGLFERVG 114
                                                                                                                        WQYLDRFFTGYYVQDYSVSEMSKDYRRLVSEFSKMGLFKTPG 109
                                                                                                                                                                              ISQADLAKHKQPGDLWISIKGKVYDISKWTKEHPGGELPLLSFAGQDVTDAFIAYHPGTA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PONT DE NEMOURS & CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plant; fatty acid; membrane-bound desaturase.
                                                                                                                                                                                                                                                                                            448 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cahoon RE,
                                                                                                                                                                                                                                       Conservative
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0110784.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US28589.
                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     delta-6 fatty acid desaturase; tariric acid;
                                                                                                                                                                                                                                                 46.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hitz WD,
                                                                                                                                                                                                                                     16;
                                                     458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   448
                                                                                                                                                                                                                                                  Score 274.5; DB 21;
Pred. No. 9.8e-24;
                                                     ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ħ
                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kinney AJ;
                                                                                                                                                                                                                                     33;
                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                 448;
                                                                                                                                                                                                                                    ۲.
                                                                                                                                                                                                                                     Gaps
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В
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                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel sphingolipid desaturase that selectively introduces a double bond into the sphingolase of the ceramide residue of sphingolipids and capnoids. A DNA sequence encoding the sphingolipid desaturase, or a vector containing the DNA sequence, can be used to produce transgenic plants, especially crop plants, with an increased or decreased delta-8-unsaturated long-chain base content or an altered delta-8-unsaturated long-chain base content or an altered delta-8-unsaturated long-chain base deficiency, to compensate for a delta-8-unsaturated long-chain base deficiency, to exclude production of delta-8-unsaturated bases, to increase tolerance or resistance to soil salinity, ion stress or toxicity, drought, wet conditions, cold or frost and/or phytopathogenic microorganisms or to alter size growth and flowering time. Cells, transgenic organisms or plants containing the DNA sequence can be used to produce sphingolipids and capnoids with unsaturated sphingobases. The sphingolipids or capnoids can be used in cosmetics, pharmaceuticals and foods and as chemical raw materials. This sequence represents a sphingolipid desaturase protein
                                                                                                                                                                                                                                                                                                      Best Loc
Matches
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                               AAY71554;
                                                                                             AAY71554 standard;
                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                      materials. This bequeive and invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transgenic plant; crop plant; delta-8-unsaturated long-chain base; tolerance; resistance; soil salinity; ion stress; toxicity; drought; cold; frost; phytopathogenic microorganism; flowering time; cosmetic; pharmaceutical; food; chemical raw material.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 15; 62pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New sphingolipid desaturase that selectively introduces double bond into sphingolipids and capnoids -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heinz E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DE19828850-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAZ44851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GVSE-) GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sphingolipid desaturase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sphingolipid desaturase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000-127549/12.
                                                                                                                                                                             77
                                                                                                                                                                                                         72
                                                                                                                                                                                                                                        17
                                                                                                                                                                                                                                                         52;
                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                           TAWKHLDKLFTGYHLKDYQVSDISRDYRKLASEFAKAGMFEKKG
                                                                                                                                                                                                         SVRPLLRRFFVG-RLTDYTVPPASADFRRLLAQLSSAGLFERVG 114
                                                                                                                                                                                                                                        KYITSKELKKHNNPNDLWISILGKVYNVTEWAKEHPGGDAPLINLAGQDVTDAFIAFHPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zaehringer U,
                                                                                                                                                                                                                                                                                                                                                                     458 AA;
                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98DE-1028850.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98DE-1028850
                                                                                              Protein;
                                                                                                                                                                                                                                                                                                                     46.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sld1; sphingobase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schmidt H,
                                                                                                                                                                                                                                                                                                        19;
                                                                                                450
                                                                                                                                                                                                                                                                                                                       Score 274.5; DB Pred. No. 1e-23;
                                                                                                ₿
                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sperling P;
                                                                                                                                                                                                                                                                                                                                      DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ceramide;
                                                                                                                                                                                                                                                                                                        32;
                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                       458;
                                                                                                                                                                                                                                                                                                      ۲.
                                                                                                                                                                                                                                                                                                      Gaps
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Soybean sphingolipid desaturase

#2

12-OCT-2000

(first entry)

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RESULT 7
ABG73418
ID 78418
ID 78418
ID 78418
AC ABG7
XX ABG7
XX Ever
XX Delt
KW maiz
KW maiz
KW ever
XX Octa
KW ever
XX Octa
XX US20
PN US20
PF 21-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 50; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is a sphingolipid desaturase from clone sel.pk0017,b4:fis isolated from soybean seedling cDNA library, sel. The present sequence is useful for producing transgenic plants having altered levels of sphingolipid desaturase which in turn would alter the fatty acid composition. The enzyme is also useful for producing polyclonal or monoclonal antibodies. The polynucleotide is useful as primer or probe for screening cDNA libraries to isolate desired full-length cDNA clones.
                                                                                                                      maize; tobacco; peanut; carrot; oil seed
octadecatetraenoic acid; alpha-linolenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polynucleotide encoding delta-6 desaturase enzyme useful for producing transgenic plants and for producing antibodies specific to which is useful for screening cDNA expression libraries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Soybean; sphingolipid desaturase; membrane-bound desaturase; transgenic plant; fatty acid.
    21-DEC-2001; 2001US-0029756.
                             08-AUG-2002.
                                                      US2002108147-A1
                                                                                  Oenothera biennis.
                                                                                                                                                 Delta-6-desaturase; enzyme; delta-12-desaturase; sunflower;
                                                                                                                                                                             Evening primrose delta-6-desaturase
                                                                                                                                                                                                         16-APR-2003
                                                                                                                                                                                                                                                           ABG73418 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cahoon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycine
                                                                                                        evening
                                                                                                                                                                                                                                   ABG73418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-JUN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200032790-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UQ ( OQUQ)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000-412336/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
                                                                                                                                                                                                                                                                                                                              69
                                                                                                                                                                                                                                                                                                                                                      72 SVRPLLRRFFVG-RLTDYTVPPASADFRRLLAQLSSAGLFERVG 114
                                                                                                                                                                                                                                                                                                                                                                                                  12 RMISTKELQAHAAADDLWISISGDVYDVTPWLRHHPGGEVPLITLAGQDATDAFWAYHPP
                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            max.
                                                                                                          primrose.
                                                                                                                                                                                                                                                                                                                              TAWSHLEKFFTGYHLSDFKVSEVSKDYRKLASEFSKLGLFDTKG 112
                                                                                                                                                                                                                                                                                                                                                                                  KYITSEELKGHNKEGDLWISIQGKVYNVSDWVKEHPGGDVPISNLAGQDVTDAFIAYHPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 47-48; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PONT DE NEMOURS &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         450 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cahoon RE,
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                      (first
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48.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 271.5; DB 21 Pred. No. 2.2e-23; 1; Mismatches 32;
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                                                                                                                                                                             #2
                                                                                                                        rape; gamma-linolenic acid
acid; delta-15-desaturase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                450;
                                                                                                                                    soybean;
nic acid;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                      GLA;
                                                                                                                                                                                                                                                                                                                                                                                  68
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Best Local S
Matches 53
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19-SEP-1997;
10-OCT-1991;
                                                                                                                                                                                                                                   for producing a plant (such as sunflower, soybean, maize, tobacco, peanut, carrot or oil seed rape plant) with increased gamma-linolenic acid (GLA) content by transforming a plant cell with the nucleic acid or vector and regenerating a plant with increased GLA content from the plant cell, for inducing or increasing production of GLA in an organism lacking in or producing low levels of GLA and for inducing production of or production cacid in at least one of a plant deficient or lacking in or producing low levels of octadecaterraenoic acid, a bacterium which produces alpha-linolenic acid or a bacterium which exhibits a delta-15-desaturase activity on a GLA substrate. This sequence represents an evening primrose delta-6-desaturase polypeptide.
                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a nucleic acid encoding an evening primrose delta-6-desaturase polypeptide. The nucleic acid, a vector comprising nucleic acid or a nucleic acid encoding delta-12-desaturase, is useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel nucleic acid encoding evening primrose delta-6-desaturase, for producing plant with increased gamma linolenic acid content, for inducing octadecatetraenoic acid production in plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 15; Fig 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-066659/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-JAN-1992;
14-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (THOM/) THOMAS
67 TAWRHIDPLFTGYYLKDFEVSEISKDYRRILNEMSRSGIFEKKG
                                                                                         12 RMISTKELQAHAAADDLWISISGDVYDVTPWLRHHPGGEVPLITLAGQDATDAFMAYHPP
                              72 SVRPLLRRFFVG-RLTDYTVPPASADFRRLLAQLSSAGLFERVG
                                                                  7
                                                                                                                                      53,
                                                                                                                                                    Similarity
                                                                  KYITAEDLRRHNKSGDLWISIQGKVYDVSRWAAEHPGGEVPLLMLAGQDVTDAFIAYHPG
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                                                                                                                                      Conservative
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97US-0934254.
91US-0774475.
91US-0817919.
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94US-0307382.
97US-0789936.
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                                                                                                                                                    45.5%;
51.0%;
                                                                                                                                    Score 269.5; DB 2
Pred. No. 3.8e-23;
7; Mismatches 33
                                                                                                                                      33;
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                                                                                                                                      Indels
                                                                                                                                                                      Length
 110
                                  114
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AAU79851
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PD US63
PN US63
PN 13-C
PR 13-C
PR 13-C
                                                                                                                                                                                                                                    RESULT
                                                                                                                 delta6-desaturase; sunflower; soybean; peanut; carrot; oil seed rape; gamma li
  13-OCT-1992;
                     19-SEP-1997;
                                           12-MAR-2002
                                                               US6355861-B1
                                                                                  Oenothera biennis
                                                                                                       chilling tolerance;
                                                                                                                                                Evening primrose delta6-desaturase
                                                                                                                                                                     15-JUL-2002
                                                                                                                                                                                            AAU79851;
                                                                                                                                                                                                                 AAU79851 standard;
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                                                                                                                                                                       (first
  92US-0959952
                      97US-0934254.
                                                                                                                                                                                                                 Protein;
                                                                                                         evening
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                                                                                                          primrose
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Best Local Similarity
Matches 52; Conser
 13-OCT-1992;
19-SEP-1997;
10-OCT-1991;
08-JAN-1992;
14-SEP-1994;
28-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               primrose Delta6-desaturase. The nucleic acid and a vector expressing the nucleic acid are useful for producing a plant such as sunflower, soybean, maize, tobacco, peanut, carrot or oil seed rape plant, with increased gamma linolenic acid (GLA) content, and also for inducing or increasing production of GLA in a bacteria or plant deficient, lacking in or producing low levels of GLA. The nucleic acid is also useful for inducing chilling tolerance in plants. This is the amino acid sequence of the evening primrose delta6 desaturase involved in the production of gamma increase.
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08-JAN-1992;
14-SEP-1994;
28-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel nucleic acid encoding evening primrose delta6-desaturase which converts linoleic acid to gamma linolenic acid useful for producing gamma linolenic acid in transgenic plant or bacteria -
                                                                                                                                                                                                                                     Delta-6-desaturase; enzyme; delta-12-desaturase; sunflower; soybean; maize; tobacco; peanut; carrot; oll seed rape; gamma-linolenic acid; GLA; octadecatetraenoic acid; alpha-linolenic acid; delta-15-desaturase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention describes an isolated nucleic acid encoding an evening
                                                                                                                                                                                             Oenothera biennis.
                                                                                                                                                                                                                                                                                               Evening primrose delta-6-desaturase
                                                                                                                                                                                                                                                                                                                                                                                     ABG73416 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Column 45-48; 53pp; English.
                                                                                                      21-DEC-2001; 2001US-0029756.
                                                                                                                                   08-AUG-2002.
                                                                                                                                                                                                                                                               Delta-6-desaturase; enzyme; delta-12-desaturase; sunflower;
                                                                                                                                                                                                                                                                                                                              16-APR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          452 AA;
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ilarity 49.5%; Pred. No. 1e-22;
Conservative 18; Mismatches
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92US-0959952.
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91US-0774475.
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94US-0307382.
97US-0789936.
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92US-0817919.
94US-0307382.
97US-0789936.
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RESULT 10
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Best Local S
Matches 52
13-OCT-1992;
19-SEP-1997;
10-OCT-1991;
08-JAN-1992;
14-SEP-1994;
28-JAN-1997;
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                                                                                                                                                                                                                                                                                                                                                                               Borago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Delta-6-desaturase; enzyme; delta-12-desaturase; sunflower; soybean; maize; tobacco; peanut; carrot; oil seed rape; gamma-linolenic acid; octadecatetraenoic acid; alpha-linolenic acid; delta-15-desaturase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Borage delta-6-desaturase
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DB; ABX15367.
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52; Conserv
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91US-0774475.
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49.5%; Pred. No. 1e-22;
tive 18; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLA;
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ARPSULT 11
AARP8455
ID AAR98
XX AAR98
XX BORAG
DT 15-SE
XX Delta
XX Delta
XX Delta
XX Chill
XX Chill
XX Chill
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a nucleic acid encoding an evening primrose delta-6-desaturase polypeptide. The nucleic acid, a vector comprising the nucleic acid or a nucleic acid or a nucleic acid or a sunflower, soybean, malze, tobacco, peanut, carrot or oil seed rape plant) with increased gamma-linolenic acid (GLA) content by transforming a plant cell with the nucleic acid or vector and regenerating a plant with increased GLA content from the plant cell, for inducing or increasing production of GLA in an organism lacking in or producing low levels of GLA and for inducing production of GLA in an organism lacking in or producing low levels of EAA and for inducing production of GLA producing low levels of octadecatetraenoic acid, a bacterium which produces alpha-linolenic acid or a bacterium which exhibits a delta-15-desaturase activity on a GLA substrate. This sequence represents a borage delta-6-desaturase polypeptide.
                                                                                                                                                                          Region
                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                               Delta-6-desaturase; gamma-linolenic acid; transgenic plant; polyunsaturated fatty acid; octadecatetraeonic acid; chilling resistance; oilseed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acid encoding evening primrose delta-6-desaturase, for producing plant with increased gamma linolenic acid content, for inducing octadecatetraenoic acid production in plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-066659/06
                   28-DEC-1995;
                                                      11-JUL-1996.
                                                                                                                                           Region
                                                                                                                                                                                                                                                                Borago officinalis.
                                                                                                                                                                                                                                                                                                                                                                      Borage delta-6-desaturase
                                                                                                                                                                                                                                                                                                                                                                                                          15-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR98455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR98455 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 15; Fig 11; 55pp; English.
                                                                                        WO9621022-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 AFHPASTWKNIDKFFTGYYLKDYSVSEVSKDYRRLVFEFSKMGLYDKKG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AYHPPSVRPLLRRFFVG-RLTDYTVPPASADFRRLLAQLSSAGLFERVG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQIKKYITSDELKNHDKPGDLWISIQGKAYDVSDWVKDHPGGSFPLKSLAGQEVTDAFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AADV-RMISTKELQAHAAADDLWISISGDVYDVTPWLRHHPGGEVPLITLAGQDATDAFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               448
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                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                   95WO-IB01167
                                                                                                                       /label= Metal_box-2
                                                                                                                                                         /label= Metal_box-1
                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                            label= Lipid_box
                                                                                                                                                                             . 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.1%; Score 261; DB 24;
47.7%; Pred. No. 3.9e-22;
tive 20; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             448
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                                                                                                                                                                                                                                                                                                                                   borage;
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RESULT 12
AAW67471
ID AAW67471
XX AAW677
XX AAW677
XX DOT 02-MB
XX Upstr
KW Upstr
KW lipid
XX Borag
XX Borag
XX Borag
XX Borag
XX Upstr
KW Lipid
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Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linoleic acid to gamma-linolenic acid (GLA). Its sequence was deduced from that of the delta-6-desaturase gene (ART30395) isolates from a borage membrane-bound polysomal library. The sequence is distinct from that of Synechocystis delta-6-desaturase (AAR98456). Expression of the desaturase in transgenic plants, esp. sunflower, soybean, maize, tobacco, peanut, carrot or oilseed rape, results in increased GLA prodn. Alteration of the plant membrane lipids as a result of expression of the desaturase may also result in increased resistance to chilling.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transgenic plants comprising the borage delta-6-desaturase gene show increased production of gamma linolenic acid and having increased resistance to chilling
                                                                                                           15-OCT-1998
                                                                                                                                                                                                                                               Domain
                                                                                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Borago officinalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Upstream region; regulatory region; sunflower; albumin; seed; expression; lipid metabolism; delta-6 desaturase; transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Borage delta-6 desaturase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW67471 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Borage delta-6-desaturase (AAR98455) catalyses the conversion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Page 52-53; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Freyssinet GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-DEC-1994;
                                                                                                                                                               WO9845460-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 AYHPPSVRPLLRREFVG-RLTDYTVPPASADFRRLLAQLSSAGLFERVG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 AADV-RMISTKELQAHAAADDLWISISGDVYDVTPWLRHHPGGEVPLITLAGQDATDAFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQIKKYITSDELKNHDXPGDLWISIQGKAYDVSDWVKDHPGGSFPLKSLAGQEVTDAFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         448 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                               373..377
                                                                                                                                                                                                                                                                                                    196..200
                                                                                                                                                                                                                                                                                                                            /note= "His-rich metal
                                                                                                                                                                                                                                                                                                                                                                                 /note= "cytochrome b5 haem-binding motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                    note= "His-rich metal"
                                                                                                                                                                                                                                                                     note= "His-rich metal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 258; DB 17;
Pred. No. 8.7e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                    binding
                                                                                                                                                                                                                                                                     binding motif"
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                                                                                                                                                                                                                                                                                                                               motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 448;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66
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09-APR-1997; 09-APR-1998;

97US-0831570 98WO-US07178.

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ARBSULT 13
AAW98130
ID AAW98
XX AAW98
XX AAW98
XX AAW98
XX BORAG
XX DALLAR
KW Lrans
KW Gamma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Delta-6 desaturase; borage; oleosin; AtS21; promoter; transgenic plant; seed; lipid; fatty acid; oilseed; vegetable oil; gamma-linolenic acid; octadecatetraenoic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence corresponds to the borage (Borago officinalis) delta-6 desaturase enzyme. The encoding lipid metabolism gene is an example of a heterologous gene which can be expressed at high levels in a seed specific manner in transgenic plants, when placed under control
  WPI; 1999-180333/15
                                      Li Z,
                                                                                                                  09-APR-1997;
                                                                                                                                                      09-APR-1998;
                                                                                                                                                                                                                                                                                         Binding-site
                                                                                                                                                                                                                                                                                                                             Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                          Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Borago officinalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Borage delta-6 desaturase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW98130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW98130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the sunflower albumin gene 5' regulatory region (AAV34397).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Fig 1; 38pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New sunflower albumin 5' altered lipid metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-583201/49.
N-PSDB; AAV34398.
                                                                                                                                                                                                                                   WO9845461-A1
                                                                              (RHON )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (RHON ) RHONE-POULENC AGROCHIMIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51;
                                        Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                            RHONE-POULENC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AYHPPSVRPLLRRFFVG-RLTDYTVPPASADFRRLLAQLSSAGLFERVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AADV-RMISTKELQAHAAADDLWISISGDVYDVTPWLRHHPGGEVPLITLAGQDATDAFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQIKKYITSDELKNHDKPGDLWISIQGKAYDVSDWVKDHPGGSFPLKSLAGQEVTDAFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ď,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AFHPASTWKNLDKFFTGYYLKDYSVSEVSKDYRKLVFEFSKMGLYDKKG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         448 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                        TL;
                                                                                                                    97US-0831575
                                                                                                                                                      98WO-US07179
                                                                                                                                                                                                                                                                                           /note= "r
                                                                                                                                                                                                                                                                                                                               196..200
                                                                                                                                                                                                                                                                                                                                                                      156..163
                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                         /note=
                                                                                                                                                                                                                                                                                                                                                   /note=
                                                                                                                                                                                                                                                                                                                                                                                      note= "cytochrome b5 haem-binding motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46.8%;
                                                                            AGROCHIMIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ą,
                                                                                                                                                                                                                                                                                                                                               "metal binding,
                                                                                                                                                                                                                                                                     "metal binding,
                                                                                                                                                                                                                                                                                                         "metal binding,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  regulatory region - useful in plant seeds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 258; DB
Pred. No. 8.7e
21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             258; DB 19;
No. 8.7e-22;
                                                                                                                                                                                                                                                                         histidine-rich motif'
                                                                                                                                                                                                                                                                                                                                                 histidine-rich
                                                                                                                                                                                                                                                                                                             histidine-rich motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
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n example
s in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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RESULT 14
AAY51349
ID AAY51
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Best Local S
Matches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is borage delta-6 desaturase, an enzyme that catalyses the conversion of linoleic acid to gamma-linolenic acid (GLA). Delta-6 desaturase cDNA (see AAX24917) was isolated from a borage membrane-bound polysomal cDNA library using a partial clone, obtained from an EST database search, as probe. The borage delta-6 desaturase nucleic acid can be operably linked to the seed-specific 5' regulatory region (see AAX24916) of the Arabidopsis thaliana oleosin AtS21 gene in claimed expression cassettes of the invention. Transgenic plants, e.g. sunflower, soybean, maize, tobacco, cotton, peanut, oilseed rape or Arabidopsis are obtained that show increased levels of GLA or octadecatetrasenic acid. The levels of desirable fatty acids in oilseed crops can be manipulated to provide seed oils of use in human health and industrial applications.
                                                                                                                                                                                                                                                                                                                                                                                                              Sphingolipid desaturase; sld1; sphingobase; ceramide; capnoid; transgenic plant; crop plant; delta-8-uneaturated long-chain base; tolerance, resistance; soil salinity; ion stress; toxicity; drought; cold; frost; phytopathogenic microorganism; flowering time; cosmetic;
                                                                                                                                  Heinz
                                                                                                                                                                                                                                              27-JUN-1998;
                                                                                                                                                                                                                                                                                   30-DEC-1999.
                                                                                                                                                                                                                                                                                                                      DE19828850-A1.
                                                                                                                                                                                                                                                                                                                                                           Helianthus annuus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sunflower HADES protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY51349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY51349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid containing oleosin 5'-regulatory region - useful for modulating fatty acid synthesis and lipid metabolism in plants, particularly to increase content of gamma-linolenic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
                                                                                                                                                                                                         27-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-APR-2000
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                                                                                                                                                                      (GVSE-)
                                                                                             2000-127549/12
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                                                                                                                                                                    GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AFHPASTWKNLDKFFTGYYLKDYSVSEVSKDYRKLVFEFSKMGLYDKKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AYHPPSVRPLLRRFFVG-RLTDYTVPPASADFRRLLAQLSSAGLFERVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQIKKYITSDELKNHDKPGDLWISIQGKAYDVSDWVKDHPGGSFPLKSLAGQEVTDAFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AADV-RMISTKELQAHAAADDLWISISGDVYDVTPWLRHHPGGEVPLITLAGQDATDAFM
                                                                                                                              Zaehringer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    448 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                              98DE-1028850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43.6%; Score 258; DB 20;
46.8%; Pred. No. 8.7e-22;
tive 21; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                              chemical raw
                                                                                                                                  Schmidt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           448
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                                                                                                                                Έ
                                                                                                                             Sperling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ۵,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Disclosure; Page 33-34; 62pp; German

sphingolipid desaturase that selectively

introduces double

capnoids

sphingolipids and

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RESULT 15
AAU79830
ID AAU79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peanut; carrot; oil
chilling tolerance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   delta6-desaturase; sunflower;
peanut; carrot; oil seed rape;
                          08-JAN-1992;
14-SEP-1994;
                                                                             13-OCT-1992;
10-OCT-1991;
                                                                                                                                                                                                             12-MAR-2002.
                                                                                                                                                                                                                                                             US6355861-B1.
                                                                                                                                                                                                                                                                                                                                        Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Borago officinalis delta6-desaturase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU79830;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU79830 standard; Protein; 448 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                          19-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Borago officinalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 AYHPPSVRPLLRRFFVG-RLTDYTVPPASADFRRLLAQLSSAGLFERVG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQIKKYITSDELKNHDKPGDLWISIQGKAYDVSDWVKDHPGGSFPLKSLAGQEVTDAFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AADV-RMISTKELQAHAAADDLWISISGDVYDVTPWLRHHPGGEVPLITLAGQDATDAFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           448 AA;
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92US-0959952.
91US-0774475.
92US-0817919.
94US-0307382.
97US-0789936.
                                                                                                                                                          97US-0934254.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                     /label= Metal_box_2
                                                                                                                                                                                                                                                                                                                                                                                                                /label= Lipid_box
                                                                                                                                                                                                                                                                                                                                                             label= Metal_box_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sunrlower; soybean; maize; tobacco;
  seed rape; gamma linolenic acid; GLA;
  borage.
                                                                                                                                                                                                                                                                                                                                                                                           . 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43.6%; Score 258; DB 21;
46.8%; Pred. No. 8.7e-22;
tive 21; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                             . 163
                                                                                                                                                                                                                                                                                                                                          377
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(RHON ) RHONE-POULENC AGROCHIMIE

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밁
                                                                                                                                                        Query Match
Best Local S
Matches 51
                                                                                                                                                                                                                                                                                    primrose Delta6-desaturase. The nucleic acid and a vector expressing the nucleic acid are useful for producing a plant such as sunflower, soybean, maize, tobacco, peanut, carrot or oil seed rape plant, with increased gamma linolenic acid (GLA) content, and also for inducing or increasing production of GLA in a bacteria or plant deficient, lacking in or producing low levels of GLA. The nucleic acid is also useful for inducing chilling tolerance in plants. This is the amino acid sequence of the borage delta6 desaturase involved in the production of gamma linoleic acid.
                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acid encoding evening primrose delta6-desaturase which converts linoleic acid to gamma linolenic acid useful for producing gamma linolenic acid in transgenic plant or bacteria -
                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention describes an isolated nucleic acid encoding an evening primrose Delta6-desaturase. The nucleic acid and a vector expressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 9; Column 31-34; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2002-380944/41.
62
                                     67 AYHPPSVRPLLRRFFVG-RLTDYTVPPASADFRRLLAQLSSAGLFERVG 114
                                                                                                                                                        51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TL;
                                                                            2 AAQIKKYITSDELKNHDKPGDLWISIQSKAYDVSDWVKDHPGGSFPLKSLAGQEVTDAFV
                                                                                                                   8
                                                                                                                                                                             Similarity
                                                                                                         AADV-RMISTKELQAHAAADDLWISISGDVYDVTPWLRHHPGGEVPLITLAGQDATDAFM
  AFHPASTWKNLDKFFTGYYLKDYSVSEVSKDYRKLVFEFSKMGLYDKKG
                                                                                                                                                                                                                                       448
                                                                                                                                                          Conservative
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                                                                                                                                                      43.6%; Score 258; DB 23;
46.8%; Pred. No. 8.7e-22;
tive 21; Mismatches 35;
                                                                                                                                                                                             Length 448;
                                                                                                                                                          Indels
                                                                                                                                                          <u>ب</u>
                                                                                                                                                          Gaps
                                                                              61
                                                                                                                     66
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Job time : 11.4957 secs Search completed: January ,-2004, 06:36:55

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Result
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Listing first 45 summaries
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Maximum DB seq length: 200000000
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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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592
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          Copyright
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T5246T
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RDM196
FRDBHNP
RDBHNP
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S352241
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nitrate reductase cytochrome b5 [imp cytochrome b5 con itrate reductase nitrate reductase nitrate reductase nitrate reductase nitrate reductase nitrate reductase nitrate reductase nitrate reductase nitrate reductase nitrate reductase nitrate reductase nitrate reductase nitrate reductase nitrate reductase nitrate reductase nitrate reductase nitrate reductase nitrate reductase nitrate reductase nitrate reductase nitrate reductase nitrate reductase nitrate reductase nitrate reductase nitrate reductase nitrate reductase nitrate reductase nitrate reductase nitrate reductase nitrate reductase cytochrome b5 - co nitrate reductase linolecyl-CoA desa nitrate reductase
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RESULT 2  A84900  hypothetical protein At2g46210 [imported] - Arabidopsis thalian C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change C;Accession: A84900 R;Lin, X; Kaul, S; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L. Nature 402, 761-768, 1999 A;Title: Sequence and analysis of chromosome 2 of the plant Ara A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: A84900 A;Status: preliminary A;Rotalus: preliminary A;Rotalus: preliminary A;Cross-references: GB:AE002093; NID:g3702328; PIDN:AAC62885.1; C;Genetics:	Ouery Match 46.4%; Score 274.5; DB 2; Length 458; Best Local Similarity 50.0%; Pred. No. 6e-21; Best Local Similarity 50.0%; Pred. No. 6e-21; Matches 52; Conservative 19; Mismatches 32; Indels 1; Gaps  Qy 12 RMISTKELQAHAAADDLWISISGDVYDVTPWLRHHPGGEVPLITLAGQDATDAFMAYHPP	phingolipid desaturase (EC 1.14.99) [similarits: Helianthus annuus (common sunflower) 15-Feb-1997 #sequence_revision 13-Mar-1997 #textion: S68358	30 152 25.7 911 1 RDTONH 31 152 25.7 911 2 T08105 32 151 25.5 141 2 T15210 33 151 25.5 917 1 RDMUNH 34 149.5 25.3 135 1 CBRT5M 35 149.5 25.3 135 1 T27107 36 149.5 25.3 137 2 S46307 37 148 25.0 920 2 S52301 38 147 24.8 573 1 S06600 39 147 24.8 573 1 T08108 40 146.5 24.7 916 2 T08108 41 146.5 24.7 916 2 S07554 42 145 24.5 898 1 RDBJNH 45 144.5 24.4 501 2 S51160  ALIGNMENTS
<pre>chaliana _change 02-Feb-2001 m.I.; Town, C.D.; Fujii, C.Y.; Nen, S.E.; Umayam, L.; Tallon, L.; g, S.L.; Fraser, C.M.; Venter, J. ant Arabidopsis thaliana. 2885.1; GSPDB:GN00139</pre>	Length 458;  Indels 1; Gaps 1;  LITLAGODATDAFMAYHPP 71	com	nitrate reductase nitrate reductase probable cytochrom nitrate reductase cytochrome b5 - vi cytochrome b5 - ri hypothetical prote nitrate reductase L-lactate dehydrog nitrate reductase nitrate reductase nitrate reductase nitrate reductase nitrate reductase nitrate reductase nitrate reductase nitrate reductase nitrate reductase nitrate reductase nitrate reductase nitrate reductase

A;Gene: At2g46210

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RESULT 4
T47950
                                                                                                                A;Cross-references: EMBL:AL132962; PIDN:CAB71088.1
A;Experimental source: cultivar Columbia; BAC clone F2A19
A;Experiing, P.; Zaehringer, U.; Heinz, E.
J. Biol. Chem. 273, 28590-28596, 1998
A;Title: A sphingolipid desaturase from higher plants. Id
A;Reference number: Z22986; MUID:99003197; PMID:9786850
                                                                                                                                                                                                                                                                                                                                   N;Alternate names: protein F2A19.180
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence revision 20-Apr-2000 #text_change 02-Sep-2000
C;Accession: T47950; T51848
R;De Haan, M.; Maarse, A.C.; Grivell, L.A.; Mewes, H.W.; Lemcke, K.; Mayer, submitted to the Protein Sequence Database, January 2000
                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-449 < DEH>
                                                                                                                                                                                                                                                                                                A; Reference number: Z24480
A; Accession: T47950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
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                                        A; Molecule type: mRNA
A; Residues: 1-449 <SPE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                         delta-8 sphingolipid desaturase (EC 1.14.99.-) [validated] - Arabidopsis thaliana
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A;Cross-references: EMBL:AJ224160; PIDN:CAA11857.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 49
                                                                                                Accession: T51848
                                                                       Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             n 42.3%;
Similarity 47.1%;
49; Conservative 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SVRPLLRRFFVG-RLTDYTVPPASADFRRLLAQLSSAGLFERVG 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source: cultivar Drakkar
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EMBL:AJ224161; PIDN:CAA11858.1
se: cultivar Columbia; mainly green
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43.2%; Score 255.5; DB 2; 45.0%; Pred. No. 5.7e-19; tive 20; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 250.5; DB 2;
Pred. No. 1.9e-18;
7; Mismatches 37;
  parts,
                                                                                                                                         Identification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 449;
  some flowers,
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    few
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                                                                                                                                         cytochron
    roots
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C;Complex: homodimer
C;Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 reductive cytochrome: chromoprotein; electron transfer; FAD; flavoprotein; heme; homodimer; iron; m F;72-477/Domain: molybdopterin-binding domain homology <PCO>
F;546-620/Domain: cytochrome b5 core homology <CB5>
F;655-905/Domain: cytochrome b5 core homology <CBr>
F;179/Binding site: molybdopterin (Cys) (covalent) #status predicted
F;428/Disulfide bonds: interchain #status predicted
F;581,604/Binding site: heme iron (His) (axial ligands) #status predicted
F;751,879/Binding site: NADP (Lys, Cys) #status predicted
F;758/Binding site: FAD (Tyr) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Diolez, A.; Langin, T.; Gerlinger, C.; Brygoo, Y.; Daboussi, M.J. Gene 131, 61-67, 1993
A;Title: The nia gene of Fusarium oxysporum: Isolation, sequence and A;Reference number: JN0803; MUID:93380674; PMID:8370541
A;Accession: JN0803
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nitrate reductase (NADPH) (EC 1.7.1.3) - fungus (Pusarium oxysporum) C;Species: Pusarium oxysporum C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-JC;Accession: JN0803; S35748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ś
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: sld1
A;Map position: 3
A;Note: F2A19.180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-905 < DIO >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Introns:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: nia
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                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local Similarity
                                                                                                                                                                                                                            Local
607
                                                                                                                                             12 RMISTKELQAHAAADDLWISISGDVYDVTPWLRHHPGGEVPLITLAGQDATDAFMAYHPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    604/1
                                                 72 SVRPLLRRFFVGRLTDYTVPPASAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 AYHPPSVRPLLRRFFVG-RLTDYTVPPASADFRRLLAQLSSAGLFERVG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 DAADVRMISTKELQAHAAADDLWISISGDVYDVTPWLRHHPGGEVPLITLAGQDATDAFM
                                                                                                                                                                                                                            Similarity
NAKAMLPTYHIGTLDEESRAILSGD
                                                                                                   RKITIEELKAHSGEEEPWFVVKGEVYDGTPYLSGHPGGAASIFGAAGQDATEEFMAIHSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EETEKKYITNEDLKKHNKSGDLWIAIQGKVYNVSDWIKTHPGGDTVILNLVGQDVTDAFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AFHPGTAWHHLDHLFTGYHIRDFQVSEVSRDYRRMAAEFRKLGLFENKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T.; Gerlinger, C.; Brygoo, Y.; Daboussi,
                                                                                                                                                                                                                         29.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24; Mismatches
                                                                                                                                                                                                                         Score 177; DB 1;
Pred. No. 2.1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 236.5; DB 2
Pred. No. 5.6e-17;
                                                                                                                                                                                                    Mismatches
631
                                                 96
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hypothetical protein T1K7.28 - Arabidopsis thaliana (Species: Arabidopsis thaliana (Mouse-ear cress) (Species: Arabidopsis thaliana (Mouse-ear cress) (Spate: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001 (Spate: 02-Mar-2001) #spate: 02-Mar-2001 #spate: 03-Mar-2001 
C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dev

; Alonso, swar, K.;

RESULT A86390

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C.A.; Li, J.H.; Li, Yenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A; Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Maurer, P.
submitted to the EMBL Data Library,
".Deference number: $52857
cytochrome b5 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 24-Oct-2000 #sequence_revision 24-Oct-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                           F;535-609/Domain: cytochrome b5 core homology <CB5>
F;645-894/Domain: cytochrome-b5 reductase homology <CBR>
F;169/Binding site: molybdopterin (Cys) (covalent) #status predicted F;570,593/Binding site: heme iron (His) (axial ligands) #status pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 reductase; beme; iron; metalloprotein; molybdenum; molybdopterin; oxidoreductase; phosi F;62-467/Domain: molybdopterin-binding domain homology <PCO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nitrate reductase (NADH) (EC 1.7.1.1) - Beauveria bassiana C;Species: Beauveria bassiana C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_C;Accession: $52857
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A; Residues: 1-894 < MAU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: A; Accession: S52857
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A;Molecule type: DNA
A;Residues: 1-135 <STO>
                                                                               T52469
                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cross-references: EMBL:X84950; NID:g693925; PIDN:CAA59336.1; PID:g693926
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Superfamily: cytochrome b5; cytochrome b5 core homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;Cross-references: GB:AE005172; NID:g9797763; PIDN:AAF98581.1; GSPDB:GN00141
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,64/Binding site: heme iron (His) (axial ligands) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                   71
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                                                                                                                                                                                                                                                                                                         11 VRMISTKELQAHAAADDLWISISGDVYDVTPWLRHHPGGEVPLITLAGQDATDAFMAYHP 70
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                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                   PSVRPLLRRFFVGRLTD 87
                                                                                                                                                                                                                                                              VRIISLEELKAHEGEMEPWFVVNGHVYNGTPYLDNHPGGATSIINAAAQDATEEFWTIHS
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                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                            29.4%; Score 174; DB 2; 40.3%; Pred. No. 4.3e-10;
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  #text_change
                                                                                                                                                                                                                                                                                                                                                                                                  Length 894;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               predicted
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nitrate reductase (NADH) (EC 1.7.1.1) nia-1 - common tobacco C;Species: Nicotiana tabacum (common tobacco) C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change C;Accession: S04838; S05696 R;Vaucheret, H.; Kronenberger, J.; Rouze, P.; Caboche, M. Plant Mol. Biol. 12, 597-600, 1989
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A;Molecule type: mRNA
A;Residues: 1-134 <FUK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Fukuchi-Mizutani, M.; Mizutani, M.; Tanaka, Y.; Kusumi, T.; Ohta, Plant Physiol. 119, 353-361, 1999
A;Title: Microsomal Electron Transfer in Higher Plants: Cloning and A;Reference number: Z25274
A;Accession: T52469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Description: acts as electron carrier for membrane-bound oxygenases C;Superfamily: cytochrome b5; cytochrome b5 core homology C;Keywords: electron transfer; heme; iron; membrane protein; metalloprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 05-May-2000 C;Accession: T14454
C;Accession: T14454
R;Kearns, E.V.; Keck, P.; Somerville, C.R.
submitted to the EMBL Data Library, March 1992
A;Description: Nucleotide sequence of cDNA for cytochrome b5 from cauliflow.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytochrome b5 - wild cabbage
C;Species: Brassica oleracea (wild cabbage)
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F;40,64/Binding site: heme iron (His) (axial ligands) #status
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A; Reference number: S04838
A; Accession: S04838
                                              A; Title: Complete nucleotide sequence of the two homeologous tobacco nitrate reductase
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Pred. No. 1.5e-10;
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S46306
cytochrome
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C;Complex: homodimer
C;Complex: homodimer
C;Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 reductase in complex in complex reductase (NADH); flavoprotein; heme; homodimer; iron; f;79-471/Domain: molybdopterin-binding domain homology <PCO>
F;79-471/Domain: cytochrome b5 core homology <CB5>
F;654-904/Domain: cytochrome-b5 reductase homology <CBR>
F;654-904/Domain: cytochrome-b5 reductase homology <PCO>
F;183/Binding site: molybdopterin (Cys) (covalent) #status predicted
F;462/Disulfide bonds: interchain #status predicted
F;566,589/Binding site: heme iron (His) (axial ligands) #status predicted
F;718,876/Binding site: NAD (Lys, Cys) #status predicted
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A;Molecule type: mRNA
A;Residues: 1-140 <FUK>
A;Cross-references: EMBI
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A; Molecule type: DNA
A; Residues: 1-35, 'P'
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Plant Physiol. 119,
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                                            RESULT
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Best Local :
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Electron Transfer in
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  tobacco
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C;Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 reduction content of the core homology; cytochrome-b5 reduction content of the core homology cytochrome content of the cytochrome b5 core homology cytochrome cytochrome b5 core homology cytochrome cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 reductase homology cytochrome-b5 re
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                                                                                                                     F;796,956/Binainy or F;835/Binding site:
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C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 05-May-2000
C;Accession: S46306; S33157
C;Accession: S46306; S3157
Plant Mol. Biol. 25, 527-537, 1994
A;Title: Tobacco cytochrome b(5): cDNA isolation, expression analysis and in vitro proteb
A;Reference number: S46306; MUID:94325476; PMID:8049375
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C;Complex: homodimer
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F;8-83/Domain: cytochrome b5 core homology <CB5>
F;43,67/Binding site: heme iron (His) (axial ligands) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: protein
A;Residues: 'D',622-623,'Y',624,'IK',627,'Y',628,'XNXKXT',635,'LILHYKX',643,'DL',646,'K',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Title: On the presence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Superfamily: cytochrome b5; cytochrome b5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: nit-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: S07176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-982 <MOL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: S16292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1-139 < SMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: S46306
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Best Local
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 HPPSVRPLLRRFFVGRLTDYTVP 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 DVRMISTKELQAHAAADDLWISISGDVYDVTPWLRHHPGGEVPLITLAGQDATDAFM-AY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33;
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                                   Similarity
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   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sence of a heme-binding domain homologous to cytochrome b5 in S07176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL: X71441; NID: g296385; PIDN: CAA50575.1;
                                   28.0%;
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   19;
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Pred. No. 4.1e-10;
                                   Score 165.5; DB 1;
Pred. No. 3.8e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
   Mismatches
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   38;
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Indels
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A;Introns: 338/1; 385/1; 462/3
C;Complex: homodimer
C;Superfamily: nitrate reductase (NADH); cytochrome b5 core homology; cytochrome-b5 reductases chromoprotein; electron transfer; FAD; flavoprotein; heme; homodimer; iron; F;79-471/Domain: molybdopterin-binding domain homology <PCO>
cytochrome b5 At2g32720 [similarity] - Arabidopsis thaliana
N;Alternate names: protein F24L7.14
C;Species: Arabidopsis thaliana (mouse-ear cross)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 02-Mar-2001
C;Accession: T00796; F84736
R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, February 1998
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R;Calza, R.; Huttner, E.; Vincentz, M.; Rouze, P.; Galangau, F.; Vaucheret, H.; Cherel, Mol. Gen. Genet. 209, 552-562, 1987
Mol. Gen. Genet. 209, Fragments complementary to tobacco nitrate reductase mRNA and en A;Reference number: S22779
A;Accession: S22779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: S25375
A; Accession: S25375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nitrate reductase (NADH) (EC 1.7.1.1) nia-2 - common tobacco C;Species: Nicotiana tabacum (common tobacco) C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 03-Jun-2002 C;Accession: S04839; S25375; S22779
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A; Residues: 171-724 < CAL>
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                                                                                                                                                                                                                             T00796
                                                                                                                                                                                                                                                          RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  422/Disulfide bonds: interchain #status predicted
566,589/Binding site: heme iron (His) (axial ligands) #status
718,876/Binding site: NAD (Lys, Cys) #status predicted
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-references: EMBL:X06134; NID:g19894; PIDN:CAA29497.1; PID:g929750
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Biol. 12, 597-600, 1989
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                                                                                                                                                                                                                                                                                                                                                                                                   61 ATDAFMAYHPPSVRPLLRRFFVGRL--TDYTVPP-----ASADFRRLLAQL 104
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C.; Moureaux, T.; Rouze, P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 904;
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                                     S.M.;
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A;Introns: 29/3; 52/1
C;Superfamily: cytochrome b5; cytochrome b5 core homology
C;Keywords: heme; iron; metalloprotein
F;5-80/Domain: cytochrome b5 core homology <CB5>
F;5-80/Domain: cytochrome b5 core homology <CB5>
F;40,64/Binding site: heme iron (His) (axial ligands) #st
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A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.: euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
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C;Genetics:
A;Gene: F24L7.14; At2g32720
A;Map position: 2
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## ALIGNMENTS

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Z22549; CAA80270.1; N0803; JN0803; JN0803; JN0803; JN0803; JN0803; JN0803; JN0803; JN0803; Cyt_B5_reductase. ro; IPR001199; Cyt_B5_reductase. ro; IPR001572; Euk_Mb_oxred. ro; IPR001709; PPN cyt_redctse. ro; IPR001709; PPN cyt_redctse. ro; IPR00143; Oxred_PAD/NAD(P). PP00143; Oxred_PAD/NAD(P). PP00173; heme_1; 1. PP00174; MO-Co_diner; 1. PP00175; NAD_binding_6; 1. PP00174; oxidored_molyb; 1. pR00176; CYTB5RDTASE.	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	development of a homologous transformation system.";  Gene 131:61-67(1993).  -!- FUNCTION: Nitrate reductase is a key enzyme involved in the first step of nitrate assimilation in plants, fungi and bacteria.  -!- CATALYTIC ACTIVITY: Nitrite + NADP(+) + H(2)O = nitrate + NADPH.  -!- COPACTOR: REQUIRES PAD, A HEME GROUP (CALLED CYTOCHROME B-557) AND ONE MOLYBDENUM ATOM.  -!- SUBUNIT: Homodimer (By similarity).  -!- SUBUNIT: Homodimer (By similarity).  -!- SIMILARITY: CONTAINS 1 Cytochrome b5 heme-binding domain.  -!- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE CT-TERMINAL DOMAIN.	<pre>ium oxysporum. ryota; Fungi; Ascomycota; Pezizomycotina; Sordariomyc rreomycetidae; Hypocreales; mitosporic Hypocreales; E raxID=5507; raxID=5607; RNCE FROM N.A. RN=50380674; PubMed=8370541; RN=50380674; PubMed=8370541; RN=corporation oxygonym isolation semisore.</pre>	JLT 1 FUSOX STANDARD; PRT; 905 AA. P39863; 01-FEB-1995 (Rel. 31, Created) 01-FEB-1995 (Rel. 31, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Nitrate reductase [NADPH] (EC 1.7.1.3) (NR).

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PRINTS; PR00407; EUMOPTERIN.

PRINTS; PR00371; PPNCR.

PRODOM; PD006612; CYE_B5; 1.

PROSITE; PS00191; CYTŌCHROME_B5_1; 1.

PROSITE; PS00255; CYTOCHROME_B5_2; 1.

PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.

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                                                                                         This SWISS-PROT entry is copyright. It is produced through a continuous the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Clavicipitaceae; Cordyceps.
NCBI_TaxID=176275;
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PRINTS; PRO0367; EUMOPTERIN.
PRINTS; PRO0371; PPNCR.
PROD00612; CYC B5; 1.
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                                                        STRAIN=cv. Columbia;
MEDLINE=99087489; PubMed=9872454;
Nakamura Y., Sato S., Asamizu E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR005066; Mo-Co_dImer:
InterPro; IPR001433; Oxred FAD/NAD(P)
Pfam; PF00970; FAD binding-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
InterPro;
InterPro;
Tabata S.; "Structural analysis of Arabidopsis thaliana chromance features of the regions of 1,013,767 bp
                                                                                                                                                                                                                               STRAIN=cv. Columbia;
MEDLINE=99097071; PubMed=9880378;
Fukuchi-Mizutani M., Mizutani M., Tanaka
"Microsomal electron transfer in higher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam;
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                                                                                                                                                                                                           heterologous expression of
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                    SEQUENCE FROM N.
                                                                                                                                                                                            Arabidopsis.";
                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=3702;
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n; PF00173; heme 1; 1.
n; PF00175; NAD_binding_1; 1.
n; PF00174; oxidored_molyb; 1
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IPR001834; Cyt_B5_reductase.
IPR000572; Euk_Mb_oxred.
IPR001709; FPN_cyt_redctse.
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Pred. No. 9.9e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERCHAIN (POTENTIAL).
IRON (HEME AXIAL LIGAND)
IRON (HEME AXIAL LIGAND)
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MOLYBDENUM-PTERIN (POTENTIAL).
INTERCHAIN (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D0ED234BF1B1322B CRC64;
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                                                                                                                                                                                                                                                     Tanaka Y.,
                                                                         Kaneko T.,
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                                                                                                                                                                                                                                 plants: cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Å
                                                                                                                                                                                                                                                     Kusumi T.,
                                      chromosome
                                                                           Kotani H., Miyajima
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                    covered by sixteen
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DT 01-FEB
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DE CYBS.
OS Brassi
OC Eukary
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RN [1]
RP SEQUEN
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Matches 31
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P40934;

01-FEB-1995 (Rel. 3

01-FEB-1995 (Rel. 3

16-OCT-2001 (Rel. 4
STRAIN=cv. Caurre.
STRAIN=cv. Keck P., Somerve.
Kearns E.V., Keck P., Somerve.
"Nucleotide sequence of cDNA for
"Nucleotide sequence of cDNA for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AB007801; BAA74839.1; -.
EMBL; AB015476; BAB09732.1; -.
EMBL; F20001; CAA23377.1; -.
PIR; T52469; T52469.
                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Spermatophyta; Magnoliophyta; eudicotyle eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                   Brassica oleracea (Cauliflower)
Eukaryota; Viridiplantae; Strep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IRR001199; Cyt_BS.
Pfam; PF00173; heme 1; 1.
PRINTS; PR00363; CYTOCHROMEBS.
PRODOm; PD000612; CYt_B5; 1.
PROSITE; PS00191; CYTOCHROME B5 1; 1.
PROSITE; PS00195; CYTOCHROME B5 2; 1.
Electron transport; Transmembrane; Hen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is
                                                                 SEQUENCE FROM N.A., AN STRAIN=cv. Cauliflora;
                                                                                                                                                                                               Cytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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DNA Res. 5:297-308(1998).
                                                                                                          NCBI_TaxID=3712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P00171; 1EHB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ke R., Laudie M., Raynal M., Delseny M.;
mitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
FUNCTION: Membrane bound hemoprotein which function as an elecarrier for several membrane bound oxygenases (By similarity)
SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE
CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY)
SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
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64
                                                                                                                                                                                                                                                                   STANDARD;
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31,
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                                                                                AND SEQUENCE
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Last sequence update)
Last annotation updat
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IRON (HEME AXIAL LIGAND) (E
IRON (HEME AXIAL LIGAND) (E
NSS -> ARA (IN REF. 3).
W; 9CC01C60F7C873FD CRC64;
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Pred. No. 3.5e
23; Mismatches
                                                                                                                                     eptophyta; Embryophyta; Tracheophyta;
eudicotyledons; core eudicots; Rosid
                                      C.R.;
cytochrome
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                                       cauliflower
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SIMILARITY).
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                                                                                                                                      Rosidae;
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Matches 30
                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=cv. Xanthi, TISSUE=Leaf;
Vaucheret H., Kronenberger J., Rouze
"Complete nucleotide sequence of the
reductase genes.";
Plant Mol. Biol. 12:597-600(1989).
-i- FUNCTION; Nitrate reductase is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOBAC
NIAL TOBAC
STANDAGE,
P11605;
01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
28-FEB-2003 (Rel. 41, Last annotation updat
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METAL
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                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eu Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.
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Pfam; PF00173; heme_1; 1.

PRINTS; PR001363; CYTOCHROMEB5.

ProDom; PD000612; Cyt_B5; 1.

PROSITE; PS00191; CYTOCHROME B5 1; 1.

PROSITE; PS0255; CYTOCHROME B5 2; 1.

Electron transport; Transmembrane; Heme; Iron; Microsome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nicotiana tabacum (Common tobacco)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; T14454; T14454.
HSSP; P00171; 1EHB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M87514; AAA32990.1; -.
Step of nitrate assimilation in plants, fungi and bacteria. CAPALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)(0) = nitrate + NF COPACTOR: EACH SUBUNIT OF THE ENZYME CONTAINS 1 EQUIVALENT HEME IRON, AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS. THE GROUP IS CALLED CYTOCHROME B-557.
ENZYME REGULATION: REGULATED BY THE NITROGEN SOURCE AND CONBY THE CIRCADIAN RHYTHM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           carrier for several membrane bound oxygenases. SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND CYTOPLASMIC SIDE OF THE BUDOPLASMIC RETICULUM (B SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: Membrane bound hemoprotein which
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASEKKVLGFEEVSQHNKTKDCWLIISGKVYDVTPFWDDHPGGDEVLLSSTGKDATNDFED
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IRON (HEME AXIAL LIGAND) (
IRON (HEME AXIAL LIGAND) (
K -> N.
K -> N.
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Pred. No. 4.4e
23; Mismatches
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homeologous
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RESULT 6
CYB5_TOBAC
ID CYB5_TOBAC
AC P49098;
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R InterPro; IPRO011934; Cyt B5_reductase.

R InterPro; IPRO01193; Eyk M5_oxred.

R InterPro; IPRO01792; Euk M5_oxred.

R InterPro; IPRO01792; FPN Cyt redctse.

R InterPro; IPRO01793; FPN Cyt redctse.

R InterPro; IPRO01433; Oxred FAD/NAD(P).

Pfam; PF00179; FPN Cot inding 6; 1.

Pfam; PF00173; heme 1; 1.

Pfam; PF00174; oxidored molyb; 1.

Pfam; PF00175; NAD binding 1; 1.

Pfam; PF00174; oxidored molyb; 1.

PF1NTS; PR00406; CYTBSEDTASE.

PRINTS; PR00363; CYTOCHROMEBS.

PRINTS; PR00363; CYTOCHROMEBS.

PRINTS; PR00371; FPNCR.

PROSITE; PS00191; CYT_BS; 1.

PROSITE; PS00191; CYT_CHROME B5 1; 1.

PROSITE; PS00191; CYT_CHROME B5 1; 1.

PROSITE; PS00191; CYT_CHROME B5 1; 1.

PROSITE; PS00191; CYT_CHROME B5 1; 1.

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PROSITE; PS00191; CYT_CHROME B5 1; 1.

PROSITE; PS00191; CYT_CHROME B1 10; 1.

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PROSITE; PS00191; CYT_CHROME B1 1; 1.

PROSITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Spermatophyta; Magnoliophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core en NCBI TaxID=4097;
                                                                                                                                                01-FEB-1996
01-FEB-1996
28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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SIMILARITY: TO EUK
N-TERMINAL DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: Contains 1 cytochrome b5 heme-binding dor SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C-TERMINAL DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                 CTEEFDAIHSDKAKKLLEEFRIGELLTTGYTSDSPGNSVHGSSSFSSFLAPI 632
                                                                                                                                                                                                                                                                                                                                                                         ATDAFMAYHPPSVRPLLRRFFVGRL--TDYTVPP-----ASADFRRLLAQL 104
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237
422
566
589
904 AA;
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(Rel.
(Rel.
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                                                                                                                                                                                                                                 STANDARD;
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41,
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35.7%;
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Last
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                                                                                                                                                sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 167; Ub 1,
No. 5.6e-10;
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IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
W; 85642BDA723EE154 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLYBDENUM-PTERIN (POT
INTERCHAIN (POTENTIAL)
                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                               136
                                                                                                                                                update)
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                                                                  core eudicots
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IP PLANT MOI. Biol. 25:527-537(1994).

IP PLANT MOI. Biol. 25:527-537(1994).

IP PLANT MOI. Biol. 25:527-537(1994).

IP PLANT MOI. BIOL. 25:527-537(1994).

CC -:- FUNCTION CY EACHY A KEY ROLE IN THE MODIFICATION BY

OXYGENASES. MAY PLAY A KEY ROLE IN THE MODIFICATION BY

OXYGENASES. MAY PLAY A KEY ROLE IN THE MENOPLASMIC RETICULUM, WHICH IN

CC DESATURATION OF PLATTY ACIDS IN THE BENOPLASMIC RETICULUM, WHICH IN

CC DEVELOPMENTALLY REGULATED PRODUCTION OF LARGE AMOUNTS OF STORAGE

CLIPIDS, IS INVOLVED IN THE REDUCTION OF CYTOCHROME P-450 AND

MAY THEREFORE BE INVOLVED IN FLAVONOID BIOSYNTHESIS IN THE PETALS.

C-I- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE

CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).

CC TISSUE SPECIFICITY: IS HIGHLY EXPRESSED IN DEVELOPING SEEDS,

MODERATELY EXPRESSED IN FLOWERS, AND IS EXPRESSED AT LOW
                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X71441; CAA5U5/5...,
EMBL; X68140; CAA48240.1; -...
HSSP; P04166; 1B5M.
InterPro; IPR001199; Cyt_B5.
                                                                                                  P08619;
01-AUG-1988
01-MAY-1992
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                            METAL
METAL
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Bukaryota; Fungi; Ascomycota; P.
Sordariomycetidae; Sordariales;
NCBI_TaxID=5141;
                                    Neurospora crassa.
Eukaryota; Fungi;
                                                                    Nitrate reductase NIT-3.
                                                                                                                                                                   NIA_NEUCR
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Electron transport; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRODOM; PD000612; CYt B5; 1.
PROSITE; PS00191; CYTOCHROME B5_1; 1.
PROSITE; PS50255; CYTOCHROME B5_2; 1.
Electron transport; Transmembrane; Heme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith M.A., Stobart A.K., Shewry P.R., I Tobacco cytochrome b5: cDNA isolation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smith M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94325476; PubMed=8049375; Smith M.A., Stobart A.K., Shewry P.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
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uctase [NADPH] (EC 1.7.1.3) (NR)
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Pred. No. 9.4e
16; Mismatches
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IRON (HEME AXIAL LIGAND) (BY SIMILARITY).

IRON (HEME AXIAL LIGAND) (BY SIMILARITY).

LA -> EF (IN REF. 1; CAA48240).

MISSING (IN REF. 1; CAA48240).

; DACE9EA695B2835F CRC64;
                     Pezizomycotina;
s; Sordariaceae;
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                     Sordariomycetes;
Neurospora.
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InterPro; IPROULTS, inding_6; 1.

Pfam; PF00173; heme_1; 1.

Pfam; PF00173; heme_1; 1.

Pfam; PF03404; Mo-co_dimer; 1.

R Pfam; PF00174; NAD binding_1; 1.

R Pfam; PF00174; oxidored_molyb; 1.

R Pfam; PF00186; CYTBSEDTASE

R PRINTS; PR00406; CYTBSEDTASE

DR PRINTS; PR00363; CYTOCHROMEB5.

THINTS: PR00407; EUMOPTERIN.
                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-eor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ukamoto P.M., Marzluf G.A., "Nitrate reductase of Neurospora crassa: the functional role individual amino acids in the heme domain as examined by site-directed mutagenesis.";
Mol. Gen Genetary (Const. 1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=74-OR23-1A / FGSC 987;
MEDLINE=93241176; PubMed=8479443;
Okamoto P.M., Garrett R.H., Marzluf G.A.;
"Molecular characterization of conventional and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMB0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "On the presence of a heme-binding domain homologous to cytochrome in Neurospora crassa assimilatory nitrate reductase."; EMBO J. 2:1909-1914(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=74-OR23-1A / FGSC MEDLINE=91287699; PubMed:
                                                                                                                                                                                                                              EMBL; X61303; CAA43600.1; -. HSSP; P00171; 1F03.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MUTAGENESIS
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l. Gen. Genet. 238:8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . Gen. Genet. 240:221-230(1993).

FUNCTION: Nitrate reductase is a key enzyme involved in step of nitrate assimilation in plants, fungi and bacter CATALYTIC ACTIVITY: Nitrite + NADP(+) + H(2)O = nitrate COFACTOR: EACH SUBUNIT CONTAINS 1 EQUIVALENT OF FAD, HEM AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS. THE HEME GROUPS
                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Contains 1 cytochrome b5 heme-binding don SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PATHWAY: Nitrate assimilation (denitrification). SUBUNIT: Homodimer. INDUCTION: ITS EXPRESSION IS HIGHLY REGULATED AN TO NITRATE INDUCTION AND TO NITROGEN REPRESSION.
                                                                                                                                                                                                                                                                                                                                                                                                                                              N-TERMINAL DOMAIN
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                                                                                                                              j [PR001199; Cyt B5.
j [PR001194; Cyt B5_reductase.
j [PR0010572; Euk_mb_oxred.
j [PR001506; Mo-co_dimer.
o; [PR001433; Oxred_FAD/NAD(P).
FO0970; FAD_binding_6; 1.
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CYTOCHROME_B5_1;
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PubMed=1829499;
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28-FEB-2003 (Rel. 41, Last ar
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                                                                                                                                                                                                                                                                                                                                                        Calza R., Huttner B., Vincentz M., Rouze P., Galangau F., Vaucheret H., Cherel I., Meyer C., Kronenberger J., Caboche M.; "Cloning of DNA fragments complementary to tobacco nitrate reductase mRNA and encoding epitopes common to the nitrate reductases from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nicotiana tabacum (Common tobacco)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.
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                   N-TERMINAL DOMAIN.
- SIMILARITY: Contain
- SIMILARITY: TO FAD/
C-TERMINAL DOMAIN.
                                                                                                                                                                                      Gen. Genet 209:552-562(1987).

PUNCTION: Nitrate reductase is a key enzyme involved in the first punction of the first seep of nitrate assimilation in plants, fungi and bacteria.

CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.

COPACTON: EACH SUBUNIT OF THE ENZYME CONTAINS 1 EQUIVALENT OF FIHEME IRON, AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS. THE HEME GROUP IS CALLED CYTOCHROME B-557.
                                                                                                       SUBUNIT: Homodimer.
SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN
                                                                                                                                                ENZYME REGULATION: REGULATED BY THE CIRCADIAN RHYTHM.
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. Biol. 12:597-600(1989).
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                                                               cytochrome
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Pred. No. 8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IRON (HEME AXIAL LIGAND) (BY SIMILARIT TRON (HEME AXIAL LIGAND) (BY SIMILARITY FLAVUN-BINDING DOMAIN (BY SIMILARITY) NADP (BY SIMILARITY).
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INTERCHAIN (POTENTIAL).
HEME-BINDING (BY SIMILARITY).
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                                           CYTOCHROME
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Matches 40
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PRINTS; PRO0303; CYTOCHROMEBS.

PRINTS; PR003071; EUMOPTERIN.

PRINTS; PR00371; FPNCR.

PRODOM; PD000612; CYt B5; 1.

PROSITE; PS00191; CYTOCHROME B5_1; 1.

PROSITE; PS00195; CYTOCHROME B5_2; 1.

PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.

Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Mo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001199; Cyt_B5.

InterPro; IPR001834; Cyt_B5 reductase.

InterPro; IPR001834; Cyt_B5 reductase.

InterPro; IPR001709; FPN_cyt_redctse.

InterPro; IPR001709; FPN_cyt_redctse.

InterPro; IPR001433; Oxred_FAD/NAD(P).

Pfam; PF00173; heme_1; 1.

Pfam; PF00174; NAD binding_1; 1.

Pfam; PF00174; NAD binding_1; 1.

Pfam; PF00174; Oxidored_molyb; 1.
STRAIN=cv. Columbia;
STRAIN=cv. Columbia;
MEDLINE=20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea
Fuili C.Y., Mason T.M., Bowman C.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                  CY52 ARATH
048845;
16-OCT-2001
                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotytedons; core eudicots; Rosid

eurosids_II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable cytochrome b5 isoform 2.
ATZG33720 OR F24L7.14.
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EMBL; X06134; CAA29497.1; -.
PIR; S04839; RDNTNS.
HSSP; P17571; 2CND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PF00175; NAD bInding 1; 1.
PF00174; oxidored moTyb; 1.
S; PR00406; CYTBSEDTASE.
S; PR00363; CYTOCHROMEBS.
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15; Mismatches 43
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INTERCHAIN (POTENTIAL).
IRON (HEME AXIAL LIGAND) (B)
IRON (HEME AXIAL LIGAND) (B)
MW; 75196875A3561D69 CRC64;
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                          T.P., Benito M.-I., Town (Barnstead M.E., Feldblyum
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01-AUG-1992
01-AUG-1992
28-FEB-2003
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Pfam; PF00173; heme_1; 1.

PRINTS; PR00363; CYTOCHROMEB5.

ProDom; PD000612; Cyt_B5; 1.

PROSITE; PS00191; CYTOCHROME B5_1; 1.

PROSITE; PS50255; CYTOCHROME_B5_2; 1.

Electron transport; Transmembrane; Heme;
                                                                                                                                                                                                                                                                                                                                                                                                              NAR-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HORVU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- FUNCTION: Membrane bound hemoprotein which function as an electrorier for several membrane bound oxygenases (By similarity).
-i- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE. BOUND TO THE CYTOPLASMIC SIDE OF THE ENDOPLASMIC RETICULUM (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L., Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam Moffat K.S., Cill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M., Venter T.
Miyazaki J., Juricek M., Warner R.L.;
"Characterization and sec
                                                                                                                                                                                                                                                                             Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Stre
Spermatophyta; Magnoliophyta;
Triticeae; Hordeum.
                                                                                                 STRAIN=cv. Himalaya;
MEDLINE=91375416; PubMed=1896007;
                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                      NCBI_TaxID=4513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nitrate reductase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AC003974; AAC04491.1;
PIR; T00796; T00796.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.", \label{eq:chaliana}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P04166; 1B5M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EAKIFTLSEVSEHNQAHDCWIVINGKVYNVTKFLEDHPGGDDVLLSSTGKDATDDFEDVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 23, Created)
(Rel. 23, Last sequence update)
(Rel. 41, Last annotation update)
uctase [NAD(P)H] (EC 1.7.1.2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127
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64
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          sequence of
                                                                     Angelis
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yta; Liliopsida;
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Pred. No. 1.5e-10;
9; Mismatches 32
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IRON (HEME AXIAL LIGAND)
IRON (HEME AXIAL LIGAND)
; B405F5430F5716C1 CRC64;
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Pai G., Van Aken S., T.H.,
          novel
                                                                            Schnorr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         891
                                                                                                                                                                                                                                                                                                                Embryophyta; Tracheophyta;
; Poales; Poaceae; Pooidea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Iron; Microsome;
          nitrate
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                                                                     K.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32;
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             reductase from
                                                                            Kleinhofs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ХВ)
ХВ)
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RESULT 11
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Best Local S
Matches 37
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InterPro; IPRO01199; Cyt_B5_reductase.

InterPro; IPRO010572; Euk_Mb_oxred.

InterPro; IPRO01709; FPN cyt_redctse.

InterPro; IPRO01709; FPN cyt_redctse.

InterPro; IPRO01433; Oxred_FAD/NAD(P).

InterPro; IPRO01212; Phe hydroxylase.

Pfam; PF003103; heme_1; 1.

Pfam; PF003404; Mo-co dimer; 1.

Pfam; PF003404; Mo-co dimer; 1.

Pfam; PF00175; NAD binding_1; 1.

Pfam; PF00176; Oxidored molyb; 1.

Pfam; PF00177; EUMOPTERIN.

PRINTS; PR00407; EUMOPTERIN.

PRINTS; PR00407; EUMOPTERIN.

PRINTS; PR00410; PHEHYDRXLASE.

PRINTS; PR00410; PHEHYDRXLASE.

PROSITE; PS00151; CYTOCHROME B5_1; 1.

PROSITE; PS00152; CYTOCHROME B5_2; 1.

PROSITE; PS001559; MOLYBOPTERIN EUK; 1.

PROSITE; PS001559; MOLYBOPTERIN EUK; 1.
                                                                                                                                                                                                                                                                                     DISULFID
METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X60173; CAA42739.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- FUNCTION: Nitrate reductase is a key enzyme involved in the step of nitrate assimilation in plants, fungi and bacteria.
-!- CATALYTIC ACTIVITY: Nitrite + NAD(P)(+) + H(2)O = nitrate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         barley.";
                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; S:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GROUP IS CALLED CYTOCHROME 8-557. SUBUNIT: Homodimer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Contains 1 cytochrome b5 heme-binding dor SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INDUCTION: By nitrate.
SIMILARITY: TO EUKARYOTIC MOLYBDOFTERIN OXIDOREDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COFACTOR: EACH SUBUNIT OF THE ENZYME CONTAINS 1 EQUIVALENT OF FAD, HEME IRON, AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS. THE HEME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAD (P) H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-TERMINAL DOMAIN
                                                                                                                              509
                                                                566
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                                                                                                                                                                                                          Similarity
                                                              TEEFDAIHSAKARGLLEMYRVGELIVTGNDYSPQSSNADLAAIV
                                                                                             TDAFMAYHPPSVRPLLRRFFVGRL----TDYTVPPASADFRRLL 101
                                                                                                                           PFMSTASAQFTM----SEVRRHASKDSAWIVVHGHVYDCTAFLKDHPGGADSILINAGSDC
                                                                                                                                                           PAASKDAADVRMISTKELQAHAAADDLWISISGDVYDVTPWLRHHPGGEVPLITLAGQDA 61
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221
406
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573
891 AA;
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                                                                                                                                                                                                                                                                                                ; Flavoprotein; FĀD; NAD; NADP; Heme; Molybdenum; lation; Multigene family.

8 168 MOLYBDENUM-PTERIN (POTENTIAL).
1 221 MOLYBDENUM-PTERIN (POTENTIAL).
6 406 INTERCHAIN (POTENTIAL).
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221
406
550
573
                                                                                                                                                                                                         27.3%;
                                                                                                                                                                                                                                                       98630 MW;
                                                                                                                                                                                        16;
                                                                                                                                                                                     Pred. No. 2.16
5; Mismatches
                                                                                                                                                                                                         Score 161.5; DB 1
Pred. No. 2.1e-09;
                                                                                                                                                                                                                                                     IRON (HEME AXIAL LIGAND)
IRON (HEME AXIAL LIGAND)
; AA47EC52FC1EFD13 CRC64;
                                                                                                                                                                                        44;
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                                                                                                                                                                                          Indels
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(BY SIMILARITY)
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00363; CYTŌCHROMEBS.
PRINTS; PR00407; EUMOPTERIN.
PRODOM; PD000612; CYt_BS; 1.
PROSITE; PS00191; CYTŌCHROME B5_1; 1.
PROSITE; PS00255; CYTOCHROME B5_2; 1.
PROSITE; PS00559; MOLYBDOPTERIN_EUK; PARTIAL.
PROSITE; PS00559; MOLYBDOPTERIN_EUK; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; S17197; S17197.
HSSP; P04166; 1B5M.
InterPro; IPR001199; Cyt_B5.
InterPro; IPR000572; Euk_Mb_oxred.
InterPro; IPR005066; Mo-co_dimer.
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-I- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
-I- COFACTOR: EACH SUBUNIT OF THE ENZYME CONTAINS 1 EQUIVALENT OF FAD HEME IRON, AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS. THE HEME GROUP IS CALLED CYTOCHROME B-557.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cannons A.C., Iida N., Solomonson L.F. "Expression of a cDNA clone encoding Chlorella nitrate reductase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chlorella vulgaris.
Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;
Chlorellaceae; Chlorella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X56771; CAA40090.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=91354204; PubMed=1883330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: Homodimer.
SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-TERMINAL DOMAIN.

SIMILARITY: Contains 1 cytochrome b5 heme-binding dom
SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES
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274 HSLKAKKQLLEYYIGELAEEGQEAAASD 301
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PF03404; Mo-co
                                                                                                                                                                                                            29;
                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                         assimilation.
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                                                                                                      AGAKSFTMAEVETHTTMESAWFVVDGKVYDATPFLKDHPGGADSILLVAGIDATDEFNAI
                                                   HPPSVRPLLRRFFVGRLTDYTVPPASAD
                                                                                                                                            ADVRMISTKELQAHAAADDLWISISGDVYDVTPWLRHHPGGEVPLITLAGQDATDAFMAY
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274
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318 AA;
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318
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33.0%;
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Pred. No. 7.
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IRON
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AXIAL LIGAND)
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Pfam; PF00174; oxidored molyb; 1.
PRINTS; PR00406; CYTB5RDTASE.
PRINTS; PR00363; CYTOCHROWEB5.
PRINTS; PR00407; EUMOPTERIN.
PRINTS; PR00371; FPNCR.
                                                                                                                                                                                                                                                                                                                     InterPro; IPRO01
Pfam; PF00173; P
Pfam; PF00173; P
Pfam; PF03404; P
Pfam; PF00175; P
Pfam; PF00174; C
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SEQUENCE FROM N.A.
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STRAIN=cv. TLRL13; TISSUE=Leaf;
MEDLINE=93292981; PubMed=8514183;
MEDLINE=93292981; PubMed=8514183;
MEDLINE=93292981; PubMed=8514183;
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P36859;
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PETHY
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                                                                ProDom; PD000612; Cyt_B5; 1.
PROSITE; PS00191; CYTTOCHROME_B5_1; 1.
PROSITE; PS50255; CYTTOCHROME_B5_2; 1.
PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
Oxidoreductase; Flavoprotein; FAD; NAD;
Nitrate assimilation; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salanoubat M., Ha D.B.D.;
"Analysis of the petunia nitrate reductase apoenzyme-encoding first step for sequence modification analysis.";
  DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interPro;
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SY THE CIRCADIAN RHYTHM.

SUBUNIT: Homodimer (By similarity).

DEVELOPMENTAL STAGE: MAXIMUM EXPRESSION 2 HOURS AFTER SUN EXPRESSION FOUND 2 HOURS BEFORE AND 8 HOURS AFTER SUN SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTAS N-TERMINAL DOMAIN.

SIMILARITY: Contains 1 cytochrome b5. heme-binding dom SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: Nitrate reductase is a key enzyme involved in the first step of nitrate assimilation in plants, fungi and bacteria. CATALYTIC ACTIVITY: Nitrite + NADH(+) + H(2)O = nitrate + NADH. COPACTOR: EACH SUBUNIT OF THE ENZYME CONTAINS 1 EQUIVALENT OF FIHEME IRON, AND MOLYBDENUM-PTERIN AS PROSTHETIC GROUPS. THE HEME GROUP IS CALLED CYTOCHROME B-557.
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o; IPR001334; Cyt_B5_reductase.
o; IPR001572; Euk_Mb_oxred.
o; IPR001709; FPN cyt_redctse.
o; IPR001709; FPN cyt_redctse.
o; IPR001433; Oxred_FAD_NAD(P).
F00970; FAD_binding_6; 1.
F00173; heme 1; 1.
F00144; Mo-co_dimer; 1.
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                         MOLYBDENUM-PTERIN
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                                                                                               Heme; Molybdenum;
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                                                                                                                                                                                                                                                                                                                                                      RX MEDLINE-21016719; PubMed=11130712;
RX Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA Hhite O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creesy T.H., Dewar K.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creesy T.H., Dewar K.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Marziali A.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Marziali A.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Kim C.J., Fanda M., Juros J.S., Maiti R., Marziali A.,
RA Kim C.J., Fanda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Langin Hopser S., Lee J.M., Learzo M., Rooney T., Rowley D.,
RA Pai G., Peterson J., Pham P. K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sakano H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
Witch Back T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
"Sequence and analysis of chromosome 1 of the plant Arabidopsis
                     SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=cv. Columbia;

Shinozaki K., Davis R.W., Ecker J.R., Theolog.

F "RIKEN Arabidopsis full length cDNA clones (R
T SSP consortium (Salk/Stanford/PGEC).";

Submitted (MAR-2002) to the EMBL/GenBank/DDB.
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P11832; Q9CA18;
01-OCT-1989 (Rel
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Nitrate reductase (NADH) 1 (EC 1.7.1.1) (NR1).
NIA1 OR ATIG77760 OR T32E8.9.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METAL
METAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wilkinson J.Q., Crawford N.M.;
"Identification and characterization of
of Arabidopsis thaliana with mutations
structural genes NIA1 and NIA2.";
Mol. Gen. Genet. 239:289-297(1993).
   MEDLINE=89091069;
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Query Match
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Matches 39
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PRINTS; PR00363; CYTOCHROMEBS.
PRINTS; PR00363; EUMOPTERIN.
PRINTS; PR00407; FUNCR.
PRINTS; PR00410; PHEHYDRXLASE.
PRODOM; PD00612; CYT B5; I.
PROSITE; PS00191; CYTOCHROME B5 1; 1.
PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.
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                                                                                                                                             VARIANT
CONFLICT
SEQUENCE
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PIR; S35228; S35228.
HSSP; P17571; 2CND.
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-!- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.
-!- COFACTOR: EACH SUBUNIT OF THE ENZYME CONTAINS 1 EQUIVALENT OF FAD, HEME IRON, AND MOLYBDENUM-PIERIN AS PROSTHETIC GROUPS. THE HEME GROUP IS CALLED CYTOCHROME B-557.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          interPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     erPro; IPRO01199; Cyt_B5.
erPro; IPR001834; Cyt_B5_reductase.
erPro; IPR001834; Cyt_B5_reductase.
erPro; IPR00572; Euk_Mb_oxred.
erPro; IPR001709; FPN_cyt_redctse.
erPro; IPR001709; FPN_cyt_redctse.
erPro; IPR001433; Oxred_FAD/NAD(P).
erPro; IPR001221; Phe_hydroxylase.
im; PF00970; FAD_binding_6; 1.
im; PF00970; FAD_binding_6; 1.
im; PF00970; NAD_binding_1; 1.
im; PF00175; NAD_binding_1; 1.
im; PF00175; NAD_binding_1; 1.
im; PF00175; NAD_binding_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE SPECIFICITY: ROOT, LEAF, AND MISCELLANEOUS: WHEN MUTATED CONFERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: Homodimer.
TISSUE SPECIFICITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Contains 1 cytochro
SIMILARITY: TO FAD/NAD-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHLORATE.
SIMILARITY: TO EUKARYOTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-TERMINAL DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C-TERMINAL DOMAIN.
                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                        assimilation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :3309-3314(1988).
                                                                                                                                         197
251
436
580
603
198
17
917
                                                                                                                                                                   1959; MOLYBDOPTERIN_EUK; 1.

Be; Flavoprotein; FAD; NAD; Heme; Molybdenum;
nilation; Multigene family; Herbicide resistance.

MOLYBDENUM-PTERIN (POTENTIAL).

197 197 MOLYBDENUM-PTERIN (POTENTIAL).

136 436 INTERCHAIN (POTENTIAL).

136 436 INTERCHAIN (POTENTIAL).

130 580 IRON (HEME AXIAL LIGAND) (BY SIMIL).

130 603 IRON (HEME AXIAL LIGAND) (BY SIMIL).

131 A -> R (IN REF. 1).
                                                                                                                                             Ä,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J., Nam H., den Boer B.G.W., Goodman H.M.;
1) in Arabidopsis thaliana encoding nitrate
                                                                                                                                             103040
                                     26.9%;
35.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytochrome b5 heme-binding don-
BINDING CYTOCHROME REDUCTASES
                                                                                                                                             Œ;
16;
                                     Score 159.5;
Pred. No. 3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLYBDOPTERIN OXIDOREDUCTASES IN THE
                                                                                                                                         -> R (IN REF. 1).
6FD3ED46B9F63825
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHOOT.
RESISTANCE TO
                                     .6e-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       as its content
                                                                      DB 1;
   43
;
                                                                                                                                             CRC64;
                                                                      Length 917;
   Indels
                                                                                                                                                                                                                                                     (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         restrictions
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13;
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MBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THE
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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50
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PRINTS; PRO0406; CYTBSRDTASE.
PRINTS; PRO0363; CYTCCHROMEBS.
PRINTS; PRO0407; EUMOPTERIN.
PRINTS; PR00371; FPNCR.
PRO050m; PD000612; CYtC.B5; 1.
PROSITE; PS00191; CYTCCHROME B5 1; 1.
PROSITE; PS00559; MOLYBDOPTERIN EUK; 1
PROSITE; PS00559; MOLYBDOPTERIN EUK; 1

NAD; بر بر

Heme; Molybdenum;

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THE SECOND RESERVANCE OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE P
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                                                                                                                                                                                                                                  InterPro; IPRO0119; Cyt_B5.
InterPro; IPRO01834; Cyt_B5 reductase.
InterPro; IPRO01872; Euk_Mb_oxred.
InterPro; IPR000572; Euk_Mb_oxred.
InterPro; IPR001709; FPN cyt_redctse.
InterPro; IPR005066; Mo-co_dimer.
InterPro; IPR001433; Oxred_FAD/NAD(P).
Pfam; PF00970; PAD binding_6; 1.
Pfam; PF00173; heme 1; 1.
Pfam; PF00174; Maj binding_1; 1.
Pfam; PF00174; Oxidored_mol_b; 1.
Pfam; PF00174; Oxidored_mol_b; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIA1 PHAVU
P39865;
01-FEB-1995
01-FEB-1995
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last seq
28-FEB-2003 (Rel. 41, Last ann
Nitrate reductase (NADH) 1 (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=cv. Saxa; TISSUE=Shoot; Hoff T., Stummann B.M., Henningsen K.W.; "Cloning and expression of a gene encoding reductase in bean (Phaseolus vulgaris).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DAWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phaseolus vulgaris (Kidney bean) (French bean).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.

NCBI TaxID-3885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Physiol. Plantarum 82:197-204(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Step of nitrate assimilation in plants, fungi and CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nit COPACTOR: REQUIRES FAD, A HEME GROUP (CALLED CYTOC AND ONE MOLYBDENUM ATOM.

SUBUNIT: Homodimer (By similarity).

SUBLIARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUC N-TERMINAL DOMAIN.

SIMILARITY: Contains 1 cytochrome b5 heme-binding SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C-TERMINAL DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; X53603; CAA376
S25445; S25445.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P17571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATDAFMAYHPPSVRPLLRRFFVGRL--TDYTVPP-----ASADFRRLLAQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence update)
annotation update)
(EC 1.7.1.1) (NR-1
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HROME REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ₽
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              domain.
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B-557)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
InterPro; IPR001199; Cyt B5.

InterPro; IPR001199; Cyt B5.

InterPro; IPR005804; FA desat fam.
Pfam; PF00487; FA desaturase; 1.

Pfam; PF00173; heme_1; 1.

ProDom; PD0001612; Cyt B5; 1.

ProDom; PD001081; FA desat_fam; 2.

PROSITE; PS00191; CYTCCHROME_B5_1; FALSE_NEG.
PROSITE; PS00191; CYTCCHROME_B5_2; 1.

PROSITE; PS50255; CYTCCHROME_B5_2; 1.

PROSITE; PS50255; CYTCCHROME_B5_2; 1.

PROSITE; PS50255; CYTCCHROME_B5_2; 1.

PROSITE; PS50255; CYTCCHROME_B5_2; 1.

PROSITE; PS50255; CYTCCHROME_B5_2; 1.

PROSITE; PS50255; CYTCCHROME_B5_1; NEME_BINDING.

PROSITE; PS50255; CYTCCHROME_B5_1; NEME_BINDING.

PROMAIN

53 53 IRON (HEME_AXIAL LIC
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METAL
                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O9DEX7;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
Delta-5/delta-6 fatty acid desaturase (EC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BRARE
                                                                                                                                                                                                                      EMBL; AF309556; AAG
HSSP; P00173; 1JEX.
                                                                                                                                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        activities.";
Proc. Natl. Acad. Sci. U.S.A. 98:14304-14309(2001).
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                                                                                                                                                                                                     ZFIN; ZDB-GENE-011212-1; fads2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hastings N., Agaba M., To
Sargent J.R., Teale A.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21592990; PubMed=11724940;
Hastings N., Agaba M., Tocher D.R., Leaver M.J., Dick J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Liver;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vertebrate fatty acid desaturase with deltas and deltas
                                                                                                                                                                                                                                                                                                                                                                                                                PATHWAY: Polyunsaturated fatty acid biosynthesis.
SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: Fatty acid desaturase with both delta-5 and delta-6 activities. May represent a component of the polyunsaturated fatty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acid biosynthesis pathway.
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; Pred. No. 3.9e-09;
16; Mismatches 34
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IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
, A212A128BB4EE661 CRC64;
 HEME-BINDING. IGAND) (BY SIMILARITY).
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MOLYBDENUM-PTERIN (POTENTIAL).
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(EC 1.14.19.-).
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SEQUENCE
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                                                                                  75 PLLRRFFVGRLTDYTVPPAS-----ADFRRLLAQLSSAGLFE 111
                                                                                                                                                                               Similarity
                                                      KYLKPLLIGEL-EASEPSQDRQKNAALVEDFRALRERLEAEGCFK 127
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52032 MW;
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              2004, 06:30:57
                                                                                                                                                                                                                        IRON (HEME AXIAL LIGAND) (BY SIMILARITY).; 6AA25A1DC1DC0F65 CRC64;
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Post-processing: Minimum Match 0%
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592
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

16	15	14	13	12	11	10	9	89	7	6	ຫ	4	w	ν.	<b>_</b>	Result No.
180	193.5	195	236.5	236.5	249	250.5	258	258	262.5	263.5	267.5	274.5	282.5	306	592	Score
30.4	32.7	32.9	39.9	39.9	42.1	42.3	43.6	43.6	44.3	44.5	45.2	46.4	47.7	51.7	100.0	Query
464	459	477	449	449	448	449	448	448	446	448	448	458	446	446	469	Query Match Length DB
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Q9y1w0 dictyosteli	Q944w4 pythium irr	0	Q9zrp7 arabidopsis	Q81b96 arabidopsis	Q817i7 argania spi	_	O04353 borago offi	٠,	Q9zty9 ricinus com	Q8vzz2 echium gent	Q8vzz1 echium pita	Q43469 helianthus	Q9fr82 borago offi	Q8lld7 aquilegia v	Q9ztu8 triticum ae	Description

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25.8	25.9	26.0	•	26.1	•	•	26.3	•	26.9	27.0		27.1	•	•	28.0	•	28.1	28.3							29.6	9	29.9	30.2
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Q96h07 homo sapien	Q944w3 pythium irr		Q8h0n8 phytophthor	O24651 olea europa	Ο.	Q9fuc2 ricinus com		Q43042 petunia hyb	3	Q96ve8 ustilago ma	Q42497 chlorella v	Q90ze8 oncorhynchu	Q9sdy3 chlamydomon	Q8x1x0 monascus an	Q98sw7 oncorhynchu	O48618 olea europa			Q9dex6 cyprinus ca	Q9p942 hansenula a	O96099 dictyosteli		Q8ay64 sparus aura		Q9fdw8 arabidopsis	Q92237 gibberella	10	Q8j259 tuber borch

## ALIGNMENTS

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Query Match 100.0%; Score 592; DB 10; Length 469; Best Local Similarity 100.0%; Pred. No. 3.1e-54;	Heme. SEQUENCE 469 AA; 52617 MW; 16F223CC1F79740D CRC64;	ITE; PS00038;	PS50255;		PD000612;	S; PR00363;	PF00173; heme 1; 1.	Pfam; PF00487; FA desaturase; 1.	InterPro; IPR001092; HLH basic.	Theorem, cycles.	1357; FOCT/I; 1130. C; 155		- I SIMILARITY: BELONGS TO THE CYTOCHROME BS FAMILY.	d (OCT-1997) to the EMBL/GenBank/DDBJ	genes.";	d by over	Delhaize E., Hebb D.M., Gardner R.C., Richards K.D.;	STRAIN=cv. ET3;	SEQUENCE FROM N.A.	[1]	NCBI TaxID=4565;	Triticeae; Triticum.	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Triticum aestivum (Wheat).	S276.		Last annotation	(TrEMBLrel.	01-MAY-1999 (TrEMBLrel. 10, Created)	•	Q9ZTU8 PRELIMINARY; PRT; 469 AA.	ULT 1

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"Isolation and characterization of a cDNA encoding a delta sphingolipid desaturase from Aquilegia vulgaris.";

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

-!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.

REMBL, AF406816; AAN03619.1;

R InterPro; IPR001199; Cyt B5.

R InterPro; IPR001199; Cyt B5.

R InterPro; IPR005804; FA desat fam.

InterPro; PR00487; FA desaturase; 1.

R Pfam; PF00487; FA desaturase; 1.

R Pfam; PF00173; heme 1; 1.

R PF10Dom; PD001081; FA desat fam; 1.

R PRODOm; PD001081; FA desat fam; 1.

R PROSITS; PS50255; CYTOCHROME B5-2; 1.
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01-MAR-2001
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Q8LLD7;
                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnoliophyta; eudicotyledons;
Asteridae; lamiids; Boraginaceae; Borago.
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Sphingolipid long chain base delta 8 desaturase.
Aquilegia vulgaris.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta
Spermatophyta; Magnoliophyta; eudicotyledons; Ranun
               SEQUENCE FROM N.A. MEDLINE=21092516;
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01-OCT-2002
                                                                                                                                                             Borago officinalis (Bourrache) (Borage).
                                                                                                                                                                                    SLD1.
                                                                                                                                                                                                      Delta 8-sphingolipid
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                                                                         NCBI_TaxID=13363;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  446 AA; 51273 MW; 76366DB0EB956D09 CRC64;
                                                                                                                                                                                                                   (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 22, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                 PubMed=11162428;
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51.5%;
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Pred. No. 5.3e-24;
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eudicotyledons; Ranuncu
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                                                                                                                    Embryophyta;
edons; core eu
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                                                                                                                                       Tracheophyta;
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ProDom; PD000612; CVt B5; 1.
ProDom; PD001081; FA desat fam; 1.
PROSITE; P850255; CYTOCHROME_B5_2; 1.
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InterPro; IPR005804; FA_desat_fa
InterPro; IPR00587; FA_desaturase; 1.
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Sperling P., Libisch B., Zaehringer U., Napier J.A.,
"Functional identification of a delta 8-sphingolipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Libisch B., Michaelson L.V., Lewis M.J., Shewry P.R., N
"Chimeras of Delta6-fatty acid and Delta8-sphingolipid
Diochem. Biophys. Res. Commun. 279:779-785(2000).
                                                                                                                                                                                                                                                                                   Pfam; PF00173; heme
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99
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                                                                                                                                                 Similarity
TAWKNIENLFTGYHLEDYLVSEISKDYRKLASEFSKAGLFEKKG
                      SVRPLLRRFFVG-RLTDYTVPPASADFRRLLAQLSSAGLFERVG
                                                                                               RMISTKELQAHAAADDLWISISGDVYDVTPWLRHHPGGEVPLITLAGQDATDAFMAYHPP
                                                                 KYISVGELEKHNOLGDVWISIOGKVYNVTDWIKKHPGGDVPIMNLAGODATDAFIAYHPG
                                                                                                                                                                                                  446 AA;
                                                                                                                                 Conservative
                                                                                                                                                                                                50926 MW;
                                                                                                                                               47.7%;
51.9%;
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                                                                                                                                               Score 282.5;
Pred. No. 1.6
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desaturase
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Q43469; 01-NOV-1996 01-NOV-1996 01-OCT-2002 SEQUENCE FROM N.A.
STRAIN-cv. inbred line HA89;
TISSUB=Cotyledons of developing sunfl
MEDLINE-21116801; PubMed=11171153;
Sperling P., Blume A., Zaehringer U.,
"Further characterization of delta 8-Helianthus annuus (Common sunflower).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; campanulids; Asterales; Asteraceae; Asteroideae;
Heliantheae; Helianthus. STRAIN=cv. inbred line HA89; TISSUB=Cotyledons of developing s MEDIINE=96028121; PubMed-7588718; Sperling P., Schmidt H., Heinz E higher plants."; Biochem. Soc. Trans. SEQUENCE FROM N.A. SLD1 Delta-8 Q43469 desaturases."; !- SIMILARITY: BELONGS TO T MBL; X87143; CAA60621.1; -. SSP; P00171; 1F03. cytochrome b5-containing J. Biochem. TaxID=4232; 1996 (TrEMBLrel. 01, Created)
1996 (TrEMBLrel. 01, Last sequence update)
2002 (TrEMBLrel. 22, Last annotation update)
sphingolipid desaturase. IPR001199; Cyt_B5 PRELIMINARY; 232:798-805(1995) 28:638-641 (2000) Heinz E.; HH fusion PRT; CYTOCHROME sunflower fruits; sunflower U., Heinz E.; 8-sphingolipid protein 458 A 85 fruits; similar desaturases ូ plant acyl lipid from

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RESULT CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF CANCEL OF
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Best Local S
Matches 51
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Best Local S
Matches 52
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Q8VZZ1;
01-MAR-2002 (TrEMBLrel. 2
01-MAR-2002 (TrEMBLrel. 2
01-OCT_2002 (TrEMBLrel. 2
Q8VZZ2
Q8VZZ2;
01-MAR-2002
01-MAR-2002
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-- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
EMBL; AY055118; AAL23581.1; --
InterPro; IPR001199; Cyt B5.
InterPro; IPR005804; FA Gesat fam.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00487; FA_desaturase; 1.
Pfam; PF00173; heme_1; 1.
ProDom; PD001612; Cyt_B5; 1.
ProDom; PD001081; FA_desat_fam; 1.
PROSITE; PS50255; CYTOCHROME_B5_2; 1.
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Eukaryota; Viridiplantee; Streptophyta; Embryo
Spermatophyta; Magnoliophyta; eudicotyledons;
Roteridae; lamiids; Boraginaceae; Echium.
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ProDom; PD001081; FA desat fam; 1.
PROSITE; PS50255; CYTOCHROME_B5_2; 1.
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Pfam; PF00173;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      448 AA; 51394 MW; 4B6D6EA4905DE263 CRC64;
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  (TrEMBLrel.
                                                                        PRELIMINARY;
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Last sequence update)
Last annotation update)
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Pred. No. 1.2e
19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                     Score 267.5; DB 10; Length Pred. No. 6.3e-20; O; Mismatches 32; Indels
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InterPro; IPR005804; FA desat_fam.
Iftam; PF00487; FA desaturase; 1.
Pfam; PF00173; heme_1; 1.
ProDom; PD000612; Cyt B5; 1.
ProDom; PD001081; FA desat_fam; 1.
PROSITE; PS50255; CYTOCHROME_B5_2; 1
                                                                                                     -i- SIMILARITY: BELONGS TO EMBL; AF005096; AAD01240.1; HSSP; P00171; 1T517
                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Malpighiales; Euphorbiaceae; Ricinus.

MCBI_TaxID=3988;
                                                                                                                                                                                                                                                                                                                                    O9ZTY9, PRELIMINARY; PRT; 446 AA.
O9ZTY9;
O1-MAY-1999 (TrEMBLrel. 10, Created)
O1-MAY-1999 (TrEMBLrel. 10, Last sequence up
O1-OCT-2002 (TrEMBLrel. 22, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maroto F.G., Alonso D.L., Garrido J.-A.S., Ferron M.V., Ruiz "Cloning and Molecular Characterization of the D6-Desaturase Echium: Functional Expression in Yeast and Tobacco."; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
EMBL; AY055117; AAL23580.1; -.
                                            HSSP; P00171; 115U;
InterPro; IPR001199; Cyt B5.
InterPro; IPR005804; FA_desat_
Pfam; PF00487; FA_desaturase;
Pfam; PF00173; heme_1; 1.
       Pfam; PF00173; heme 1; 1.
Probom; PD000612; Cyt B5; 1.
Probom; PD001081; FA desat fam; 1.
PROSITE; PS50255; CYTOCHROME_B5_2;
                                                                                                                                                                                                                                                                                                               Desaturase/cytochrome b5 protein. Ricinus communis (Castor bean).
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Spermatophyta; Magnoliophyta; eudicotyled
Asteridae; lamids; Boraginaceae; Echium.
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Pred. No. 1.
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5_2; 1.
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Matches 51
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004353;
01-JUL-1997
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Q9SAU5;
01-MAY-2000
                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; lamiids; Boraginaceae; Borago.
                                                                                            Delta 6 desaturase.
Borago officinalis (Bourrache) (Borage).
                                                                                                                                     01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00173; heme 1; 1.
ProDom; PD000612; Cyt B5; 1.
ProDom; PD001081; FA desat fam; 1.
PROSITE; PS50255; CYTOCHROME B5_2; 1.
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InterPro; IPR001804; FA desat fam.
InterPro; IPR005804; FA desaturase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUN-1997) to the EMBL/GenBank/DDBJ-!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 EMBL; AF007561; AAD01410.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQIKKYITSDELKNHDKPGDLWISIQGKAYDVSDWVKDHPGGSFPLKSLAGQEVTDAFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AADV-RMISTKELQAHAAADDLWISISGDVYDVTPWLRHHPGGEVPLITLAGQDATDAFM
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) (TrEMBLrel. 13,
2 (TrEMBLrel. 22,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Beremand P.D., The of Plant Seed Oils
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50.9%; Pred. No. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation updat
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Pred. No. 6.4e-19;
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5; Mismatches
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Query Match
Best Local S
Matches 49
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Best Local S
Matches 51
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01-MAY-1999
01-MAY-1999
01-MAR-2003
                                                                                                                                                                                                       Pfam; PF00173; heme_1; 1.
ProDom; PD000612; Cyt_B5; 1.
ProDom; PD001081; FA desat fam; 1.
PROSITE; PS50255; CYTOCHROME_B5_2; 1.
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Pfam; PF00173; heme 1; 1.
ProDom; PD000612; Cyt B5; 1.
ProDom; PD001081; FA_desat_fam; 1.
PROSITE; PS50255; CYTOCHROME_B5_2;
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InterPro; IPR001199; Cyt B5.
InterPro; IPR005804; FA desat fam.
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"Expression of a borage desaturase cDNA containing an N-t cytochrome b5 domain results in the accumulation of high delta6-desaturated fatty acids in transgenic tobacco."; Proc. Natl. Acad. Sci. U.S.A. 94:4211-4216(1997).

-I- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytochrome b5 Fusion Protein.";
J. Biol. Chem. 273:28590-28596 (1998)
-!- SIMILARITY: BELONGS TO THE CYTOC
EMBL; AJ224160; CAA11857.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=cv. Drakkar; TISSUE=Ripening
MEDLINE=99003197; PubMed=9786850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                         Pfam; PF00487; FA_desaturase; Pfam; PF00173; heme_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sperling P., Zaehringer U., Heinz E.; "A Sphingolipid Desaturase from Higher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=3708;
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                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001199; Cyt_B5.
InterPro; IPR005804; FA_desat_
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                                      Similarity
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9 (TrEMBLrel. 10,
3 (TrEMBLrel. 23,
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                                                                                                                                                 AA;
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                                                                                                                                                 51490 MW;
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                                      42.3%; Score 250.5;
47.1%; Pred. No. 4e-
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Last annotation update)
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Pred. No. 6.4e-19;
1; Mismatches 35
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Matches 50
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Q8LB96;
Q8LB96;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Delta-8 sphingolipid desaturase.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Pfam; PF00173; heme 1; 1.
ProDom; PD000612; Cyt B5; 1.
ProDom; PD001081; FA_desat_fam;
PROSITE; PS50255; CYTOCHROME_B5_
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                               SEQUENCE FROM N.A.
Haas B.J., Volfovsky N., Town C.D., Troukhan
Feldmann K.A., Flavell R.B., White O., Salzbe
"Full-length messenger RNA sequences greatly
annotation.";
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| cloning of
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Pred. No. 5.7e-18;
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Matches 43
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InterPro; IPR005804; FA_desat_fam.
Pfam; PF00487; FA_desaturase; 1.
Pfam; PF00173; heme 1; 1.
ProDom; PD000612; Cyt_B5; 1.
ProDom; PD001081; FA_desat_fam; 1.
PROSITE; PS50255; CYTOCHROME_B5_2; 1.
                                   Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai Satou M., Seki M., Southwick A., Tang C.C., Toriumi M. Vanamaura Y., Yu G., Yu S., Shinozaki Vanamaura Y., Yu G., Yu S., Shinozaki Vanamaura Y., Yu G., Yu S., Shinozaki Vanamaura Y., Yu G., Yu S., Shinozaki Vanamaura Y., Yu G., Yu S., Shinozaki Vanamaura Y., Yu G., Yu S., Shinozaki Vanamaura Y., Yu G., Yu S., Shinozaki Vanamaura Y., Yu G., Yu S., Shinozaki Vanamaura Y., Yu G., Yu S., Shinozaki Vanamaura Y., Yu G., Yu S., Shinozaki Vanamaura Y., Yu G., Yu S., Shinozaki Vanamaura Y., Yu G., Yu S., Shinozaki Vanamaura Y., Yu G., Yu S., Shinozaki Vanamaura Y., Yu G., Yu S., Shinozaki Vanamaura Y., Yu G., Yu S., Shinozaki Vanamaura Y., Yu G., Yu S., Shinozaki Vanamaura Y., Yu G., Yu S., Shinozaki Vanamaura Y., Yu G., Yu S., Shinozaki Vanamaura Y., Yu G., Yu S., Shinozaki Vanamaura Y., Yu G., Yu S., Shinozaki Vanamaura Y., Yu G., Yu S., Shinozaki Vanamaura Y., Yu G., Yu S., Shinozaki Vanamaura Y., Yu G., Yu S., Shinozaki Vanamaura Y., Yu G., Yu S., Shinozaki Vanamaura Y., Yu G., Yu S., Shinozaki Vanamaura Y., Yu G., Yu S., Shinozaki Vanamaura Y., Yu G., Yu S., Shinozaki Vanamaura Y., Yu G., Yu S., Shinozaki Vanamaura Y., Yu G., Yu S., Yu S., Shinozaki Vanamaura Y., Yu G., Yu S., Shinozaki Vanamaura Y., Yu G., Yu S., Yu S., Shinozaki Vanamaura Y., Yu G., Yu S., Shinozaki Vanamaura Y., Yu G., Yu S., Shinozaki Vanamaura Y., Yu G., Yu S., Shinozaki Vanamaura Y., Yu G., Yu S., Shinozaki Vanamaura Y., Yu G., Yu S., Shinozaki Vanamaura Y., Yu G., Yu S., Shinozaki Vanamaura Y., Yu G., Yu S., Shinozaki Vanamaura Y., Yu G., Yu S., Shinozaki Vanamaura Y., Yu G., Yu S., Shinozaki Vanamaura Y., Yu G., Yu S., Shinozaki Vanamaura Y., Yu G., Yu S., Shinozaki Vanamaura Y., Yu G., Yu S., Shinozaki Vanamaura Y., Yu G., Yu S., Shinozaki Vanamaura Y., Yu G., Yu S., Shinozaki Van
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Sperling P., Zaehringer U., Heinz B.;
"A sphingolipid desaturase from higher
cytochrome b5 fusion protein.";
J. Biol. Chem. 273:28590-28596(1998).
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01-MAY-1999 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
02-MAR-2003 (TrEMBLrel. 23, Last annotation update)
02-MAR-2003 (TrEMBLrel. 23, Last annotation update)
03-MAR-2003 (TrEMBLrel. 10, Last annotation update)
03-MAR-2003 (TrEMBLrel. 10, Last annotation update)
03-MAR-2003 (TrEMBLrel. 10, Last sequence update)
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Feldmann K.,
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Mayer K.F.X., Quetier F., Salanoubat M.;
Submitted (NOV-1999) to the EMBL/GenBank
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Yamamura Y., Yu G., Yu S., Ecker J.R.;
"Arabidopsis cDNA clones.";
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Pred. No. 1.2e-
14; Mismatches
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edons; core eudicots; Rosidae;
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SEQUENCE
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Pfam; PF00173; heme_1; 1.
ProDom; PD000612; Cyt_B5; 1.
ProDom; PD001081; FA_desat_fam;
PROSITE; PS50255; CYTOCHROME_B5_
Heme.
SEQUENCE
                   ProDom; PD000612; Cyt B5; 1.
ProDom; PD001081; FA desat fam; 1.
PROSITE; PS50255; CYTOCHROME B5_2; 1.
                                                                                                            front-end desaturases involved in eicosapentaenoic acid biosynthesis.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIWILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
EMBL; AY082393; AAL92563.1; -.
                                                                                                                                                                                                                                                Phaeodactylum tricornutum.
Eukaryota; stramenopiles; Bacillariophyta; Bacillariophyceae;
Bacillariophycidae; Naviculales; Phaeodactylaceae; Phaeodacty
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                                                          InterPro; IPR001199; Cyt B5.
InterPro; IPR005804; FA desat_fam.
Pfam; PF00487; FA desaturase; 1.
Pfam; PF00173; heme_1; 1.
                                                                                                                                                            Domergue F., Lerchl J., Zaehringer U., Heinz E.; "Cloning and functional characterization of Phaeodactylum front-end desaturases involved in eicosapentaenoic acid
                                                                                                                                                                                                                                                                                                                01-JUN-2002
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                         Q8RXB0;
01-JUN-2002
                                                                                                                                                                                                 STRAIN-UTEX 646;
                                                                                                                                                                                                             SEQUENCE FROM N.A.
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(TrEMBLrel. 21, Last sequence up (TrEMBLrel. 22, Last annotation ty acid desaturase D6.
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ME:
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hong H., Dalta N., Mackenzie S.L., Qiu X.;
"A delta-6 fatty acid desaturase from Pythium
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ
-I- SIMILARITY: BELONGS TO THE CYTOCHROME B5 E
EMBL; AP419296; AAL13310.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001199; Cyt B5.
InterPro; IPR005804; FA_desat_fam.
Pfam; PF00487; FA_desaturase; 1.
Pfam; PF00173; heme_1; 1.
ProDom; PD000612; Cyt B5; 1.
ProDom; PD001081; FA_desat_fam; 2.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-OCT-2002 (TrEMBLrel. 22, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProDom; PD001081; FA_desat_fam; 2.
PROSITE; PS50255; CYTOCHROME_B5_2; 1.
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Result
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6: /cgn2_6/ptodata/2/iaa/backfilesl.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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RESULT 1 US-08-934-254-27 ; Sequence 27, A ; Patent No. 635 ; GENERAL INFOR ; APPLICANT:		45	44	43							36	35							
SULT 1  -08-934-254-27  Sequence 27, Application US/08934254  Patent No. 6355861  GENERAL INFORMATION: APPLICANT: Thomas, Terry L. APPLICANT: Thomas, Terry L.		119.5	119.5	119.5	121.5	121.5	126.5	126.5	127.5	127.5	128	128	128.5	128.5	128.5	128.5	128.5	128.5	129
pplications AATION: Thomas,				20.2	•			•	21.5	•	21.6	21.6	•	21.7	21.7	21.7	21.7	21.7	21.8
on US,		457	457	457	179	179	104	104	142	142	133	133	465	465	432	432	347	347	134
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IN US/08934254  TERFY L.  DEPOSITION OF GRAMA LINGUERIC ACID BY A	ALIGNMENTS	US-08-834-033A-2	US-08-833-610-4	US-08-834-655-2	US-09-227-613-21	US-09-439-261-22	US-09-178-881-5	US-08-801-972-5	US-09-178-881-3	US-08-801-972-3	US-09-227-613-22	US-09-439-261-23	US-09-227-613-38	US-09-439-261-40	US-09-227-613-9	US-09-439-261-9	US-09-227-613-40	US-09-439-261-42	US-09-041-517-1
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-934-254-27
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,254
FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 8383ZXXWVU
TELEFAX: (516) 742-4343
TELEFAX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 27:
CEDIUM OF SEG ID NO: 27:
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                                                                                                                            Query Match 44.9%; Score 266; DB 4; Length 452; Best Local Similarity 49.5%; Pred. No. 4.1e-24; Matches 52; Conservative 18; Mismatches 33; Indels
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CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, S
STREET: 400 Garden C
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STATE: New York
COUNTRY: United St
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SVRPLLRRFFVG--RLTDYTVPPASADFRRLLAQLSSAGLFERVG 114
                                        KYITAEDLRRHNKSGDLWISIQGKVYDCSRWAAEHPGGEVPLLSLAGQDVTDAFIAYHPG 66
                                                                   RMISTKELQAHAAADDLWISISGDVYDVTPWLRHHPGGEVPLITLAGQDATDAFWAYHPP
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400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     United States
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; TOPOLOGY: 11; MOLECULE TYPE: US-08-366-779-5
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                                                                                                                               Sequence 5 Patent No.
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Best Local
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                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/366,779
FILING DATE: 30-DEC-1994
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy COMPUTER: IBM PC COM
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ADDRESSEE: Scully, S
                                                             APPLICANT:
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                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Presser, Leopold REGISTRATION NUMBER: 19, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: New York
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                                                                                                                                   5, Application US/08789936
5. 5789220
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                                                      Thomas, Terry L. Reddy, Avutu S. Nuccio, Michael
                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Reddy, Avutu S.
Nuccio, Michael
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Freyssinet, Georges L.
Numberg, Andrew N.
MENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
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                                                                                             Terry L.
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46.8%; Pred. No. 3.8e-23;
tive 21; Mismatches 35; Indels
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Best Local S
                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/366,77
FILING DATE: 30-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 8383
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 230 901 SANS UR INFORMATION FOR SEQ ID NO: 5:
              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                          CITY: Garden City
                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (516) 742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                       COUNTRY: United States
                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Garden City
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 AFHPASTWKNLDKFFTGYYLKDYSVSEVSKDYRKLVFEFSKMGLYDKKG 110
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                                                                                                                      11530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                            New York
                                                                                                                                                                                           B: Scully, Scott, Murphy & Presser
400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B: Scully, Scott, Murphy & Presser
                                                                                                                                                                                                                                                                                                       Thomas, Terry L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       448 amino acids
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                                                                                                                                                                                                                                                     DELTA
: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43.6%; Score 258; DB 1;
46.8%; Pred. No. 3.8e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DELTA 6-DESATURASE
                                                                                                                                                                                                                                                                      PRODUCTION OF GAMMA LINOLENIC ACID BY DELTA 6-DESATURASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25
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US/08/934,254
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ATTORNEY/AGENT INFORMATION:

Presser,

Leopold

19,827

8383ZYXWVU

CLASSIFICATION: FILING DATE:

REGISTRATION NUMBER:

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RESULT 5
US-08-833-610-5
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
TYPE: amino acid
TOPOLOGY: linear
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                                                                       TELEX: N/A
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,610
FILING DATE: 11-APR-1997
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: RAE-VENTER, BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.123.00US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)328-4400
TELEPAX: (650)328-4477
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TELECOMMUNICATION INFORMATION:
                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: RAE-VENTER LAW GROUP, P.C. STREET: 260 SHERIDAN AVE, P.O. BOX 60039 CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (516) 742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 43.6%; Score 258; DB 4; Length 448;
Local Similarity 46.8%; Pred. No. 3.8e-23;
STRANDEDNESS:
                                     LENGTH:
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5, 5972664
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HUANG, YUNG-SHENG
THURMOND, JENNIFER
CHAUDHARY, SUNITA
                                  446 amino acids
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                                                                                                                                                                                                     US-08-834-033A-15
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Patent No.
                                                                                                                             Query Match
Best Local S
Matches 50
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amin
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                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
STREET: 2001 FERRY BUILDING
CITY: SAN FRANCISCO
                                                                                                                                                                                                                     TOPOLOGY: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                    THE TEPHONE: (415) 433-8716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/834,033A FILING DATE: 11-APR-1997 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/N SOFTWARE: WORDPERFECT 5.1
                                                                                                                                                                                                                                                                          TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 AFHPASTWKNIDKFFTGYYLKDÝSVSEVSKVYRKLVFEFSKMGLYDKKG 110
                                                                                                                           ch 42.1%; Score 249; DB 3; I Similarity 45.9%; Pred. No. 4.7e-22; 50; Conservative 21; Mismatches 36;
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AYHPPSVRPLLRRFFVG-RLTDYTVPPASADFRRLLAQLSSAGLFERVG 114
                                                     AQIKKYITSDELKNHDKPGDLWISIQGKAYDVSDWVKDHPGGSFPLKSLAGQEVTDAFV
                                                                                         AADV-RMISTKELQAHAAADDLWISISGDVYDVTPWLRHHPGGEVPLITLAGQDATDAFM 66
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                                                                                                                                                                                                                                                                                             446 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                      peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                          CGAB-300.USA
                                                                                                                                                               DB 3; Length 446;
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                                                                                                                               Indels
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                                                                                                                                                                          RESULT 8
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                                                                                                                       Sequence 5, Application US/08834033A Patent No. 6075183
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30
                                        APPLICANT:
                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: (650)328-4400
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/833,610 FILING DATE: 11-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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                                                                                                                                                                                                                        72 IMKKYYVGTLVSNELP
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                                                                                                                                                                                                                                                                                        12 EELAAHNTKDDLLLAIRGRVYDVTKFLSRHPGGVDTLLLGAGRDVTPVFEMYHAFGAADA 71
                                                                                                                                                                                                                                                                                                                        17 KELQAHAAADDLWISISGDVYDVTPWLRHHPGGEVPLITLAGQDATDAFMAYHP-PSVRP 75
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          INVENTION:
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260 SHERIDAN AVE, P.O. BOX 60039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        446 amino acids
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                                                                       MUKERJI, PRADIP
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MURKERJI, PRADIP
HUANG, YUNG-SHENG
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                       THURMOND, JENNIFER CHAUDHARY, SUNITA
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linear
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                                                          YUNG-SHENG
                                                                                                                                                                                                                                                                                                                                                       25.1%; Score 148.5; DB 40.8%; Pred. No. 8e-10; tive 14; Mismatches
Y, SUNITA
METHODS AND COMPOSITIONS FOR SYNTHESIS
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Best Local S
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                                                                                           SOFTWARE:
SEQ ID NO 23
                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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Query Match
                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/145,828A CURRENT FILING DATE: 1998-09-02
                                                                                                                                                                                       APPLICANT: Parker-B
                                                            LENGTH: 44
TYPE: PRT
                                                                                                                            NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/834
PILING DATE: 11-APR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKST NUMBER: CGAL
                                             ORGANISM: Mortierela alpina
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MOLECULE TYPE:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (415) 433-8716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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Leonard, Amanda E. Y.
                                                                                                                                                                                         Parker-Barnes, Jennifer M.
/ENTION: THE ELONGASE GENE AND USES THEREOF
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Kirchner, Stephen J.
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2001 FERRY BUILDING
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25.1%;
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Pred. No. 8e-10;
4; Mismatches
 Score 148.5;
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 DB 4;
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 Length 446;
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US-09-330-235-12
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                                                                                                  SOFTWARE: 1
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Patent No. 6459018
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NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.0
                                                                                                                                 PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1999-0 NUMBER OF SEQ ID NOS: 60
                                                                                                                                                                                                              FILE REFERENCE: 6295.US.P2
CURRENT APPLICATION NUMBER: US/09/439,261
CURRENT FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: US 08/833,610
PRIOR FILING DATE: 1997-04-11
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TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS
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stent No. 6428990
FEATURE:
NAME/KEY: VARIANT
LOCATION: (447)...(447)
                                                   TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                   LENGTH: 447
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TLE OF INVENTION: HUMAN DESATURASE GENE
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Local Similarity 40.8%;
                                                                                                                                                                              FILING DATE: 1997-0
APPLICATION NUMBER:
FILING DATE: 1998-0
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                                                                                                                   FastSEQ for Windows Version 4.0
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Leonard, Amanda E.
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4; Mismatches
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     ; ORGANISM: Candida tropicalis
US-09-912-161-2
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                                                                                                                                                                                                                                                                                                US-09-912-161-2
                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: David, Craft L.
APPLICANT: Madduri, Krishna
APPLICANT: Loper, John C.
TITLE OF INVENTION: CYTOCHROME b5
TITLE OF INVENTION: THERETO
                                                                   SOFTWARE: PatentIn version 3.1 SEQ ID NO 2
                                                                                                                                                                                                                                                           Sequence 2, Application US/09912161 Patent No. 6503734
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SEQ ID NO 10
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                                                                                                  NUMBER OF SEQ ID NOS: 45
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                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo Sapien FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                  LENGTH: 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 447
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                                                                                                                                                                                                                                                                                                                                                              IMKKYYVGTLVSNELP 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/09227613A
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; OTHER INFORMATION: Xaa = Unknown or other at position 447 US-09-439-261-46
 DB 4;
Length
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17 KELQAHAAADDLWISISGDVYDVTPWLRHHPGGEVPLITLAGQDATDAFMAYHP-PSVRP
                                     Score 148.5;
Pred. No. 8e-
                         Mismatches
                                     8e-10;
                         30;
                         Indels
                         ۲
                         Gaps
 75
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12 EELAAHNTKODLLLAIRGRVYDVTKFLSRHPGGVDTLLLGAGRDVTPVFEMYHAFGAADA 71

APPLICANT: MUKERJI, Pradip
APPLICANT: LEONARD, Amanda E.
APPLICANT: HUNNG, Yung-Sheng
TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
FILE REFERENCE: 6295.US.P1

CURRENT FILING DATE: 1999-01-08
PRIOR APPLICATION NUMBER: US/09/227,613A
CURRENT FILING DATE: 1999-01-08
PRIOR APPLICATION NUMBER: 08/833,610
PRIOR FILING DATE: 1997-04-11 FastSEQ for Windows Version

17 KELQAHAAADDLWISISGDVYDVTPWLRHHPGGEVPLITLAGQDATDAFMAYHP-PSVRP 75 Score 148.5; DB Pred. No. 8e-10; Mismatches DB 4; 30; Length 447; Indels 1: Gaps 71

12 EELAAHNTKODLLLAIRGRVYDVTKFLSRHPGGVDTLLLGAGRDVTPVFEMYHAFGAADA

FILE REFERENCE: M6368 (1010-35)
CURRENT APPLICATION NUMBER: US/09/912,161
CURRENT FILING DATE: 2001-07-24 GENE AND PROTEIN OF CANDIDA TROPICALIS AND METHODS !

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US-08-801-972-1
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Best Local Similarity
Matches 25; Conserv
                                                                                                                                          Matches
                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/801,972
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals,
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                            IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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FITLE OF INVENTION:
FITLE OF INVENTION:
                                                                                                                                                                                                                             LIBRARY: Consensus
CLONE: 2264814
                                                                                                                                                                                                                                                                                                STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                       ENGTH:
90 MLKQYYIGDIHPSDLKPES 108
                                76 LLRRFFVGRLTDYTVPPAS 94
                                                                     30 EEVAKRNSLKELWLVIHGRVYDVTRFLNEHPGGEEVLLEQAGVDASESFEDVGHSSDARE 89
                                                                                              17 KELQAHAAADDLWISISGDVYDVTPWLRHHPGGEVPLITLAGQDATDAFM-AYHPPSVRP 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 KELQAHAAADDLWISISGDVYDVTPWLRHHPGGEVPLITLAGQDATDAFMAY-HPPSVRP 75
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VENTION: A NOVEL HUMAN CYTOCHROME
                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                              linear
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                                                                                                                                                        23.1%;
                                                                                                                                      18;
                                                                                                                                 Score 136.5; DB 2;
Pred. No. 5.7e-09;
"ismatches 32;
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                                                                                                                                      Indels
                                                                                                                                                                       Length 155;
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RESULT 15

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Search completed: January Job time : 4.16063 secs
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                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Consensus
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CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM:
SOFTWARE: FastSEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 3174 FOR CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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                                                                                                   76 LLRRFFVGRLTDYTVPPAS 94
                                                                                                                                   30 EEVAKRNSLKELWLVIHGRVYDVTRFLNEHPGGEEVLLEQAGVDASESFEDVGHSSDARE 89
                                                                                                                                                                  17 КЕLQAHAAADDLWISISGDVYDVTPWLRHHPGGEVPLITLAGQDATDAFM-АҮНРРSVRP
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                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                    23.1%; Score 136.5; DB 3; 35.4%; Pred. No. 5.7e-09; tive 18; Mismatches 32;
              1, 2004, 06:38:15
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Minimum DB
Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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                                                       274.5
258
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193.5
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Match
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592
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          \begin{smallmatrix} 2 & 2 & 3 & 4 & 3 \\ 2 & 2 & 3 & 2 & 7 \\ 2 & 2 & 3 & 6 \\ 2 & 2 & 3 & 7 \\ 2 & 2 & 3 & 6 \\ 2 & 2 & 7 & 7 \\ 2 & 2 & 3 & 6 \\ 2 & 2 & 7 & 7 \\ 2 & 2 & 7 & 7 \\ 2 & 2 & 7 & 7 \\ 2 & 3 & 6 \\ 2 & 2 & 7 & 7 \\ 2 & 2 & 7 & 7 \\ 2 & 3 & 6 \\ 2 & 2 & 7 & 7 \\ 2 & 3 & 6 \\ 2 & 2 & 7 & 7 \\ 2 & 2 & 7 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 \\ 2 & 3 & 2 & 7 
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: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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US-10-340-779A-11

US-10-029-756-27

US-10-340-779A-13

US-10-029-756-5

US-09-967-477B-8

US-09-769-863-14

US-10-054-534B-14

US-10-120-637A-37

US-09-769-863-20

US-10-54-534B-20

US-10-54-534B-20

US-10-54-534B-20

US-10-54-534B-20

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US-10-967-477B-6

US-09-967-477B-2

US-09-967-477B-2
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## ALIGNMENTS

RESULT 1 US-10-340-779A-11

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Sequence 11, Application US/1034079A
Publication No. US20030152983A1
GENERAL INFORMATION:
APPLICANT: Nothaelson, Louise
APPLICANT: Nothaelson, Louise
APPLICANT: Scobart, Keith
TITLE OF INVENTION: Desaturase
FILE REFREENCE: 005407.0004
CURRENT PAPLICATION NUMBER: US/10/340,779A
CURRENT PAPLICATION NUMBER: US 09/582,034
PRIOR APPLICATION NUMBER: US 09/582,034
PRIOR PILING DATE: 1998-12-23
FRIOR PILING DATE: 1998-12-23
FRIOR PILING DATE: 1998-12-23
INUMBER OF SEQ ID NOS: 23
SOTTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 458
TYPE: PTT
ORGANISM: Helianthus annus
US-10-340-779A-11

Query Match
Best Local Similarity 50.0%; Pred. No. 3.2e-24;
Matches 52; Conservative 19; Mismatches 32; Indels 1; Gaps
12 RMISTKELOAHAADDLWISISGDYVDYDFWLRHHPGGEPLITLAGGDATDAFWAYHPP 71
Db 17 KYITSKELKGHNNPNDLWISISGDYVDYDFWLRHHPGGEPLITLAGGDATDAFWAYHPP 71
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RESULI 3
US-10-340-779A-13
; Sequence 13, Application US/10340779A
; Publication No. US20030152983A1
; GENERAL INFORMATION:
; APPLICANT: Napler, Johnathan A.
APPLICANT: Michaelson, Louise
APPLICANT: Stobart, Keith
; TITLE OF INVENTION: Desaturase
; FILE REFERENCE: 005407.00004
; CURRENT APPLICATION NUMBER: US/10/340,779A
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US-10-029-756-27
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; SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-10-029-756-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 44.9%; Score 266; DB 14; Best Local Similarity 49.5%; Pred. No. 3.2e-23; Matches 52; Conservative 18; Mismatches 33
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Publication No. US20020108147A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 8383ZYXWVU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/934,254
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/10/029,756
PILING DATE: 21-Dec-2001
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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TITLE OF INVENTION: PRODUCTION OF GAMMA LINGLENIC ACID BY A
                                                                                                                                                                                                                                                                                                                                                                               72 SVRPLLRRFFVG--RLTDYTVPPASADFRRLLAQLSSAGLFERVG 114
                                                                                                                                                                                                                                                                                                                                         67 TAWRHLDPLFTGYYYLKDFEVSEISKDYRRLLNEMSRSGIFEKKG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 RMISTKELQAHAAADDLWISISGDVYDVTPWLRHHPGGEVPLITLAGQDATDAFMAYHPP 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 452 amino acids
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US-10-029-756-5
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Matches
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Publication No. US20020108147A1
GENERAL INFORMATION:
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SEQ ID NO 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE:
                                                                                                                                                      TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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FILING DATE: 1998-12-23
APPLICATION NUMBER: UK 9814034.6
FILING DATE: 1998-06-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/029,756
                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 83
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/934,254
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Thomas, Terry L.

APPLICANT: Thomas, Terry L.

TITLE OF INVENTION: PRODUCTION OF GAMMA LINGLENIC ACID BY
DELTA 6-DESATURASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: UK 9727256.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS: ADDRESSEE: Scully,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FastSEQ for Windows Version 4.0
                                                                                                         TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 21-Dec-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                             TELEPHONE: (516) 742-4343
                                                                                                                                                                                                                                                                                                                                           NAME: Presser, Leopold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: New Yor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Garden City
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                                            DESCRIPTION: SEQ ID NO:
                                                                 TYPE: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EE: Scully, Scott, Murphy & Presser
400 Garden City Plaza
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Version #1.25

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PRIOR APPLICATION NUMBER: US 09/582,034
62 AFHPASTWKNLDKFFTGYYLKDYSVSEVSKDYRKLVFEFSKMGLYDKKG 110
                                              67 AYHPPSVRPLLRRFFVG-RLTDYTVPPASADFRRLLAQLSSAGLFERVG 114
                                                                                               2 AAQIKKYITSDELKNHDKPGDLWISIQGKAYDVSDWVKDHPGGSFPLKSLAGQEVTDAFV 61
                                                                                                                                             8 AADV-RMISTKELQAHAAADDLWISISGDVYDVTPWLRHHPGGEVPLITLAGQDATDAFM
                                                                                                                                                                                                                  43.6%; Score 258; DB 12;
46.8%; Pred. No. 2.9e-22;
                                                                                                                                                                                              ed. No. 2.9e
Mismatches
                                                                                                                                                                                                35;
                                                                                                                                                                                                                                            Length 448;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
                                                                           SOFTWARE: FastSEQ for
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                           Sequence 14, Application US/09769863
Publication No. US20030157144A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local Similarity
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Patent No. US20020156254A1
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Best Local Similarity
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LENGTH: 453
TYPE: PRT
ORGANISM: Saprolegnia diclina
-09-769-863-14
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PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 60/297,562
PRIOR FILING DATE: 2001-06-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: BNZ-001
CURRENT APPLICATION NUMBER: US/09/967,477B
CURRENT FILING DATE: 2002-04-16
                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/769,863
CURRENT FILING DATE: 2001-01-25
                                                                                                                                                                                              APPLICANT: Thurmond, Jennifer
APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: DESATURASE GENES AND USES
                                                                                                                                                                                                                                                                                                                   APPLICANT: Abbott Laboratories
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Haiping Hong
TITLE OF INVENTION: FAD4, FAD5, FAD5-2, AND FAD6, NOVEL
TITLE OF INVENTION: FATTY ACID DESATURASE FAMILY MEMBERS AND USES THEREOF
                                                                                                                                                                             FILE REFERENCE: 6763.US.O1
                                                                                                                                                                                                                                                                                                    APPLICANT:
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APPLICANT: Haiping
                                                                                                                NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RLVSWKEIREHATPATAWIVIHHKVYDISKW-DSHPGGSV-MLTQAGEDATDAFAVFHPS 67
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                                                                                                                                                                                                                                                                           Huang,
                                                                                                                                                                                                                                                             Das,
                                                                                                                                                                                                                                                                                                Mukerji, Pradip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                           Tapas
                                                                                                                                                                                                                                                                         Yung-Sheng
                                                                                              Windows Version 4.0
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SOPTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 14 LENGTH: 453
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Best Local Similarity
Matches 39; Conserv
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Best Local Similarity
Matches 39; Conserv
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Publication No.
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                                                                                                                                                                                                                                                     APPLICANT: Thurmond, Jennifer
APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
FILE REFERENCE: 6763.US.O1
CURRENT APPLICATION NUMBER: US/10/431,952
CURRENT FILING DATE: 2003-05-08
                                                                                                                          PRIOR APPLICATION NUMBER: US/09/769,863
PRIOR FILING DATE: 2001-01-25
NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Abbott Laboratories
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CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: US 09/769,863
PRIOR FILING DATE: 2001-01-25
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APPLICANT: Thurmond, Jennifer M.
APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: DESATURASE GENES AND USES
FILE REFERENCE: 6763.US.P1
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ORGANISM: Saprolegnia diclina
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Mukerji, France,
Mukerji, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, France, Fra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Das,
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Huang, Yung-Sheng
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34.8%; Pred. No. 1.2e-10;
ative 20; Mismatches 37
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US-10-120-637A-37
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                                                                                                                                                                                                Sequence 20, Application US/09769863 Publication No. US20030157144A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 37, Appropriate Publication No.
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APPLICANT:
                                                  APPLICANT: Thurmond, Jennifer
APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: DESATURASE GENES AND USES
FILE REFERENCE: 6763.US.O1
                                                                                                                                                             APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 6804.US.P1
CURRENT APPLICATION NUMBER: US/10/120,637A
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: US 09/849,199
PRIOR FILING DATE: 2001-05-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: DELTA 4-DESATURASE GENES AND USES
TITLE OF INVENTION: THEREOF
CURRENT APPLICATION NUMBER: US/09/769,863
CURRENT FILING DATE: 2001-01-25
NUMBER OF SEQ ID NOS: 32
                                                                                                                                                APPLICANT:
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ORGANISM: Saprolegnia diclina
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 ISTKELQAHAAADDLWISISGDVYDVTPWLRHHPGGEVPLITLAGQDATDAFMAYHPPSV 73
                                                                                                                                                                                                                                                                                                                                   66 PISDAVLRKYRIGKLAAAGKDEPANDSTYYSWDSDFYKVLRORVVARLEER 116
                                                                                                                                                                                                                                                                                                                                                                                                                                             15 STKELQAHAAADDLWISISGDVYDVTPWLRHHPGGEVPLITLAGQDATDAFMAYHPPSVR 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 LKLLEQYYVGDVDQSTAAVDTSISDEVKKSQSDFIASYRKLRLEVKRLGLYD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   509
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                                                                                                                         Huang, Yung
Das, Tapas
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Thurmond, Jennifer M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/10120637A
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Das, Tapas
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                                                                                                                                          Yung-Sheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.1%; Score 160.5; DB 12; 36.0%; Pred. No. 1.6e-10;
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GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Huang, Yung-Sheng
APPLICANT: Das, Tapas
APPLICANT: Das, Tapas
APPLICANT: Pereira, Suzette L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LENGTH: 470
; TYPE: PRT
; ORGANISM: Saprolegnia diclina
US-10-054-534B-20
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                                                                                                                                                                                                  Sequence 20, Application US/10431952
Publication No. US20030190733A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
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Best Local
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APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: DESATURASE GENES AND USES
FILE REFERENCE: 6763.US.P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/054,534B CURRENT FILING DATE: 2002-01-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: US 09/769,863
PRIOR FILING DATE: 2001-01-25
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                                APPLICANT: Thurmond, Jennifer
APPLICANT: Pereira, Suzette L.
TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
FILE REFERENCE: 6763.US.O1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
CURRENT APPLICATION NUMBER: US/10/431,952
CURRENT FILING DATE: 2003-05-08
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                                                                                                                                                                                                                                                                                                                                                   62 TDAFMAYHPPS--VRPLLRRFFVGRLT
                                                                                                                                                                                                                                                                                                                                                                                       18 PVAGKKA-----FTWQEVAQHNTAASAWIIIRGKVYDVTEWANKHPGGREMVLLHAGREA 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 TDAFMAYHPPS--VRPLLRRFFVGRLT 86
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Mukerji, France
Mukerji, France
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                                                                                                                                                                                                                                                                                                                   TDTFDSYHPFSDKAESILNKYEIGTFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         26.6%; Score 157.5; DB 1 ilarity 39.1%; Pred. No. 3.2e-10; Conservative 12; Mismatches 34
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39.1%;
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Pred. No. 3.2
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APPLICANT: Halping Hong
TITLE OF INVENTION: FAD5, FAD5-2, AND F
TITLE OF INVENTION: FATTY ACID DESATURASE FA
FILE REFERENCE: BNZ-001
CURRENT APPLICATION NUMBER: US/09/967,477B
CURRENT FILING DATE: 2002-04-16
PRIOR APPLICATION NUMBER: 60/236,303
PRIOR FILING DATE: 2000-09-28
PRIOR PRIOR APPLICATION NUMBER: 60/297,562
PRIOR APPLICATION NUMBER: 60/297,562
PRIOR FILING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
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US-09-967-477B-2
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; TYPE: PRT
; ORGANISM: Saprolegnia diclina
US-10-431-952-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-967-477B-6
                                                                              GENERAL INFORMATION:
APPLICANT: Xiao Qiu
APPLICANT: Haipling Hong
TITLE OF INVENTION: FAD4, FAD5,
TITLE OF INVENTION: FATTY ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/09967477B Patent No. US20020156254A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local Similarity
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                                                                                                                                                                                  Sequence 2, Application US/09967477B
Patent No. US20020156254A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US/09/769,863
PRIOR FILING DATE: 2001-01-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FASTSEQ for Windows Version 4.0
CURRENT APPLICATION NUMBER: US/09/967,477B
CURRENT FILING DATE: 2002-04-16
PRIOR APPLICATION NUMBER: 60/236,303
                                                                 FILE REFERENCE: BNZ-001
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APPLICANT: Haiping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Thraustochytrium sp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
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                                                                                                                                                                                                                                                                                                            KILAKYKIGKLVGGYEFPVFKPD 94
                                                                                                                                                                                                                                                                                                                                                                                            QEVAKHNTAKSAWVIIRGEVYDVTEWADKHPGGSELIVLHSGRECTDTFYSYHPFSNRAD 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TDAFMAYHPPS -- VRPLLRRFFVGRLT 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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FATTY ACID DESATURASE FAMILY MEMBERS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 153.5; DB 10; Pred. No. 9.4e-10;
                                                                                FAD5-2, AND FAD6, DESATURASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                   MEMBERS AND USES THEREOF
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GENERAL INFORMATION:

APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
ITITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10 (52052) B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/03-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2003-02-21
VIMBER OF SEQ ID NOS: 47374
SEQ ID NO 5090
LENGTH: 141
TYPE: PRT
ORGANISM: Caenorhabditis elegans
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Search completed: January Job time: 22.7174 secs
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PRIOR APPLICATION NUMBER: 60/297,562
PRIOR FILING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 2
LENGTH: 519
                                                                                                                                                                                                                                                     Matches
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Best Local Similarity
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Best Local Similarity
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LOCATION: 462
OTHER INFORMATION: Xaa = Gly
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                                                                                    62
                                                                                                                         66 M-AYHPPSVRPLLRRFFVGRLTDYTVP 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37; Conservative
                                                                                                                                                                                                            9 ADVRMISTKELQAH---AAADDLWISISGDVYDVTPWLRHHPGGEVPLITLAGQDATDAF 65
                                                                                                                                                                                                                                                     34; Conservative
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                                                                                    LDVGHSKDAIEMANEYLIGQLPESDVP
                                                                                                                                                                     SELRVISLDEVSKHNWEDADQSCWIVISGKVYDVTKFLNEHPGGEEVITQLAGKDATVGF
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37.8%;
                                                                                                                                                                                                                                                                       25.5%; Score 151; DB 12; 39.1%; Pred. No. 4.2e-10;
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; Pred. No. 1.9e-09;
21; Mismatches 37;
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                                                                                    88
                                                                                                                                                                                                                                                                                          Length 141;
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